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CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: PCT/US00/28066
PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: 60/159,542
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/165,914
PRIOR APPLICATION NUMBER: 60/169,914
PRIOR FILING DATE: 1999-11-17
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GENERAL INFORMATION:
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	100 367	81 TyrGlnIleAlaSerGlyLeuAlaTyrLeuH1sLysLysAsnIleIlePheCysAspLeu 	D 64
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Sequence 14, Application PC/TUSO101435
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 21 human secreted protei
FILE REFERENCE: PS726PCT
CURRENT APPLICATION NUMBER: PCT/USO1/01435
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/226,282
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 145
NUMBER OF SEQ ID NOS: 145
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SEQ ID NO 14
LENGTH: 3564
TYPE: DNA
ORGANISM: Homo:
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                                    ProValArgProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProLysVal
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; NAME/KEY: SIMILAR
; LOCATION: (136)...(1515)
; OTHER INFORMATION: 29% hc; OTHER INFORMATION: to pro
; OTHER INFORMATION: number
PCT-US01-08631-8042
                                                 Best Local
Query Match
DB:
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Pred. No.:
Score:
                                                                                                                                                                                   PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 8042
LENGTH: 2652
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                                                            APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC
FILE REFERENCE: 21272-049
                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                  ORGANISM: Homo sapiens FEATURE:
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                                  (1-728)
                                                                                                                        29% homologous to Caenorhabditis elegans contains similarity to protein kinases (Pfam:pkinase.hmm, score: 149.36),accession number AF098504,Smith-Waterman Score-427.
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LENGTH: 70
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GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS
FILE REFERENCE: SCH-1811
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CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
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                                  GAGGAGGTCGTCTGGTGCCTGGATGACAAGGCCCAACTCCTTGGTGATGTACCACTCCACC
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420 5344	1 GlnAsnProTyrProValLysAlaMetGluValValAsnSerGlySerGluValTrpTyr 	y 40 b 528	H 4
400 5284	1 TyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaArg	у 38 b 522	9 4
380 5224	1 AlaAspG	y 36	7
360 5164	CysPheLeuAlaValProValIleLysLysAsnSerTyrL          AATTCCTACC	y 34 b 513	₽ ५
5137	7	US.	_
340	1 LeuLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThrProAlaValVal	у 32	~
320 <sub>.</sub> 5137	1 LeuGlnValGlnArgSerLeuTrpThrAlaThrGluAspGlnLysIleTyrIleTyrThr 	у 30 b 510	ש ע
300 5101	1 GluLysGlyLeuMetGluValGlnArgMetCysCysProGlyMetLysValSerCysGln 	28 504	₽ ゼ
280 5041	1 TyrThrValValPheTrpAspGlyLysGluGluSerArgAsnTyrThrValValAsnThr 	y 26	$\sigma \sim$
260 4981	LaPhePheSerSerGlnGlyGlnGlu 	24 492	σ 🗸
240 4921	1 GluLysArgProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThr 	7 22 5 486	₽~
220 4861	MetMetGluCysTrpAspThrLysPro                  	y 20	σ ∨
200 4801	1 HisGinLeuGinIleAlaLysLysLeuSerLysGlyIleArgProValLeuGlyGlnPro	18 474	σ ~
180 4741	1 PheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeuGlyHis 	_	o ~
160 4681	1 ProGlyTyrGlnAlaProGluIleArgProArgIleValTyrAspGluLysValAspMet	14 462	o ~
140 4621	SerArgGlnSerPheHisGluGlyAlaLeuGlyValGluGlyThr 	, 12 5 456	U ~
120 4561	1 LysSerAspAsnIleLeuValTrpSerLeuAspValLysGluHisIleAsnIleLysLeu	7 10 5 450	U ~
4501	2 TACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTG	444	U

461 GluGluValValTrpCysLauAspAspLysAlaAssnserLeuValMetTyrHisSerThr 462 [	•	PE: DNA PE: DNA IGANISM: Homo sapiens 132-382-7	TYI ORC	US.
461 GludiuvalvalTrpCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480 462 GAGGAGTGCTGGGTGCTGGGTGATGAAGGCCAAGCCAAG		PILING DATE: 2002-04-26 OF SEQ ID NOS: 26 (E: PatentIn Ver. 2.1	SON	
461 GLUGIUWALVAITEPCYSLAUASPASPLYSALAKSNSSELEUWALMETTYFHISSETTHE 480 5465 GAGGAGCTGCTCGTCCTGCTCCTGCTCANAGCCAAAAGCTCAAAAGCTAAAACCACCAAAAGCTAAAAGCTAAAAACCACCAAAAGCTAAAAACCACCAAAAGCTAAAAACCACCACAAACCCCAAAAAAAA		NT: WEISS, BERTRAM INT: WEISS, BERTRAM F INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND S FERENCE: SCH-1811 APPLICATION NUMBER: US/10/132,382	APPL. TITLI FILE CURRI	
461 GluGludvalValTrpCysLeuAspAspLysAlaAssnSerLeuValMetTyrHisSerThr 480		382-7 ?7, Application US/1013238	SULT -10-1	· · · G &
461 GluGluvalvalTrpCysleuAspAspLysAlaAsnSerLeuvalMetTyrHisSerThr 480		GAGGCTTGCACTCGCAAGAGAAGG 626	624	₽ 5
461 GLUGLUVALVELTEPCYSLEWASPASPLYSALAASISETLEWVALMENTYPHISSETH: 480	4	GCTGGGGCGCCAGGGAGTTCGACATTTCTACCAGTCCTACGAGGAGCTGGGCCGGGT	618	) <u>p</u>
461 GluGluvalvalTrpcysLeuAspAspLysAlaAsnSerteuValMetTyrHsSerThr 480	20	GlyTrpGlyAlaArgGluPheAspIlePheTyrGlnSerTyrGluGluLeuGlyArgLe	70	
461 GlugluvalvalTrpCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480	18	GACACTGTTGTGCACCTTTGAAAATGAAAACACAGAGTGGTGCCTGGCCGTCTGGAG	Ø	₽
461 GlugluvalvalTrpCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480	0	AspThrValValCysThrPheGluAsnGluAsnThrGluTrpCysLeuAlaValTrpAr	68	S
461 GluGluValValTrpCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480	12	LeuLysalaargGluLeuThrProHisGlyValLeuValAspAlaAlaValValAlaLy	606	р <b>ў</b>
461 GluGluValTypCysLeuAspAspLysAlaAsnSerLeuValMetTyrH1sSerThr 480	6064	VALILEVALITEGAL PERSONAL PROPERTY OF THE PROPE	60	p 5
461 GluGluValValTrpCySLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480	8 0	CASSICUTION TO THE CONTRACT CONTRACT CASCASSICATION OF THE CONTRACT CASCASSICATION OF THE CONTRACT CASCASSICATION OF THE CONTRACT CASCASSICATION OF THE CA		? ;
461 GluGluValValTrpCySLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480		GlnAlaValLysIleLeuAlaValArgAspLeuIleTrpValProArgArgGlyGlyAs	5 6 8	2 2
461 GluGluValValTrpCySLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480	9 2	SeraspargSerGluH1saspLeuThrProMetaspGlyGluThrPheSerGlnH1sLe	588	ρ. δ
461 GluGluValValTrpCySLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480	88	SerValProPheSerThrAspCysGluAspSerAspMetLeuH1SThrProGlyAlaAl 	582 582	다 2
461 GluGluValValTrpCySLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480	i co ci	CCACCCGGCCAGGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTACCAAGTTCTTC	76	p d
461 GluGluValValTrpCySLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480	7 0		70	p 2
461 GluGluValValTrpCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 480	4 1	ProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGl 	64	DF OA
461 GluGluValYalTrpCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 48	64	ProvalargProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProLysVa 	50	da Ao
461 GluGluValValTrpCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 48 	ŭ o	ThTTyrGlnLeuCysAlaArgTyrPheCysGlyValProSerProLeuArgAspMe 	52 4	Db dy
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320	301 LeuGlnValGlnArgSerLeuTrpThrAlaThrGluAspGlnLysIleTyrIleTyrThr	δ
300 5237	281 GluLysGlyLeuMetGluValGlnArgMetCysCysProGlyMetLysValSerCysGln	B 5
280 5177	261 TyrThrValValPheTrpAspGlyLysGluGluSerArgAsnTyrThrValValAsnThr 	p Q
260 5117	241 PheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGlu 	ρ Q
240 5057	221 GluLysArgProLeuAlsLeuSerValValSerGlnMetLysAspProThrPheAlaThr 	g Q
220 4997	201 GluGluValGlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysPro	β δ
200 4937	181 HisGlnLeuGlnIleAlaLysLysLeuSerLysGlyIleArgProValLeuGlyGlnPro	. B . 63
180 4877	161 PheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeuGlyHis 	p 4
160 4817	141 ProGlyTyrGlnAlaProGluIleArgProArgIleValTyrAspGluLysValAspMet 	B &
140 4757	121 SerasptyrglyIleSerargGlnSerPheH1sGluGlyAlaLeuGlyValGluGlyThr 	P Q
120 4697	101 LysSerAspAsnIleLeuValTrpSerLeuAspValLysGluHisIleAsnIleLysLeu 	A d
100 4637	81 TyrGlnIleAlaSerGlyLeuAlaTyrLeuHisLysLysAsnIleIlePheCysAspLeu 	. p. Q
80 4577	61 GluAsnAlaArgAspSerSerPheIleProLeuGlyHisMetLeuThrGlnLysIleAla  \	g Q
60 4517	41 HisproLeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSer	p Qy
40 4457	21 AlaSerMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIle	g Qy
20 4397	1 MetLeuArgHisLeuArgAlaThrAspAlaMetLysAsnPheSerGluPheArgGlnGlu 	g Qy
	IS-09-836-392-21 (1-728) x US-10-132-382-7 (1-7229)	SD
•	Alignment Scores:       5.35e-249       Length:       7229         Icore:       3579.50       Matches:       688         Marches:       0       Conservative:       0         Percent Similarity:       94.51%       Mismatches:       1         Indels:       39         Puery Match:       93.66%       Indels:       39         BB:       40       Gaps:       1	. Pe Pr

680	alLeuValAspAlaAlaValValAlaLys	6201	Qy
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660	ValileValileGlyLeuGluLysAspSerGluAlaGlnArgGlyArgValileAlaVal	641	Qy
6200		6141	Db
640	GlnAlaValLysIleLeuAlaValArgAspLeuIleTrpValProArgArgGlyGlyAsp	621	Qу
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620	SerAspArgSerGluH1sAspLeuThrProMetAspGlyGluThrPheSerGlnH1sLeu	601	. da
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6020	SerValProPheSerThrAspCysGluAspSerAspMetLeuH1sThrProGlyAlaAla	581 5961	da Að
580	ProProArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSer	561	Db
5960		5901	Qy
560	IleLeuIleH1sGlnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSer	541	Qy
5900		5841	Db
540	ProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGln	,521	Qy
5840		5781	Db
520	ProValArgProLeuAspThrGluProProAlaAlaSerH1sThrAlaAsnProLysVal	501	Qy
5780		5721	Db
500	ThrTyrGlnLeuCysAlaArgTyrPheCysGlyValProSerProLeuArgAspMetPhe	481	Qy
5720		5661	Db
480	GluGluValValTrpCysLeuAspAspLysAlaAsnSerLeuValMetTyrH1sSerThr	461	Db Qy
5660		5601	
460	GluProTyrMetAlaProSerMetValThrSerValValCysSerSerGluGlyArgGly	441	Db
5600		5541	Qy
440 5540	rLeuGluIleCysArgArgLeu              CTGGAGATCTGCAGGCGGCTG	421 5481	Оу
420	GlnasnProTyrProValLysAlaMetGluValValAsnSerGlySerGluValTrpTyr	401	Db Oy
5480		5421	
400 5420	TyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaArg	· 381 5361	Db Oy
380	AlaAspGlyLeuValAlaValPheProValValArgGlyThrProLysAspSerCysSer	361	Db
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360 5300	ThrCysPheLeuAlaValProValIleLysLysAsnSerTyrLeuValLeuAlaGlyLeu	341 5274	Db Oy
5273		5273	Ф
340	LeuLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThrProAlaValVal	321	Qy
5273	CTCCAGGTCCAGAGATCCCTGTGGACAGCCACCGAG	5238	말

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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 7307
TYPE: DNA
CRGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS
FILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARDER OF SEQ ID NOS: 26
                                4836
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161 PheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeuGlyHis 180
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                                          ProGlyTyrGlnAlaProGluIleArgProArgIleValTyrAspGluLysValAspMet 160
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Conservative:
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501 ProValArgPro              799 CCCGTGCGGCCC 521 ProGluGlyAsp
81 ThrTyrGlnLe              39 ACCTACCAGCT
461 GluĞluValVal              679 GAGGAGGTCGTC
441 GluProTyrMetA             619 GAGCCCTACATGG
421 SerAsnGlyProGl            559 AGCAATGGGCCGGG
401 GlnAsnProTyr 
381 TyrLeuCysSer           439 TACCTGTGCTCA
361 AlaAspGlyLeuVa 
341 ThrCysPheLeu
351
01 LeuGlnValG1             16 CTCCAGGTCCA
281 GluLysGlyLeum            256 GAGAAGGGCCTCA
261 TyrThrValVal             196 TACACCGTGGTG
241 PheMetTyrGlu 
221 GluLysArgPro
201 GluGluValGln             016 GAGGAAGTGCAG
181 HisGlnLeuGln 

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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 21272-094-061
CURRENT APPLICATION NUMBER: PCT/US02/05109
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 09/810,173
PRIOR ETIING DATE: 2001-03-15
RIOR ETIING DATE: 201-03-15
NUMBER OF SEQ ID NOS: 1052
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Zhou, Ping
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Ghosh, Malabika
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ORGANISM: Homo
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AspSerAspMetLeuH1sThrProGlyAlaAlaSerAspArgSerGluH1sAspLeuThr
                                                                                       ProAlaAlaSerHisThrAlaAsnProLysValProGluGlyAspSerIleAlaAspVal
                                                                                                                                                                                                                                                        CysGlyValProSerProLeuArgAspMetPheProValArgProLeuAspThrGluPro
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                                      TGCGGGGTCCCCAGCCCCTCAGGGACATGTTTCCCGTGCGGCCCTTGGACACGGAACCC
                                                                                                                                                                                                                                                                                                AAGGCCAACTCCTTGGTGATGTACCACTCCACCACCTACCAGCTGTGTGCCCGGTACTTC
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PCT-US02-05109-456; Sequence 456; Application

ENERAL INFORMAT

PPLICANT:

APPLICANT: APPLICANT: APPLICANT:

Wang, Jian-ku Wang, Dunrui

Jian-Rui

Wehrman, Tom

APPLICANT:

APPLICANT:

Chen, Rui-hong

APPLICANT:

Yang,

Ma,

Yamazaki,

APPLICANT

PPLICANT PPLICANT: PPLICANT:

Asundi, Vinod Zhang, Jie Zhao, Qing A.

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APPLICANT: Ghosh, Malabika J.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 804
CURRENT APPLICATION NUMBER: US/09/810,173
CURRENT FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 526
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 456
LENGTH: 2839
                 Percent Similarity:
Best Local Similarity:
Query Match:
DB;
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Score:
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; LOCATION: (872)..(1831)
US-09-810-173-456
US-09-836-392-21
                                                                    Alignment Scores:
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GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
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APPLICANT:
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                                                                                                            LENGTH: 2839
TYPE: DNA
ORGANISM: HOMO:
FEATURE:
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Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
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Wang, Zhiwei
Yamazaki, Victoria
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Asundi, Vinod
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CysG1yVa1ProSerProLeuArgAspMetPheProVa1ArgProLeuAspThrG1uPro
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                                                                       SerGluAlaGlnArgGlyArgValIleAlaValLeuLysAlaArgGluLeuThrProHis
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Query Match: (DB:
                                                                                                                                                                                                                                         ; NAME/KEY: misc_feature
LOCATION: (298)...(811)
OTHER INFORMATION: Simi
OTHER INFORMATION: Run
US-09-471-275-7370
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                                                                                                  US-09-836-392-21 (1-728) x US-09-471-275-7370 (1-995)
                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                EARLIER APPLICATION NUMBER: US 60/125,453
EARLIER FILING DATE: 1999-03-19
EARLIER APPLICATION NUMBER: US 60/126,605
EARLIER FILING DATE: 1999-03-26
EARLIER FILING DATE: 1999-03-26
EARLIER FILING DATE: 1999-05-07
EARLIER FILING DATE: 1999-05-07
EARLIER FILING DATE: 1999-09-21
EARLIER FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: US 09/399,720
EARLIER APPLICATION NUMBER: US 09/399,720
EARLIER APPLICATION NUMBER: US 09/404,284
EARLIER APPLICATION NUMBER: US 09/404,284
EARLIER FILING DATE: 1999-09-21
EARLIER FILING DATE: 1999-09-21
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GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-12-23
EARLIER APPLICATION NUMBER: US 09/235,076
EARLIER FILING DATE: 1999-01-20
EARLIER APPLICATION NUMBER: US 09/234,611
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 10451
SOFTWARE: pt_CT_genes Version
SEQ ID NO 7370
                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: FEATURE:
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ITLE OF INVENTION:
ILE REFERENCE: 782
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ER APPLICATION NUMBER: US 09/240,371

ER FILING DATE: 1999-01-29

ER APPLICATION NUMBER: US 09/277,227

ER FILING DATE: 1999-03-25

ER FILING DATE: 1999-03-18

ER FILING DATE: 1999-03-18

ER FILING DATE: 1999-03-18

ER APPLICATION NUMBER: US 09/293,972

ER APPLICATION NUMBER: US 09/294,861

ER APPLICATION NUMBER: US 09/274,861

ER APPLICATION NUMBER: US 09/274,861
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LysPheSerIleAlaAspGluAspAlaArgGlnAsnProTyrProValLysAlaMetGlu
                                                         ValArgGlyThrProLysAspSerCysSerTyrLeuCysSerH1sThrAlaAsnArgSer
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                                                                                                                9034, Application
Culpepper, Janice
Leiby, Kevin R.
Vasicek, Tom
                                                                  Gearing, David
Shyjan, Andrew
                                         Holtzman, Douglas
Galvin, Katherine
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FILE REFERENCE: 1600.1152-001

CURRENT APPLICATION NUMBER: US/09/637,890

CURRENT FILING DATE: 2000-08-09

PRIOR APPLICATION NUMBER: 60/147,939

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 10217

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 9034

LENGTH: 1912

TYPE: DNA

ORGANISM: Homo sapiens

US-09-637-890-9034
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  GAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGACACTAAGCCA
                                                                                                       TTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCTGCACTGGGCCAC
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SOFTWARE: Fast
SEQ ID NO 9514
FENCTH: 1912
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/644,869
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/151,062
PRIOR FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 9708
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TyrGlnIleAlaSerGlyLeuAlaTyrLeuHisLysLysAsnIleIlePheCysAspLeu
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Holtzman, Douglas A.
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1624.00
99.68%
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PCT-US01-01354+25701
Sequence 25701, Application PC/TUS0101354
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc. et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC004PCT
CURRENT APPLICATION NUMBER: PCT/US01/01354
CURRENT FILING DATE: 2001-03-17
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                                             Percent Similarity:
Best Local Similarity:
                                                                                                                  ; TYPE: DNA ; ORGANISM: Homo sapiens PCT-US01-01354-25701
us-09-836-392-21
                                   Query Match:
                                                                                           Alignment Scores:
                                                                                                                                              NUMBER OF SEQ ID NOS: 42506
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25701
LENGTH: 18286
TYPE: NOTE THE SECOND SEQ ID NO 25701
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(1-728) x PCT-US01-01354-25701 (1-18286)
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Matches:
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ATCCCTGTCTTCCTTCCAGAATTCCTACCTGGTCTTAGCGGGCCTCGCCGGATGGGCTT
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                                                        CATCCAGGGCACGCCCACTGCTCCTGCTCTGGGGACAGAGCAAGGGGAAGCCCCCCTGGCT
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밁	14644	14644 TGAGAAAATTCTCCTCTGCTTTGAAGTCTGTCCCCTCCCCATAACTTAATCCCTTAGCAG 14703	14703	
δ	635		635	
망	14704	14704 AAACTGCATGTCTGTTGCCTCCCCTCCCGCACCTTTCTGCACACCGGCTTCACTCCCCGGA 14763	14763	
δ.	636	ArgArgGlyGly 639	639	
艮	14764	14764 GAGCACGGCTACCGACAAATCGCTTCCCCTTCTGGGTTTTGGTTGCTTAGGCGCGGGTGGA 14823	14823	
Qy	640		659	
밁	14824	14824 GATGTTATCGTCATTGGCCTGGAGAAGGATTCTGGCGCCCAGCGGGGCCGAGTCATTGCC 14883	14883	
Qy	660	660 ValLeuLysAlaArgGluLeuThrProHisGly 670		
밁	14884	14884 GTCTTAAAAAGCCCGAGAGCTGACTCCGCATGGG 14916		
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Search completed: April 15, 2003, 09:44:46 Job time: 2755 secs

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100
THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTPMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-200000000 -USER-US09836392 @CGN_1_1_438_@runat_08042003_090541_23490
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG
-NCPU-1MEQUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPOEXT-0.5 -FGAPOP-6
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                                                                                                                             Alignment Scores:
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APPLICANT: MASCHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094/749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR APPLICATION NUMBER: 50/350,435
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
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SEQ ID NO 50
LENGTH: 3112
TYPE: DNA
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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
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TAMECHIKA, ICHIRO
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Alignment :
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Query Match:
DB:
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US-10-144-771-18122
/ Sequence 18122, Application US/10144771
/ GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
/ TITLE OF INVENTION: HUMAN GENOME DISCOVERY
/ FILE REFERENCE: CL001321
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PRIOR FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIOR APPLICATION NUMBER: 08/103,744
RIOR FILING DATE: 1993-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                581 SerValProPheSerThrAspCysGluAspSerAspMetLeuH1sThrProGlyAlaAla
                                                                         641 VallleVallleGlyLeuGluLysAspSerGluAlaGlnArgGlyArgVallleAlaVal
                                                                                                                                                                                                     601 SerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLeu
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                661 LeuLysAlaArgGluLeuThrProHisGlyValLeuValAspAlaAlaValValAlaLys
                                                                                                                       621 GlnAlaValLysIleLeuAlaValArgAspLeuIleTrpValProArgArgGlyGlyAsp
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APPLICATION NUMBER: 08/104,507
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 TTAAAAGCCCGAGAGCTGACTCCGCATGGGGTGCTGGTGGATGCCGTGGTGGCAAAG
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Percent Similarity:
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; LOCATION: 192, 263
; OTHER INFORMATION:
US-10-349-781-16014
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SEQ ID NO 16014
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NUMBER OF SEQ ID NOS: 61458
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/349,781
CURRENT FILING DATE: 2003-01-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPPLICANT: Stuart, Susan G.; Stuve, Laura L.
APPLICANT: Mullahy, Sara J.; Naughton, Rebec
ITILE OF INVENTION: POLYNUCLEOTIDES OF CELLS
FILE REFERENCE: PD-1028-2 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature OTHER INFORMATION: Inc
                                                                                                                                                394 IleAlaAspGluAspAlaArgGlnAsnProTyrProValLysAlaMetGluValValAsn
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                LeuGluIleCysArgArgLeuGluProTyrMetAlaProSerMetValThrSerValVal 453
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Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 244538
SEQ ID NO 231260
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                            LOCATION: (341)..(341)
OTHER INFORMATION: n 1s
                                                                                      OTHER INFORMATION: n is
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LOCATION: (252)..(252)
OTHER INFORMATION: n is
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URRENT FILING DATE: 2001-07-26 —
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LOCATION: (222). (222)
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.OCATION: (120)..(120)
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 NAME/KEY: misc_feature
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LOCATION: (477)..(477)
OTHER INFORMATION: n 1:
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NAME/KEY: misc_feature
LOCATION: (473)..(473)
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LOCATION: (470)..(470)
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LOCATION: (450)..(450)
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LOCATION: (437)...(437)
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LOCATION: (435)..(435)
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LOCATION: (430)..(430)
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 1242491CB1
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SOFTWARE: PERL Program
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LENGTH: 2693
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APPLICANT: ISON, Craig H.
APPLICANT: ISON, Craig H.
TITLE OF INVENTION: HUMAN KINASES
FILE REFERENCE: PI-0125 PCT
CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
CURRENT FILING DATE: 2002-12,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
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BAUGHN, Mariah R.
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BOROWSKY, Mark L
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GRIFFIN, Jennifer A.
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Dyung Aina M.
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CGTGCACCTGAAGTTGCCAGAGGAAATGTCATTATAACCAACAGGCTGATGTTTATTCA
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                                                                                                     CCTGGTCATCAATACCGAAGATGGGAAAAAGAGACATACCCTAGAAAAGATGACTGATTC
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                           --HisHisGlnLeuGlnIleAlaLysLysLeuSerLysGlyIleArgPro
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-----TGGCCTATGGTTGAGAAATTAATTAAACAGTGT

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-----PheserserGlnGlyGlnGlu-----Tyr

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24	LeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIleHisProLeu 43	ω.	
222	222 CTTTGCCACCTCCACCCCAGTTTGATATCTTTGCTGGCAGCTGGGATTCGTCCCCGG 2	281	
44	44 CysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAla 63	w	
282	ATGTTGGTGATGAGTTAGCCTCCAAGGGTTCCTTGGATCGCCTGCTTCAGCAGGACAAA 341	41	
64	ArgAspSerSerPheIleProLeuGlyH1sMetLeuThrGlnLysIleAlaTyrGlnIle 83	ω	
342	GCCAGCCTCACTAGAACCCTACACACACAGGATTGCACTCCACGTA	386	
84	AlaSerGlyLeuAlaTyrLeuHisLysLysAsnIleIlePheCysAspLeuLysSerAsp 103	03 .	
387	387 GCTGATGGTTTGAGATACCTCCACTCAGCCATGATTATATATA	446	
104	AsnIleLeuValTrpSerLeuAspValLysGluHisIleAsnIleLysLeuSerAspTyr l	123	
447	AATGTGCTGCTTTTCACACTGTATCCCAATGCTGCCATCATTGCAAAGATTGCTGACTAC	506	
124	GlyIleSerArgGlnSerPheHisGluGlyAlaLeuGlyValGluGlyThrProGlyTyr	143	
507	GGCATTGCTCAGTACTGCTGTAGAATGGGGATAAAAAACATCAGAGGGCACACCAGGGTTT	566	
144	144 GlmalaProGluTleArgProArgTleValTvrAspGluLvsValAspMetPheSer 162	62	

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Remaining Prior Application
NUMBER OF SEQ ID NOS: 64
SOFTWARE: FastSEQ for Windo
SEQ ID NO 55
LENGTH: 3138
TYPE: DNA
ORGANISH: Homo sapiens
FEATURE:
NAME/KEY: CDS
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RIOR APPLICATION NUMBER: US 60/373,010
RIOR FILING DATE: 2002-04-16
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RIOR APPLICATION NUMBER: US 60/360,495
RIOR FILING DATE: 2002-02-28
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ITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
ITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 994
ITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 1
ITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 218
ITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16
ITLE OF INVENTION: 13424 MOLECUHES
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URRENT FILING DATE: 2003-02-19
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  710 AGGGTGCTGGCAGGTCGCCGG
                                    57 ThrValLeuSerGluAsnAlaArgAspSerSerPheIleProLeuGlyHisMetLeuThr 76
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CURRENT APPLICATION NUMBER: US/10/369,022
CURRENT FILING DATE: 2003-02-19
PRIOR APPLICATION NUMBER: US 60/360,495
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/370,121
PRIOR FILING DATE: 2002-04-04
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APPLICANT: Silos-Santiago, Inmaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760,
TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 31
TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615,
TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675
TITLE OF INVENTION: 13424 MOLECULES
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PRIOR FILING DATE: 2002-04-16
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                                                         AsnIleIlePheCysAspLeuLysSerAspAsnIleLeuValTrpSerLeuAspValLys
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	417	AlametGluValValAsnSerGlySerGl	408	Ϋ́
	1848	AAAGAAGGAAGTAGTCGGGGGGCAAGAAGAAGAAGGACGAACGTGGGGGCCCAGCTCCAC	1789	₽
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	405	ArgGlnAsnProTyr	385	δ.
	1731	CCCCCGCTGAGGCCATTCGCCTGACTCCCGTGGACTGTGGTGG	1687	뭥
	385	lAlaValPheProValValArgGlyThrProLysAspSerCysSerTyrLeuCysSerHi	365	VΩ
	1686	ACTOTGGATAAG-CGGAAAGGATCCGATGGGGCCAGCCCCCCTGCAAGCCCCAGCATCAT	N 4	문 5
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. ,	1585	AAGGGCAACTTCAAACGAGCCGTTCTCAAGCTACGGGAAGGCAGCCACACATCAGCCTG	1526	B
	325	AlaThrGluAspGlnLysIleTyrIleTyrThrLeuLysGlyMetCy	310	Ş
	1525	AGA	1466	日
	309		309	δ
	1465	GAGGAGCAGCTGCGGCGGGGAGCAGGAGCTGGCAGAACGTGAGATGGACATCGTGGAA	1406	밁
	309	tLysValSerCysGlnLeuGlnValGlnArgSerLeuTrpThr	295	Ϋ́O
	1405	Ã	1346	皮
	295	LysGlyLeuMetGlu-ValGlnArgMetCysCysProGlyMe	282	Ş
	1345	CTGCAGGAAGACTGGAAGCTGGAGATTCAGCACATGTTTGATGACCTTCGGACCAAGGAG	1286	밁
	281	ThrValValAsnThrG	264	δ
	1285	CGGCTTGAAGTCATCGAACAGTCAGCCCTGTTCCAGATGCCACTGGAGTCCTTCCACTCG	1226	용
	263	GluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGluTyrThrVal	244	δ
•	1225	CAGATTTCGGTAGCATCTTGAAG	1202	β
• .	243	ProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThrPheMetTyr	224	₽,
	Ν	TTTGCCCCCCTCCTGGAGGAATGCTGGGACCCAGACCCCCACGGGCG	1154	B
	223	jeuGlnAlaLeuMetMetGluCysTrpAspThrLysProGluI	204	VΩ
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	203	····-LysLysLeuSerLysGly-IleArgProValLeuGlyGlnProGluGluVal	187	Ş
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	186	luLeuLeuSerGlyGlnArgProAlaLeuGlyHisHisGlnLeuGlnIleAla	169	Ş
	1042	ATCCGTCTCTCCTCCAAAAGCAGTGATGTCTGGAGCTTCGGGGTGCTGCTGTGG	983	В
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•	128	1IleLysLeuSerAspTyrGlyIleSerArgGln	114	Q.

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117 VALITYPYTSERANGIOPTGGANGGAGAGGGCTTGAAGGGCTTGGGGGAAAGAAAGCAA 1908 117 VALITYPYTSERANGIPTGGACCCCAAACTGGGCAAAGCCTTGGGGGAAAGAAAGCAA 1908 118 PACAGTGGTCATCAAGTGGCCCAAACTGGGCCAAACCACACCACACCCCCCCC	ນ ເພດ ພ	D Qy	ğ g	Фф	Db Qq	φ γΩ	Фр	дд У	Qy Db	P 64	B 8	р <del>2</del>	DB Qy	Db Qy	ОУ	밁
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1346 AAGGAGCTTCGGAGCCGTGAGGAGGAGCTGCTGCGGGCGCACAGGAGCAGCGCTTCCAG 1405
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                                                                                                         264 ValPheTrpAspGlyLysGluGluSerArgAsnTyr-----ThrValValAsnThrGlu 281
                                                                                                                                                                              244 GluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGluTyrThrVal
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TYPE: DNA
ORGANISM: Homo sapiens
US-10-263-929-85
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US-10-263-929-85
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CURRENT FILING DATE: 2002-10-03
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APPLICANT: Galant, Ron
TITLE OF INVENTION: Alzheimer's Disease Linked Genes
FILE REFERENCE: LSD-07417
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SerPheHisGluGlyAlaLeuGlyValGluGlyThrProGlyTyrGlnAlaProGluIle 148
                                  GAGAACCACAACCTCGCAGACACGGTGCTCAAGATCACGGACTTCGGCCTCGCCCGCGAG
                                                            GluH1sIleAsn------IleLysLeuSerAspTyrGlyIleSerArgGln 128
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426	412 lAsnSerGlySerGluValTrpTyrSerAsnGlyProGlyLeu	οy	
1736	1677 GGGGCCCAGCTCCACCCTGCAGAAGGAGCGGGTGGGAGGAGAGGAGAGGCTGAAGGGGCT	Db 1	
412	luvalva	Qy	-
1676	GAAGAACTGGTCGGGGGCAAGAAGAAGGGACGAACGTG	ᅡ	
407	400 gGlnAsnProTyrProValLys	Qy	
1619	::: ::::::::::::::::::::::::::::::::::	_	
400	380 rTyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaAr	Ωу	
1566	1515 AAGCCCCAGCATCATCCCCCGGCTGAGGGCCATTCGCCTGACTCCCCGTGGAC	Db 1	
380	370yalvalargGlyThrProLysAspSerCysSe	Qy	
1514	ດ	뮍	
369	sAsnSerTyrLeuValLeuAlaGlyLeuAlaAspGlyLeuValAlaValPhéPro	Ϋ́O	
1455	- ALGVER STORM TO THE CONTROL OF THE	문 동 5	
ιω	36 AGCCAGGAGAAGCCCCGGGTCCGCAAGCGCAAGGGCAACTTCAAGCGCAGCCGCCTGCTC	, p	
337	nAlaLeuAspThrPro	Ϋ́	
1335	CCTGCTCATGTGCCAGCTG	р В	
332	312 uAspGlnLysIleTyrIleTyrThrLeuLysGlyMetCysProLeuAsnThrProGlnGl	ОУ	
1297	eccecced	망	
312	295 tLysValSerCysGlnLeuGlnValGlnArgSerLeuTrpThrAlaThrGl	Qy	
1245		-	
295	G	Qy	
1185			
281	264 ValPheTrpAspGlyLysGluGluSerArgAsnTyrThrValValAsnThrGlu	VΩ	
1125	TCATCGAACAGTCAGCCCTGTTCCAGATGCCACTGGAGTCCT	Db 1	
263	244 GluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGluTyrThrVal	Qy	
1065	042CCAGATTTCGGTAGCATCTTGAAG	рь 1	
243	224 ProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThrPheMetTyr	0y.	
1041	94TITGCCCGCCTCCTGGAGGAATGCTGGGACCCAGACCCCCACGGGCGG	ф	
223	204 GlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysProGluLysArg	ΨQ	
993	943 GTGGCTATGAATAAGCTGACGCTGCCCATTCCCTCCACGTGCCCCGAGCCC	ф	
203	- Ë	Ωу	
942	AGCTGCTGACGGGGGAGGTCCCCTACCGTGAGATCGACGCCTTGGCCGTGGCGTATGGC	ф	
186	sGlnLeuGlnIleAla	Qy	
882		뭥	
168	eSerTyrGlyMetValLeuTyr	Qy	
822	:::	ᅡ	

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APPLICANT: Sreekumar, Arun
ITILE OF INVENTION: Expression Profile of Prostate Cancer
FILE REFERENCE: UM-07221
CURRENT APPLICATION NUMBER: PCT/US02/24567
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 60/309,581
PRIOR APPLICATION NUMBER: US 60/334,468
PRIOR FILING DATE: 2001-018-02
PRIOR APPLICATION NUMBER: US 60/334,468
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin version 3.2
SEQ ID NO 86
TENGTH: 3435
                                                                                                                                                                                                                                                                                                                                     RESULT 12
PCT-US02-24567-86
                                                                                                                                                                                                                                                                                                 Sequence 86, Application PC/TUS0224567 GENERAL INFORMATION:
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452 alValCysSerSerGluGlyArgGlyGluGluValValTrpCysLeuAspAspLysAlaA 472 :::	рь Оу 2
441GluProTyrMetAlaProSerMetValThrSerV 452	Qy
2085 CACACCCAGTCGCCTGGCTTCGCCAGCCTCAATGAGATGGAGGAGTTCGCGGAGGCAG 2144	2 2 2 2
GGGGGAAGCAAACAGTGGTCATCAAGTGCCCCCAACCTGGGCAAGTCCCCCAAACA	
412 lAsnSerGlySerGluValTrpTyrSerAsnGlyProGlyLeu 426	Ωу
GGGGCCCAGCTCCACCCTGCAGAAGGAGGGGGGGGGGGG	
1900 CUSTUUUCCC CCAAAGGAAGGAAGGGAAGAAGGAAGGAAGGAAGGAAGG	Q 5
gGlnAsnProTyrProValLys	
380 rTyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaAr 400	Qy
370	Qу рь 1
331 SABISSTIYILGUVALLGUALAGIYLGUALAASPGIYLGUVALALAVALPhePro 369 ::::	B 5
AAGCTGCGGGAAGCCGCACATCAGCCTGCCCTCTGGCTTTGAGCATAAGATCACA	
338AlaValValThrCysPheLeuAlaValProValIleLysLy 351	Q
332 nAlaLeuAspThrPro	оу 1
1586TCGTGGAACGGAGCTGCACCTGCTCATGTGCCAGCTG 1623	Db 1
312 uAspGlnLysIleTyrIleTyrThrLeuLysGlyMetCysProLeuAsnThrProGlnGl 332	Qy
295 tLysValSerCysGlnLeuGlnValGlnArgSerLeuTrpThrAlaThrG1 312 :::        1534 GAGGAGCAGCTGCGGCGGCGGGAGCAGGAGCTGGCAGAACGTGAGATGGACA 1585	₽. <i>Q</i>

	990	CTGG	<b>AAGTCCATCAACATCCTGATC</b>	CCCATCATCCACCGGGACCTCA	937	밁
	113	TrpSerLeuAspValLys	LysSerAspAsnIleLeuVal	AsnIleIlePheCysAspLeuLysSerAspAsnIleLeuValT	94	γ
	936	TACAATGATGCCCCTGTG	AACTGGGCTGTGCAGGTGGCCCGGGGCATGAACTACCTAC	AACTGGGCTGTGCAGGTGG	880	B
	93	HisLysLys	AlaSerGlyLeuAlaTyrLeu	GlnLysIleAlaTyrGlnIleAlaSerGlyLeuAlaTyrLeuHisLysLys-	77	Qy
	76 879	pSerSerPheIleProLeuGlyH1sMetLeuThr :::     GTGCCACCTCACGTGCTGGTC	ArgAspSerSerPheIleProL :::    GTGCCA-	ThrValLeuSerGluAsnAlaArgAs       ::: AGGGTGCTGGCAGGTCGCCGG	57 838	pb Qy
	56 837	ProLeuSerSerLeuAsn :::   ::: CGGGGTGGTGCACTGAGC	LeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsn        	SerileHisProLeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsn ::::	39 778	Db Qy
	38 777	ValAlaLeuIleGlyIle :::      ATTGCCCTTAGGGGCGCC	AlaLeuGlnHisProCysIle                   CCCTGCAGCACCCCAACATA	GlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIle 	19 718	Db Qq
		.*	0-210-120-86 (1-3435)	-392-21 (1-728) x US-10-	09-836-	us-ċ
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٠.	607 2765	erAspArgSerGluHisA :: TGTGAGCCGCGGGCACC	-AspMetLeuH1sThrProGlyAlaAlaSerAspArgSerGluH1sA 	ysGluAspSerAspMetLeuH1sThrProGlyAlaAlaSerAspArgSerGluH1sA	588 2706	р, <b>2</b>
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412	)8AlaMetGluValVa	Qy 40
1964	8 CGGTGGGCCCCCAAAGAAGGAAGAACTGGTCGGGGGCAAGAAGAAGGAACGAAC	Db 190
407	gGlnAsnProTyrProValLys	оу 40
1907	:::	
400	0 rTyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaAr	Оу 38
38U 1854	AAAGCCCCAGCATCATCCCCCGGCTGAGGGCCATTCGCCTGACTCCCGTGGAC3	Db 180
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369 1802	1 sAsnSerTyrLeuValLeuAlaGlyLeuAlaAspGlyLeuValAlaValPhePro 1:::	Oy 35
1743	AAGCTGCGGGAAGGCGGCACCATCAGCCTGCCCTCTGGCTTTGAGCATAAGATCACA	Db 168
351	8AlavalvalThrCysPheLeuAlaValProValIleLysLy	Qу 33
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<b>ω</b> .	2 nAlaLeuAspThrPro	Ov 33
332 1623	2 uAspGlnLysIleTyrIleTyrThrLeuLysGlyMetCysProLeuAsnThrProGlnGl 6TGGTGGAAGGGGAAGGTGCAGCTGCTATGTGCAAGGTG	Qу 31 Об 158
Ū	4 GASGAGCAGCTGCCGCCGCGGAGCCAGGAGCTGGCAGAACGTGAGATGGACA	Ţ
12	5 tLysValSerCysGlnLeuGlnValGlnArgSerLeuTrpThrAlaThrGl	ຸ່່ນ
1533	AAGGAGCTTCGGAGCCGTGAGGAGGAGCTGCTGCGGGGGGGG	Db 147
295	2 LysGlyLeuMetGlu-ValGlnArgMetCysCys	Ωу 28
281 1473	4 ValPheTrpAspGlyLysGluGluSerArgAsnTyrThrValValAsnThrGlu :::	Oy 26
1413	4 CGGCTTGAAGTCATCGAACAGTCAGCCCTGTTCCAGATGCCACTGGAGTCCTTCCACTCG	Db 135
263	GluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGluTyrThrVal	ОУ 244
1353	0CCAGATTTCGGTAGCATCTTGAAG	Db 133
243	SerValValSerGlnMetLysAspProThrPheAlaThrPheMetTyr	Οy 2:
1329	2TTTGCCCGCCTCCTGGAGGAATGCTGGGACCCAGACCCCAGGGGGGG	ეხ 128
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1281	GTGGCTATGAATAAGCTGACGCTGCCCATTCCCTCCACGTGCCCCAAGCCC	13
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186	9 GluLeuLeuSerGlyGlnArgProAlaLeuGlyHisHisGlnLeuGlnIleAla	λλ 16
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68	9 ArgProArgIleVálTyrAspGluLysValAspMetPheSerTyrGlyMetValLeuTyr	_
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128 1050	4 GluH1sIleAsnIleLysLeuSerAspTyrGlyIleSerArgGln    :::    ::::   ::::   :::   :::   GAGAACCACAACCTCGCAGACACGGTGCTCAAGATCACGGACTTCGGCCTCGCCCGCGAG	2y 11 0b 99

RESULT 14 US-09-949- US-09-949- Sequence GENERAL APPLICAL TITLE OI FILE OI FILE CURRENT CURRENT CURRENT CURRENT PRIOR FI PRIOR AI PRIOR FI	Qy 6 Db 27	Qy 5 Db 27	ОУ Db 2	Qy Db 2	Qy Db 2	Qy Db 2	Qy Db 2	Оу Ор 2	Qy Db 2	. Ор 2	Qy Db 2	Qy Db 2	· Qy	Qy Db 2	Db 19
ULT 14 09-949-016-1327 69-949-016-1327 equence 1327, Application US/09949016 energy Information: Energy Information: Energy Veryer, J. Craig et al. Applicant: Veryer, J. Craig et al. TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307 CURRENT APPLICATION NUMBER: US/09/949,016 CURRENT FILING DATE: 2000-04-14 PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20 PRIOR FILING DATE: 2000-10-03	607 spleuThrProMetAspGly 613            766 GGCGGACGCCATCGGATGGG 2785	588 ysGluAspSerAspMetLeuH1sThrProGlyAlaAlaSerAspArgSerGluH1sA 607	582 alpro	562 roArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSerSerV 582	542 euileHisGlnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSerProP 562   :::	522 luGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGlnIleL 542	502 alargProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProLysValProG 522	487ArgTyrPheCysGlyValProSerProLeuArgAspMetPheProV 502     :::     :::     :::     :::    :::    :::    :::    :::	486 1a 486 	472 snSerLeuValMetTyrH18SerThrThrTyrGlnLeu	452 alvalcysSerSerGluGlyArgGlyGluGluValValTrpCysLeuAspAspLysAlaA 472 ::: :::	441GluProTyrMetAlaProSerMetValThrSerV 452	427LeuValIleAspCysAlaSerLeuGluIleCysArgArgLeu 440	412 lasnSerGlySerGluValTrpTyrSerAsnGlyProGlyLeu	)65 GGGGCCCAGCTCCACCCTGCAGAAGGAGCGGGTGGGAGGAGGAGGAGAGGGCTGAAGGGGCT 2024

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US-09-836-392-21 (1-728) x US-09-949-016-1327 (1-3143)
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Query Match:
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US-09-949-016-1327
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1327
LENGTH: 3143
TYPE: DNA
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alArgProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProLysValProG 522
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                                                                                                                                                                                                                                                                                                         alValCysSerSerGluGlyArgGlyGluGluValValTrpCysLeuAspAspLysAlaA 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGGAGCAGCTGCGGCGGCGGGAGCAGGAGCTGGCAGAACGTGAGATGGACA--
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                                                                                                                                                                                                                                    snSerLeuValMetTyrHisSerThrThrTyrGlnLeu--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lAsnSerGlySerGluValTrpTyrSerAsnGlyProGlyLeu-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TCGTGGAACGGGAGCTGCACCTGCTCATGTGCCAGCTG 149
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                                                                                      -ArgTyrPheCysGlyValProSerProLeuArgAspMetPheProV 502
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-AlaMetGluValVa 412

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Qy 39 SerIleHisproLeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsn 56		TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01455 CURRENT APPLICATION NUMBER: US/60/455,444 CURRENT FILING DATE: 2003-03-18 NUMBER OF SEQ ID NOS: 50986 SOFTWARE: FASTSEQ for Windows Version 4.0 SEQ ID NO 1697 LENGTH: 3143 TYPE: DNA ORGANISM: Homo sapiens US-60-455-444-1697 Allgament Scores:	Qy 607 spleuThrPrometAspGly 613	Qy 582 alpro	Qy 542 eulleHisGlnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerProP 562	Db , 2317CGGGGCCTCAGCCCACCGCGCGCGCGCGCGCGCGCGCGCGCGC
6 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	04 AQ QQ	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0y 0y	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		Db Oy
351 SABISETTYTLEURIAGLYLEURIARASPOLYLEUVBLALAVAIPHEPRO 369 11	2 uAspGlnLys1leTyrIleTyrThrLeuLysGlyMetCysProLeuAspThrProGlnGl	1227 CGGCTTGAAGTCATCGAACCAGTCAGCCCTGTCCAGATGCCACTGGAGGTCCTTCCACTCG 1286  264 ValPheTrpAspGlyLysGluGluSerArgAsnTyrThrValValAsnThrGlu 281  :::	204 GInPheArgArgLeuGInAlaLeuMetMetGluCysTrpAspThrLysProGluLysArg 223	169 GluLeuLeuSerglyGlnArgProAlaLeuGlyH1sH1sGlnLeuGlnIleAla 186	129 SerPheHisGluGlyAlaLeuGlyValGluGlyThrProGlyTyrGlnAlaProGluIle 148 :::             924 TGGCACAAGACCACCAAGATGAGCGCTGCGGGGACCTACGCCTGGATGGCGCCGGAGGTT 983 149 ArgProArgIleValTyrAspGluLysValAspMetPheSerTyrGlyMetValLeuTyr 168 :::::	810 CCCATCATCCACCGGGACCTCAAGTCCATCAACATCCTGATCCTGGAGGCCATC 863  114 GluHisileAsnIleLysLeuSerabpTyrGlyIleSerargGln 128     :::   :::   :::   :::   :::   :::   :::   :::   :::   :::

Search completed: April 15, 2003, 09:53:18 Job time : 562 secs

523	SerIleIleProArgLeuArgAlaIleArgLeuThrProVa	503	밁
878	ATGTGCTGCCC	868	γ
503	leThrValGlnAlaSerProThrLeuAspLysArgLysGlySerAspGlyAlaSerProP	483	밁
867	AGAGAAGGCCTCATGGAGGTGCAGAGG	840	Ş
483	463 alleuLysLeuArgGluGlySerSerHisIleSerLeuProSerGlyPheGluHisLysI 483	463	B 2
839	TCCAGGAACTACACGGTGGT	814	9
463	ser-GlnGluLysProArgValArgLys-ArgLysGlyAsnPheLysArgAlaV	446	ర్జ
813	GCCTTCTTCTCATCCCAGGGCCAGGAGTACACCGTGGTGTTTTGGGATGGAAAAGAGGAG	754	δ
445	GluargGluMetAspIleValGluArgGluLeuH1sLeuLeuMetCysGlnLeu	428	В
753	ATGTATGAACTGTGCTGTGGGAAGCAGACA	724	Qγ
427	AlaAlaGlnGluGlnArgPheGlnGluGluGlnLeuArgArgArgGluGlnGluLeuAla	408	В
723		723	ΩΥ
407	${\tt PheAspAspLeuArgThrLysGluLysGluLeuArgSerArgGluGluGluLeuLeuArg}$	388	В
723		723	Qy
387	MetProLeuGluSerPheHisSerLeuGlnGluAspTrpLysLeuGluIleGlnHisMet	368	B
723	ATGAAGGACCCGACTTTTGCCACCTTC	697	Qy
o	eGlySerIleLeuLysArgLeuGluValIleGluGlnSer/	4	문
696	CGCTGGCCCTGTCG	670	Ş
347		332	₽
669	TTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGACACTAAGCCAGAG	610	γQ
331	:::   alalaMetAsnLysLeuThrLeuProIleProSerThrCysProGluPro	315	₽.
609	AAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGCAGCCGGAGGAAGTG	559	Q.
314	GluLeuLeuThrGlyGluValProTyrArgGluIleAspAlaLeuAlaValAlaTyrGly	295	8
558	AGTTGCTGTCAGGACAGCGCCCTGCACTGGGCCCACCACCAGCTCCAGATTGCC	505	Ωγ .
294	IleArgLeuSerLeuPheSerLysSerSerAspValTrpSerPheGlyValLeuLeuTrp	275	B
504		445	δĀ
274	TrpHisLysThrThrLysMetSerAlaAlaGlyThrTyrAlaTrpMetAlaProGluVal	255	용
444	TCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACTCCTGGCTACCAGGGCCCCAGAGATC	385	Ş
254	euAlaAs	235	. <u>B</u>
384	GAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCAG	340	γ
234	ProllelleHisArgAspLeuLysSerIleAsnIleLeuIleLeuGluAlaIle	217	Ď.
339	AACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGTGT	280	δ
216	-D	198	8
279	CAAAAAATAGCCTACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAA	229	Ş
197	::    alLeuVal	184	В
228	C	169	δ

Alignment Scores:	US-10-369-022-56		ENGTH:	FastSEC	ning Prior App R OF SEQ ID NO	APPLICATION N	APPLICATION N	APPLICATION N	PRIOR APPLICATION NUMBER: US 60/382,409  PRIOR APPLICATION NUMBER: 208 60/382,409	RIOR	APPLICATION N	APPLICATION N				וכגיט		OF INVENTION: 24410, 32560, 611, 15985, 69112, 2158, 224, 615, 434  OF INVENTION: 27410, 33260, 615, 437  OF INVENTION: 05431 22245 2387 15658 55054 15314 1613 1675	TILE OF INVENTION: MILIOUS AND PARTICULATION IN INCIDENT OF TAYER OF INVENTION: PAIN AND PARTICULATION USING 9949, 14230, 76	APPLICANT: NUSURIELY OWLE DOWN APPLICANT: SILOS-SANTIAGO, AND COMPOSITIONS IN TERRATURE TITLE OF INVENTION. METHODS AND COMPOSITIONS IN TERRATURE	Millennium Pharmac	ence	-   033 - n	Db 899 sLeuValSerPheGlyArgThrLeuThrIleSerPro 911	Qy 2023 GCTGCCGTGGCAAAGGACACTGTTGTGTGCACCT 2059	Db 888 oAlaAlaSerArgFroArgLeuAspProTrpLy 899	Qy 1963 GGCCGAGTCATTGCCGTCTTAAAAGCCCGAGAGCTGCTGCATGGGGTGCTGGTGGAT 2022	Db 885ArgProArgPr 888	QY 1903 CCCAGGCGCGGTGGAGATGTTATCGTCATTGGCCTGGAGAAGGATTCTGAAGCCCAGCGG 1962	Db 876 gProThrThrLeuThrPheAlaPro	OY 1843 ACCTTCAGCCAGCACCTGCAGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTC 1902	Db 871ProGluPheProGlyAr 876	Qy 1783 CATACGCCCGGTGCCTCCGACAGGTCTGAGCATGACCCTGACCCCCATGGACGGGAG 1842	::: 854 eProArgLeuProAspProGlnAlaLeuPheProAlaArgArgArgPro	TCCCCAGCAAGTTCTTCCAGTGTGCCTTTCTCCACCGACTGCGAGGACTCAGACATGCTA	Db 837 yProProGluProAlaGlyH1sGlyProGlyProArgAspLeuLeuAspPh 854
	428 GluArgGluMetAspIleValGluArgGlu	Qy 724729 724 724 753	Db 408 AlaAlaGinGluGlnArgPheGinGluGluGlnLeuArgArgArgGluGinGluLeuAla 427	Qy 723 723	Db 388 PheAspAspLeuArgThrLysGluLysGluLeuArgSerArgGluGluLeuLeuArg 407	Оу 723 723	MetProLeuGluSerPheHisSerLeuGlnGluAspTrpLysLeuGluIleGlnHisMet	QY 697 ATGAAGGACCCGACTTTGCCACCTTC 723	Db 348 ProAspPheGlySerIleLeuLysArgLeuGluValIleGluGlnSerAlaLeuPheGln 367	QY 670 CCG	Db 332PheAlaArgLeuLeuGluCysTrpAspProAspProHisGlyArg 347	TGATGGA	Db 315 ValAlaMetAsnLysLeuThrLeuProIleProSerThrCysProGluPro 331	QY 559AGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGCAGCCGGAGGAAGTG 609	Db 295 GluLeuThrGlyGluValProTyrArgGluIleAspAlaLeuAlaValAlaTyrGly 314	OY 505 GAGTTGCTGTCAGGACAGCGCCCTGCACTGGGCCACCAGCTCCAGATTGCC 558	Db 275 IleArgLeuSerLeuPheSerLysSerSerAspValTrpSerPheGlyValLeuLeuTrp 294	QY 445 AGGCCTCGCATTGTATGATGAGAAGGTAGGTAGATATGTTCTCCTATGGAATGGTGCTCTAC 504	Db 255 TrpHisLysThrThrLysMetSerAlaAlaGlyThrTyrAlaTrpMetAlaProGluVal 274	QY 385 TCATTCCATGAGGGGGGCCCTAGGCGTGGAGGGGCACTCCTGGCTACCAGGCCCCCAGAGATC 444	Db 235 GluAsnHisAsnLeuAlaAspThrValLeuLysIleThrAspPheGlyLeuAlaArgGlu 254	QY 340 GAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCAG 384	Db 217 ProIleIleHisArgAspLeuLysSerIleAsnIleLeuIleLeuGluAlaIle 234	QY 280 AACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGGTGCCCTTGACGTCAAG 339	Db 198AsnTrpAlaValGinValAlaArgGlyMetAsnTyrLeuHisAsnAspAlaProVal 216	OY 229 CAAAAAATAGCCTACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAA 279	Db 184 ArgValLeuAlaGlyArgArgValProProHisValLeuVal 197	CGAGAACGCCAGAGATTCTTCCTTTATACCCCTGGGAC	LeuValMetGluTyrAlaArgGlyGlyAla	QY 115 AGCATCCACCCGCTCTGCTTCGCCCTGGAGCTCGCGCCGCTCAGCAGCCTCAAC 168	Db 144 GlnGluhlahrgLeuPheGlyhlaLeuGlnHisProAsnIleIleAlaLeuArgGlyhla 163	QY 55 CAGGAGGCCAGCATGCTGCAGCGCCCCTGCATCGTGGCGCTCATCGGCATC 114	US-09-836-392-8_COPY_22_2205 (1-2184) x US-10-369-022-56 (1-953)	Query Match:       7.82%       Indels:       351         DB:       6       Gaps:       38	t Similarity: 31.96% Conservative: ocal Similarity: 22.35% Mismatches:	317.50 Matches:

1497	ACCACCTACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCAGCCCCCTCAGGGACATG	1438	δ
775	pSerAspGluAlaProAlaAlaProSerPr	764	문
1437	GGGAGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACTCC	1378	Qy
764	:::        ::::: 	744	DЬ
1377	TGCAGCTCTGAGGGCAGA	1355	Qy
744	aArgProHisGlyArgArgGluAspValGlyProGlyLeuGlyLeuAlaProSerAlaTh	724	D
1354	GCCCCCTCCATGGTTACGTCAG	1333	Qy
724	lyArgPheProArgGlyLeuSerProProAl	704	B
1332		1321	δĀ
704	rgAlaAlaAspGlyGluGluGlnArgArgTr	684	밁
1320	TG	1276	δ
684	sGlyAlaArgArgCysAspLeuAlaLeuLeuGlyCysAlaThrLeuLeuGlyAlaVa	664	Вb
1275	AGCGGCTCTGAGGTCTGGTACAGCAATGGGCCGGGC	1240	δ
664	yAlaArgAlaProTrpGluProThrProSerAlaProProAlaArgTrpGlyHi	646	뮍
1239	ATCGCGGATGAAGACGCACGCCAGAACCCCCTACCCCAGTGAAGGCCATGGAGGTGCTCAAC	1180	Qy
646	ThrProSerTyrLeu-SerValProLeuProAlaGluProSerProGl	631	B
1179		1120	Qy
630	MetGluGluPheAlaGluAlaGluAspGlyGlySerSerValProProSerProTyrSer	611	뭥
1119		1060	Ş
610	roGlyPheAlaSer-LeuAsnGlu	603	밁
1059		1000	οy
603	ysGlnTrpSerSerAlaProAsnLeuGlyLysSerProLysHisThrProIleAlaP	583	₽
999	TGCCCCTTAAACACACCCCAACAGGCC	973	δō
583	hrLeuGlnLysGluArgValGlyGlyGluGluArgLeuLysGlyLeuGlyGluGlySerL	563	밁
972	CTGTGGACAGCCACCGAGGACCAGAAAATCTACATCTACACCCTCAAGGGCATG	919	δ
563	roLysLysGluGluLeuValGlyGlyLysLysGlyArgThrTrpGlyProSerSerT	543	밁
918		898	δõ
543	erSerSerGlySerSerSerGlyGlySerG	523	망
897	TGGGATGAAGGTGAGCTGC	879	Q
523	еÞт	503	8
878	ATGTGCTGCCC	868	Q
503	OT)	483	D
867		840	Qy
483	SerSerHisIleSerLeuF	463	₽
839		814	Qy
463	Ser-GlnGluLysProArgValArgLys-ArgLysGlyAsnPheLysArgAlaV	446	밁
813	GCCAGGAGTACACCGTGGTGTTTTG	754	Qy

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                                                        US-09-836-392-8_COPY_22_2205 (1-2184) x US-60-426-964-2 (1-953)
                                                                                                                Query Match:
                                                                                                                                  Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                    ; ORGANISM: homo sapiens
US-60-426-964-2
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                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Silos-Santiago,
                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Methods and compositions for treating TITLE OF INVENTION: Methods and compositions for treating TITLE OF INVENTION: pain and painful disorders using 16314, FILE REFERENCE: MPIIO2-189PIM CURRENT APPLICATION NUMBER: US/60/426,964 CURRENT FILING DATE: 2002-11-15 NUMBER OF SEO ID NOS. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/60426964
                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID |
SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                        LENGTH: 95
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55 CAGGAGGCCAGCATGCTGCAGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATC 114
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                                                                                                                Conservative: Mismatches: Indels:
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PRIOR FILING DATE: 2001-08-31
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                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/240,542 FILING DATE: 2000-10-13
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                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/238,389 FILING DATE: 2000-10-06
                          APPLICATION NUMBER: US
                                                                                            FILING DATE: 2000-09-14
                                                                                                                  APPLICATION NUMBER: US 60/232,654
                                                                                                                                          APPLICATION NUMBER: US 60/234,902 FILING DATE: 2000-09-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU-YOUNG, Janice; TÂNG, Y. Tom;
AZINZAI, Yalda; BURRILL, John D.;
MARCUS, Gregory A.; ZINGLER, Kurt A.;
LU, Dyung Aina M.; LAL, Preeti G.;
RAMKUMAR, Jayalaxmi; WARREN, Bridget A.;
KEARNEY, Liam; POLICKY, Jennifer L.;
THANGAVELU, Kavitha; BURFORD, Neil
                                                                                                                                                                                                              ATION NUMBER: US 60/236,499
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LU, Yan; ISON, Craig H.;
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                                                                                                                                                                                         DATE: 2000-09-29
                                                                      TION NUMBER: US 60/231,357
2000-08-31
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; OTHER INFORMATION: Incyte ID No: 55052990CD1
US-10-288-798-12
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733 CTGTGCTGTGGGAAGCAGACAGCCTTCTTCTC-ATCCCAGGGCCAGGAGTACACCGTGGT
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                                                                                 CTGGCCCTGTCGGTGGAGCCAGATGAAGGACCCGACTTTTGCCACCTTCATGTATGAA
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Qy 1455 TGCCCGTACTTCTGCGGGGT	/22AISH1SAIGAIG	1395 GTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACCTCCACCCTACCAGCTGTG	704 AlaThrSerThrProGlnLeuThrProThrAsnSerLeuLysArgGlyGlyAla	1347 TACGTCAGTCGTGTGCAGCTCTGAGGGCAGAGGGGAGGAGGTCGTCTG	Db 684 GluAspGlyAspGlyProSerSerAspGlyIleHisGluGluProThrProValAsnSer 703	QY 1302GAGATCTGCAGGCGGCTGGAGCCCTACATGGCCCCCCTCCATGGT 1346	:668GlnHisSerProSerGlnSerTyrLeuCysIleProPheProArgGly	OV 1254 CTGGTACAGCAATGGGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCT 1301	Qy 1194 CGCACGGCAGAACCCCTACCCAGTGAAGGCGTCAACAGCGCTTCTGAGGT 1253	641 ProAlaLeuProGlyPheThrSerLeuMetGluMet	QY 1134 CTGCTCCTACCTGTGCTCACACACACCAGCCCAAGTTCAGCATCGCGGATGAAGA 1193	Db 622 GlyTyrLysGlnTrpSerSerAlaProAsnLeuValLysGlyProArgSerSer 640	Qy 1080CGCCGATGGGCTTGTGGCTGTGTTTCCCGTGGTGCGGGGCACCCCAAAGGACAG 1133	Db 602 GlyThrLeuGlyGlnLysGluLeuAlaSerGlyAspGluGlyLeuLysSerLeuValAsp 621	Qy 1074 GGGCCT 1079	Db 582 luGluGlyGluGluGluLysArgAlaProLysLysLysGlyArgThrTrpGly-Pro 601	ATTCCT	562 leGlnLeuThrProGlyGluSerSerLysThrTrpGlyArgSerSerValValProLysG			1002 GGATACTCCAGCTGTCACCTGCTTCTTGGCCGTGCCTGTTA		963	VSG1yLysPheArqLysSerArqLeuLysLeuLysAspG1yAsmArq1leSerLeuProS	- 40% TAGATATATATATATATATATATATATATATATATATAT	917	Db 463 GluLeuLeuArgArgGluGlnGluLeuAlaGluArgGluIleAspIleLeuGluA 482	QY 867 GATGTGCCCTGGGATGAAGGTGAGCTGCCAGGTCCAGAGAT 916	Db 443 GluLeuArgThrTrpGluGluLeuThrArgAlaAlaLeuGlnGlnLysAsnGlnGlu 462	QY 843 GAA		403
CURRENT FILING DATE: 2003-02-25	FITTE DEFENDANCE, DE-COOM HEN	i ii ii	T: ZINGLER, Kurt T: LAL, Preeti G.	NT: TANG, Y. TOM; AZIMZAI, Yalda NT: BURRILL, John D.; MARCUS, Gregor	cki S.; LU, Yan q H.; AU-YOUNG, Janice K.	335		; APPLICANT: INCYTE GENOMICS, INC.; BANDMAN, Olga ; APPLICANT: NGUYEN, Danniel B.; WALIA, Narinder K.	12, Application US/10362892 INFORMATION:	RESULT 13	942	CCACA 1981		Ofense Central Control to the Control of Con	902	882 rProSerGinProSerSerHisArgArgThrProSerAspGiyAlaLeuLysProGinThr	1797 TGCCTCCGACAGGTCTGAGCATGACCTGACCCCCATGGACGGGGAGACCTTCAGCCAGC	862	Qy 1786ACGCCCGGTGC 1796	845 uAlaProProLeuSerProCysThrHisAsnProLeuValAsnValArgVa	Qy 1734 TTCTTCCAGTGTGCCTTTCTCCACCGACTGCGAGGACTCAGACATGCTACAT 1785	rLeuLeuArgSerAspSerAspGluIleValValTyrGluMetProValSerProValGl	1692 GGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTCCCCCAGCAAG	IleSerGluCysAsnSerThrArgSe	Qy 1635 GGAATCACTCACTGACTACTGCTCCATGTCCTCCTACTCCTCATCCCCACCCCGCCA 1691	805	1575 CATCGCGGACGTGAGCATCTACAGTGAGGAGCTGGGCACGCAGATCCTGATCCACCA		OLJEVOVOVOTORULJOSLOVERRECIONERROLINOSIONEN ETTJORGODREJOSEN 1681 1681	1488	746 LeuLeuGluAlaGlyLysCysGlnLeuLeuProLeuGluGluProGluProProAlaArg	Qy 1476 1487

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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 55052990CD1
JS-10-362-892-12
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SEQ ID NO 12
LENGTH: 1097
TYPE: PRT
ORGANISM: Homo sapiens
322 ArgAlaSerMetPheSerLysGlySerAspValTrpSerTyrGlyValLeuTrpGlu 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 ArgHisAspProAspGluAspIleSerGlnThrIleGluAsnValArgGlnGluAlaLys 193
                                     448 CCTCGCATTGTATATGATGAGAAGGTAGATATGTTCTCCTATGGAATGGTGCTCTACGAG 507
                                                                          302 HisArgThrThrLysMetSerAlaAlaGlyThrTyrAlaTrpMetAlaProGluValIle 321
                                                                                                                                                                                                                                                                  388 TTCCATGAGGGGGGCCCTAGGCGTGGAGGGCACTCCTGGCTACCAGGCCCCCAGAGATCAGG 447
                                                                                                                                                                                                   331 --- GACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCAGTCA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                              181 GAGAACGCCAGAGATTCTTCCTTTATACCCCCTGGGACACATGCTCACCCAAAAAATA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 ATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCCG 126
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APPLICATION NUMBER: US 60/232,654
FILING DATE: 2000-09-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/240,542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/234,902 FILING DATE: 2000-09-22 APPLICATION NUMBER: US 60/236,499 FILING DATE: 2000-09-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/231,357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/238,389 FILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                        ValAsnTrpAlaValGlnIleAlaArgGlyMetAsnTyrLeuLeuAspGluAlaIleVal 262
                                                                                                                                                            GlyAspLeuSerAsnLysIle---LeuLysIleThrAspPheGlyLeuAlaArgGluTrp 301
                                                                                                                                                                                                                                         ProIleIleHisArgAspLeuLysSerSerAsnIleLeuIleLeuGlnLysValGluAsn 282
                                                                                                                                                                                                                                                                                                                                                 ------GCCTACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAA-------
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Conservative:
Mismatches:
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652	1 ProAlaLeuProGlyPheThrSerLeuMetGluMet	. 64	뫄
GA 1193	4 CTGCTCCTACCTGTGCTCACACACACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATGAA	113	Qy
er 640	<pre>2 GlyTyrLysGlnTrpSerSerSerAlaProAsnLeuValLysGlyProArgSerS</pre>	62	D)
AG 1133	0CGCCGATGGGCTGTGTGTGTGTTTTCCCGTGGTGCGGGGCACCCCAAAGGAC	108	Qy
sp 621	2 GlyThr	60	Db
1079	4 GGGCCT	107	Qy
ro 601	2 luGluGlyGluGluGluLysArgAlaProLysLysGlyArgThrTrpGly-F	58	Д
GC 1073	6	104	Ωy
sG 582	<pre>2 leGlnLeuThrProGlyGluSerSerLysThrTrpGlyArgSerS</pre>	56	В
1045	5	104	Qy
BI 562	2 eulleAsnSerArgSerSerProProAlaSerProThrIleIleProArgLeuArgAla	54	фd
1045	2 GGATACTCCAGCTGTCGTCACCTGCTTCTTGGCCGTGCCTGTTA	100	Qy
rL 542	2 erAspPheGlnHis	52	ДD
TT 1001	3 CAAGGACATGTGCCCCTTAAACACACCCC	96	Qy
os 522	<pre>2 ysGlyLysPheArgLysSer</pre>	50	Дb
CT 962	7TCTACA	94	Qy
gL 502	2 rgGluLeuAsnIleIleHisGlnLeuCysGlnGluLysProArgValLysLysA	48	ДD
946	7	91	Qy
uA 482	3 GluLeuArgArgArgGluGlnGluLeuAlaGluArgGluIleAspIleLeuGl	46	р.
916	7 GATGTGCTGCCCTGGGATGAAGGTGAGCTGCCAGCTCCAGGTCCAGAGAT		Qy
lu 462	   3 GluLeuArgThrTrpGluGluGluLeuThrArgAlaAlaLeuGlnGlnLysAsnGlnG	44	Дb
AG 866	GAAGGGCCTCATGGAGGTGCAC	84	Qy
ys 442		42	뫄
GA 842	2 GTTTTGGGATGGAAAAGAGGAGTCCAGGAACTACACGGTGGTGAACA	79	Qy
eu 422	3 LeuThrThr	40	Дb
GT 791	3 CTGTGCTGTGGGAAGCAGACAGCCTTCTTCTC-ATCCCAGGGCCAGGAGTACACCGTG	73	Qy
1n 402	4ProSerPheThrAsnIleLeuAspG	. 39	фd
AA 732	3 CTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCCGACTTTTGCCCACCTTCATGTATG	. 67	Qγ
393	8PheAlaLysLeuMetGluAspCysTrpAsnProAspProHisSerArg-	37	da da
CG 672	3 TTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGACACTAAGCCAGAGAAGCGAC	61	Qy
377	2 A	36	뫄
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al 361	::   :::    :::	34	말
558	TTGCTGTCAGGACAGCGCCCTGCACT	508	Qγ

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PCT-US02-39126-13
, Sequence 13, Application PC/TUS0239126
; GENERAL INFORMATION:
, APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: KABLE, Amy E.
                                                                                                            RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                           rProSerGlnProSerSerHisArgArgThrProSerAspGlyAlaLeuLysProGluTh 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lGluArgPheLysArgAspProAsnGlnSerLeuThrProThrHisValThrLeuThrTh 882
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                                                                                                                                                                                                                                       luSerSerSerPheLeuPheProPhePheValProProGlnGlyMetLeuLysThrP 942
                                                                                                                                                                                                                                                                               AGATGTTATCGTCATTGGCCTGGAGAAGGATTCTGAAGCCCAGCGGGGCCGAGTCATTGC 1976
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                                                                                                                                                                                                                                                                                                                                                                 CCTGCAGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCCAGGCGCGGTGG 1916
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PRIOR APPLICATION NUMBER: US 60/340,235
PRIOR FILING DATE: 2001-12-07
PRIOR PPLICATION NUMBER: US 60/343,007
PRIOR FILING DATE: 2001-12-19
PRIOR PPLICATION NUMBER: US 60/343,546
PRIOR FILING DATE: 2001-12-21
PRIOR PILING DATE: 2001-12-21
PRIOR PPLICATION NUMBER: US 60/354,388
PRIOR APPLICATION NUMBER: US 60/354,388
PRIOR APPLICATION NUMBER: US 60/357,675
PRIOR FILING DATE: 2002-02-04
PRIOR FILING DATE: 2002-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score:
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SEQ ID NO 13
LENGTH: 1081
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OTHER INFORMATION: Incyte ID No:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             URRENT APPLICATION NUMBER: PCT/US02/39126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TLE OF INVENTION: KINASES AND PHOSPHATASES LE REFERENCE: PF-1315 PCT
                                                                                                              181
                                                                                                                                                                                                                                                                                                                           174 ArgHisAspProAspGluAspIleSerGlnThrIleGluAsnValArgGlnGluAlaLys
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                              238
                                                                                                                                                                                                                                          194 LeuPheAlaMetLeuLysHisProAsnIleIleAlaLeuArgGlyValCysLeuLysGlu
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                                                                                                            GAGAACGCCAGAGATTCTTCCTTTATACCCCTGGGACACATGCTCACCCAAAAAATA---
                                                                                                                                                        ProAsnLeuCysLeuValMetGluPheAlaArgGlyGlyProLeuAsnArgValLeuSer
                                                                                                                                                                                                -----CTCTGCTTCGCCCTGGAGCTCGCGCCGCTCAGCAGCCTCAACACCGTGCTGTCC
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EMERLING, Brooke M.
RAMKUMAR, Jayalaxmi
JIN, Pei
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SPRAGUE, William W.
ZEBARJADIAN, Yeganeh
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SWARNAKAR, Anita
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                          GCCTACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAA------
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Matches:
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	leGlnLeuThrProGlyGluSerSerLysThTTrpGlyArqSerSerValValProLysG	GGATACTCCAGCTGTCGTCACCTGCTTCTTGGCCGTGCCTGTTA	::: LysArgLysSerL		ysGlyLysPheArqLysSerArqLeuLysLeuLysAspGlyAspArqIleSerLeuPros	GCCLUSTBURGENCKCCBKBURCCBGARARAS gGluLeuAsnIleIleIleHisGlnLeuCysGlnGluLysProArgValLysLysArgL	₽		GAAGGGCCTCATGGAGGTGCAGAG	pAsnTrpLysHisGluIleGlnGluMetPheAspGlnLeuArgAlaLysGluLys		CTGTGCTGTGGGAAGCAGACAGCCTTCTCTC-ATCCCAGGGCCAGGAGTACACCGTGGT     :::::::       :::    LeuThrThrIleGluGluSerGlyPhePheGluMetProLysAspSerPheHisCysLeu				AGAAGCGACCG	AAGAAGCTGTCCAAGGGCATCCGGCCCGGTTCTGGGGCAGCGGAGGAAGTGCAG        ::::    AlaMetAsnLysLeuAlaLeuProIleProSerThrCysProGluPro	Glyval		CTCGGATTGTATATGATGAGAAGGTAGATATGTTCTCCTATGGAATGGTGCTCTAGGAG 			- GlyAspLeuSerAsnLysIleLeuLysIleThrAspPheGlyLeuAlaArgGluTrp		AACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGGTGGTCCCTT	243 ValAsnTrpAlaValGlnIleAlaArgGlyMetAsnTyrLeuHisAspGluAlaIleVal 262
1073	1045	1045 562	542	1001	962 522	502	482	916	866 462	442	842	791 422	402	732	393	672	612 377	361	558	507 341	321	447	301	282	330	262
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GAGC  ::: uAla	rGln	gPhe TCC?	lGlu	:	gSer	) 1	GACG	2 - G	uLys	TTCC		uVa]	GGT	TGG	rsei	CAG	pG13	- 662	ACAC	;	900	aLei	r Lys	cec	rLeu	<del>]</del>

8 GGTCTGAGGATGACCTGACCC	1808 903	. Qy
3 ProSerGinProSerSerHisArgArgThrProSerAspGlyAlaLeuLysProGluThr 902	00 1	da 42
3 GluArgPheLysArgAspProAsnGlnSerLeuThrProThrH1sValThrLeuThrThr	. 86	D D
8 GCCAGGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCAGCAAGCTTCCTTC	1688	Qy
3 ProValGluAlaProProLeuSerProCysThrHisAsnProLeuValAsnValArgVal 86	843	DЬ
9CATCCCACTGCTCCATGTCCTCCTACTCCTCATCCCCACCCC 168	164	γo
ThrArgSerLeuLeuArgSerAspSerAspGluIleValValTyrGluMetProValSer 84	<b>6</b> 0	Db :
AATCACTCACTG	163	Q .
7 TCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCAGATCCTGATCCACCAGG 163 	157 80	da Yo
SerProProSerArgLysLeuPheLysLysGluGluProMetLeuLeuLeuGlyAspP	7	Дb
ACACGGCCAACCCAAAGGTGCCTGAGGG	1541	Qy
6 GluGluLysLysArgArgGluGlyLeuPheGlnArgSer	76	Db
4 CATG	149	γQ
6 Le	74	DЬ
6CCCCAGCCCCTCAGGGA 149	147	φ
	72	Db
5 TECCCEGTACT	145	VΩ
2ArgArg 72	72	ДQ
5 GTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTAC	139	ν.
	704	Db
TACGTCAGTCGTGTGCAGCTCTGAGGGCAGAGGGGGAGG	1347	γo
4 GluAsp	68	Db Db
2GGAGATCTGCAGGCGGCTGGAG	130	Qγ
	66	Db
4 CTGGTACAGCAATGGGCCGGGCCTCCTTG	125	Qy
3	65	Дb
4 CGCACGGCAGAACCCCTACCCAGTGAAGGCCATGGAGGTGGTCAA	119	δō
ProAlai	641	B
CTGCTCCTACCTGTGTCACACAC	1134	Q
2 GlyTyrLysGlnTrpSerSerAlaProAsnLeuValLysGlyProArgSerSer 640	622	Д
CGCCGATGGGCTTGTGGCTGTTTTCCCGTGGTGCGGGCACCCCAA	1080	Qγ
  2 GlyThrLeuGlyGlnLysGluLeuAlaSerGlyAspGluGlyLeuLysSerLeuValAsp 621	602	DЬ
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	- 279 1 216	CAAAAATAGCCTACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAA	198	B 5
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	r 183	AGCATCCACCCGCTCTGCTTCGCCCTGGAGCTCGCGCCGCTCAGCAGCCTCAA :::::	115 164	유 성
•	C 114 a 163	5 CAGGAGGCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATC	144	Ag Ag
		5-392-8_COPY_22_2205 (1-2184) x US-10-263-929-187 (1-954)	-09-836-	SD
		t Scores: 2.76e-07 Length: 954 312.50 Matches: 194 Similarity: 33.548 Conservative: 77 sal Similarity: 24.018 Mismatches: 258 ttch: 7.708 Gaps: 29	ignmen ed. NC ore: rcent st Loc ery Ma	Per Sc Pr DB
		H: 954 PRT VISM: Homo sapiens 3-929-187	-01-	us:
•		W FILING DATE: 2002-10-03 OF SEQ ID NOS: 213 ARE: PatentIn version 3.2	CURRENT F NUMBER OF SOFTWARE:	
		VENTION: Alzheimer's NCE: LSD-07417	TITLE OF IN FILE REFERE CURRENT APE	
		e 187, Application US/10263929 . INFORMATION: ANT: Kim, Jaeseob	PLI	
	٠	-929-187	RESULT 15 US-10-263-	US
		ThrProSer 1	005	용 성
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		CAGAGTGGTGCCTGGCCGTCTGGAGGGGCTGGGGCCCCAGGGAGTTCGAC	2075	2 0
	2074	TGGTGGATGCTGCCGTGGTGGCAAAGGACACTGTTGTGTGCACCTTTGAAAATGAAAACA  LeuAspProTrpTrpPheValSerProSerHisAlaArgSer	2015 981	유 양
	980	CCCAGCGGGCCGAGTCATTGCCGTCTTAAAAGCCCGAGAGCTGACTCCGCATGGGGTGC	1955 963	å Š
_	1954 1962	GCGGTGGAGATGTTAȚCGTCATTGGCCTGGAGAAGGATTCTGAAG 	1910 943	음 성
Ĭ.	190 942	GCCAGCACCTGCAGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTT	1850 923	岛 장

1159	TCCCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTCCTACCTGTGCTCACACACAC	1104	, Qy
538	SerGlySerSerSerGlyGlySerGlyThrTrp	528	Db
1103	TATTAAAAAGAATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTTGTGGCTGTGTT	1044	Qy
527	LeuThrProValAspCysGlyGlySerSer	518	ф
1043	ij	984	Оy
517	IleProArgLeuArgAlaIleArg	510	망
983	CCTTAA	936	Qy
509	LysGlySerAspGlyAlaSerProProAlaSerProSerIle	496	ДĎ
935	AGGTGAGCTGCCAGCTCCAGGTCC	876	γQ
495		476	Db
875		846	Qγ
475	LysGlyAsnPheLysArgSerArgLeuLeuLysLeuArgGluGlyGlySerHisIleSer	456	망
845		828	γΩ
455	   ArgGluLeuHisLeuLeuMetCysGlnLeuSerGlnGluLysProArgValArgLysArg	436	망
827	GAACTACAC	819	Qy
435	GluGluGlnLeuArgArgArgGluGlnGluLeuAlaGluArgGluMetAspIleValGlu	416	ф
818		· 818	Qy
415	Lys GluLeuArgSerArgGluGluLeuLeuArgAlaAlaGlnGluGlnArgPheGln	396	ДЬ
818		818	Qy
395		376	da
818	GGTGTTTTGGGATGGAAAAGAGGAGTCCAG	789	Qy
375	ArgLeuGluVallleGluGlnSerAlaLeuPheGlnMetProLeuGluSerPheHisSer	356	Db
788	GCCTTCTTCTC-A	730	γQ
355	ProAspPheGlySerIleLeuLys	348	Ъ
729	CCGCTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACCTTCATGTAT	670	Qy
347	PheAlaArgLeuLeuGluGluCysTrpAspProAspProHisGlyArg	332	ДЬ
669	AGGCG	610	Qγ
331	ValalaMetAsnLysLeuThrLeuProIleProSerThrCysProGluPro	315	Δb
609	AAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGCAGCCGGAGGAAGTG	559	Qy
314	GluLeuLeuThrGlyGluValProTyrArgGluIleAspAlaLeuAlaValAlaTyrGly	295	DЬ
558	GAGTTGCTGTCAGGACAGCGCCCTGCACTGGGCCCACCACCAGCTCCAGATTGCC	505	Qy
294	pSerPheGlyValLeuLeuT	275	ď
504	TGTTCTCCTATG	445	Qy
274	TrpHisLysThrThrLysMetSerAlaAlaGlyThrTyrAlaTrpMetAlaProGluVal	255	Db
444	ACTCCTGGCTACCAGGCCCCAGAGA	385	Qy
254	:::        ::::     ::::   ::::   ::::   ::::   ::::   ::::	235	В

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                                                                                                                                                                                                                                   1745 TGCCTTTCTCCACCGACTGCGAGGACTCAGACATGCTACATACGCCCGGTGCTGCCTCCG 1804
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                                                                                                                                                                                   806 ProGlyGlnSerLeuThr-----ProThrHisValThrAlaValCysAlaValSerArg
                                                                                                                                                                                                                                                                                    786 hrPro-SerProSerThrAsnProLeuValAspLeuGluLeuGluSerPheLysLysAsp 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               676 uGlyCysAlaThrLeuLeu-GlyAlaValGlyLeuGlyAlaAspValAlaGluAlaArgA 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 657 SerAlaPro-ProAlaArgTrpGlyHisGlyAlaArgArgArgCysAspLeuAlaLeuLe 676
844 Gly-HisGlyProGly 848
                                                                                       824 GlyHisArgArgThrProSerAspGlyAlaLeuGlyGlnArgGlyProProGluProAla 843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     578 GlyLeuGlyGluGlySerLysGln-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----SerProTyrSerThrProSerTyrLeuSerValProLeuProAlaGluProSer 645
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Search completed: April 15, 2003, 07:26:16 Job time: 81 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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-MODEL-frame+_p2n.model -DEV-xlh
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Maximum DB seq length: 2000000000
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                                                                                                                        -Q-/cgn2_1/USFTO_spool/US09836392/runat_08042003_090541_23458/app_query.fasta_1.903
-DB-Pending_Patents_NA_Main -QFMT-fastap -SUFFIX=P2n.rnpm -MINNATCH=0.1
-LOOPEXT-0 -UNITS-bits -START=1 -END--1 -MATRIX-blosum62
-TRANS-human40.cd1 -LIST-45 -DCCALIGN-200 -THR_SCORE-pct -THR_MAX=100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-2000000000 -USER-US09836392_eCGN_1_1_2551_@funat_08042003_090541_23458
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPEXT-0.5 -FGAPOP-6
                                                                                                      -YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                               Pending_Patents_NA_Main: *
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cgn2_6/ptodata/1/pna/PCTUS_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

5 6 357		1 3822 2 3822	Result
			Score N
97.5	99.8	100.0	Query Match I
2652 7015	3579	3496 3496	Query e Match Length DB ID
4 H	بـر نـر	32	. B
	٠	PCT-US00-28066-8 2 US-09-836-392-8	DB ID
Sequence 5042, Appli	Sequence 37, Appl Sequence 14, Appl	Sequence 8, Appli Sequence 8, Appli	Description

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TITLE OF INVENTION: AILLING OF TILE REFERENCE: PT020PCT
CURRENT APPLICATION NUMBER: PCT7US00/28066
CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: 60/159,542
PRIOR APPLICATION NUMBER: 60/165,914
PRIOR APPLICATION NUMBER: 60/165,914
PRIOR FILING DATE: 1999-11-17
PRIOR APPLICATION NUMBER: 60/189,027
PRIOR FILING DATE: 2000-03-14
NUMBER: OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 3496
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US00-28066-8
 Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                    RESULT 1
PCT-US00-28066-8
; Sequence 8, Application PC/TUS0028066
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Protein Tyrosine Kinase |
; TITLE OF INVENTION: ANTIBODIES
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10 US-09-902-319-440
10 US-09-342-216-440
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Length:
Matches:
Conservative:
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Sequence 38919, A
Sequence 25704, A
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Sequence 4, Appli
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Sequence 7, Appli
Sequence 3, Appli
Sequence 456, App
Sequence 456, App
Sequence 7370, Ap
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Sequence 9514, Ap
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15552, A.
11416, A.
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                             PheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGlu-
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              TTCTTGGCCGTGCCTGTTATTAAAAAGAATTCCTACCTGGTCTTAGCGGGCCTCGCCGAT 1086
                                             GGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAGCTGCCAGCTCCAG
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700	lyAlaArgGluPheAspIlePheTyrGlnSerTyrGluGluLeuGlyArgLeuGluAl	681	ДĎ
2166	GCCCCAGGGAGTTCGACATTTTCTACCAGTCCTACGAGGAGCTGGGCCGGCTGGAGGCT	2107	γQ
680	$\verb alValCysThrPheGluAsnGluAsnThrGluTrpCysLeuAlaValTrpArgGlyTr $		dd
2106	GTTGTGTGCACCTTTGAAAATGAAAACACAGAGTGGTGCCTGGCCGTCTGGAGGGGCTGG		, Qy
660	laArgGluLeuThrProHisGlyValLeuValAspAlaAlaValValAlaLysAspThr	641	рb
2046	CGAGAGCTGACTCCGCATGGGGTGCTGGTGGATGCTGCCGTGGTGGCAAAGGAC	1987	Qy
640	allieGlyLeuGluLysAspSerGluAlaGlnArgGlyArgVallleAlaValLeuLys	621	Дb
1986	ATTGGCCTGGAGAAGGATTCTGAAGCCCAGCGGGGCCGAGTCATTGCCGTCTT	1927	γQ
620	1ArgAspLeuIleTrpValProArgArgGlyGlyAspValIle	601	Db
1926	TGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCCAGGCGCGGTGGAGATGTTAI	1867	VQ
600	ArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLeuGlnAla	581	рь
1866	GGTCTGAGCATGACCTGACCCCCATGGACGGGGAGACCTTCAGCCAGC	1807	Qy
580	roPheSerThrAspCysGluAspSerAspMetLeuHisThrProGlyAlaAlaSerAsp	561	Дb
1806	TCAGACATGCTACATACGCCCGGTGC	1747	γQ
560	rgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSerSerVal	541	Дb
1746	CAGGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTCCCCAGCAAGTTCTTCCAGTGT	1687	γQ
540	HisglnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSerProPro	521	Дb
1686	TCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCTACTCCTCATCCCC		γQ
520	IleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGlnIleLeu	501	рb
1626	GGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCAGATCCTG	1567	γо
500		481	Db
1566	GGCCCTTGGACACGGAACCCCCGGCAGCCAGCCAACACGCCAAACCCCAAAGGTGCCTGAG	1507	Qy
480	GlnLeuCysAlaArgTyrPheCysGlyValProSerProLeuArgAspMetPheProVal	461	ф
1506	AGCTGTGTGCCCGGGTACTTCTGCGGGGGTCCCCCAGCCCCCTCAGGGACATGTTTTCCCGTG	1447	Qy
460		441	Db
1446	CGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACTCCACCACCTAC	1387	Qy
440	lValCysserSerGluGlyArgGlyGluGlu	421	Дb
1386	ACATGGCCCCCTCCATGGTTACGTCAGTCGTGTGCAGCTCTGAGGGCAGAGGGGAGGA	1327	Qy
420	oGlyLeuLeuValIleAspCysAlaSerLeuGluIleCysArgArgLeuGluPro	401	ДĎ
1326	GGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCTGGAGATCTGCAGGCGGCTGGAGCCC	1267	Qy
400	ProTyrProValLysAlaMetGluValValAsnSerGlySerGluValTrpTyrSerAsn	381	Db <sup>"</sup>
1266	CCTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTACAGCAA	1207	Qy
380	CysSerHisThralaAsnArgSerLysPheSerIleAlaAspGluAspAlaArgGlnAsn	361	DЬ
1206	GCTCACACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATGAAGACGCACGGCAGAAC	1147	Qγ
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PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 145
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 59
LENGTH: 706
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FILE REFERENCE: PS726PCI
CURRENT APPLICATION NUMBER: PCT/US01/01435
CURRENT FILING DATE: 2001-01-17
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CURRENT APPLICATION NUMBER: PCT/USO1/11988
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
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Sequence 1621, Application US/09833245
(GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION UNMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
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PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN Ver. 2.1
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GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS
FILE REFERENCE: SCH-1811
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn
SEQ ID NO 6
LENGTH: 1987
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CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
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TYPE: PRT
ORGANISM:
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                                                                                                                 FILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 2013
                                                                                                                                                                                                  Sequence 2, Application GENERAL INFORMATION:
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TITLE OF INVENTION: MEMBR
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TYPE: PRT
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Matches:
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	360 1445	301 AAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTA 	Qy Db
	300 1425	241 TACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTG	Qy Db
	240	181 GAGAACGCCAGAGATTCTTCCTTTATACCCCTGGGACACATGCTCACCCAAAAAATAGCC 	D Q
	180 1385	121 CACCCGCTCTGCTTCGCCCTGGAGCTCGCGCCGCTCAGCAGCCTCAACACCCGTGCTGTCC	당 왕
	120 1365	61 GCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATC	B &
	60 1345	1 ATGCTGAGGCACCTGCGGGCCACCGATGCCATGAAGAACTTCTCCGAGTTCCGGCAGGAG 	D Qy

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	BGGCTTTGCACTCGCAAGAGA 2181	_	Ş
2006	GlyTrpGlyAlaArgGluPheAspIlePheTyrGlnSerTyrGluGluLeuGlyArgLeu	1987	ф
2160	GCTGGGGCGCCAGGGAGTTCGACATTTTCTACCAGTCCTACGAGGAGCTGGGCCGGCT	2101	γQ
1986	AspThrValValCysThrPheGluAsnGluAsnThrGluTrpCysLeuAlaValTrpArg	1967	. pb
2100	ACACTGTTGTGTGCACCTTTGAAAATGAAAACACAGAGTGGTGCCTGGCCGTCTGGA	2041	Qy
1966	LeuLysAlaArgGluLeuThrProHisGlyValLeuValAspAlaAlaValValAlaLys	1947	ДD
2040	TAAAAGCCCGAGAGCTGACTCCGCATGGGGTGCTGGTGGATGCTGCCGTGGTGGCAAA	1981	. Qy
1946	lava	1927	Db
1980	TTATCGTCATTGGCCTGGAGAAGGATTCTGAAGCCCAGCGGGGCCGAGTCATTGCC	1921	Qy
1926	ValLysIleLeuAlaValArgAspLeuIleTrpValProArgArgGlyGlyAs	1907	Db
1920	AGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCCCAGGCG	1861	Qy
1906	rGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLe	1887	Db
1860	CCGACAGGTCTGAGCATGACCTGACCCCCATGGACGGGG	1801	Qy
1886	alProPheSerThrAspCysGluAspSerAspMetLeuHisThrProGlyAlaAl	1867	ф
1800	GTGTGCCTTTCTCCACCGACTGCGAGGACTCAC	1741	Qy
1866	ProProArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSer	1847	Db
1740	CACCCCCCAGCCAGCTGCCAGGTCCCCCCTCAAGCCTCCCCAGCTCCCCAGCAAGTTCTTC	1681	Qy
1846	GluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSe	89	da
1680	TCCTGATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCT		Qy
1826	ProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGln	1807	Db
1620	CTGAGGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCAG	1561	Qy
1806	roLysVal		Db
1560	CCGTGCGCCCTTGGACACGGAACCCCCGGCAGCCAGCCACACGGCCAAACCCAAAGGTG	1501	· Qy
1786	ThrTyrGlnLeuCysAlaArgTyrPheCysGlyValProSerProLeuArgAspMetPhe	1767	DЬ
1500	CCTACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCAGCCCCCTCAGGGACATGTTT	4	γо
1766	GluGluValValTrpCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr	1747	фa
1440	AGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACTCCACC	1381	γQ
1746	GluProTyrMetAlaproSerMetValThrSerValValCysSerSerGluGlyArgGly	1727	DЬ
1380	AGCCCTACATGGCCCCCTCCATGGTTACGTCAGTCGTGTGCAGGCTCTGAGGGCAGAGGG	1321	VΩ
1726		1707	dg.
1320	GCAATGGGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCTGGAGATCTGCAGGCGGCTG	1261	οy
1706	GlnAsnProTyrProValLysAlaMetGluValValAsnSerGlySerGluValTrpTyr	1687	Db
1260	GAACCCCTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTAC	1201	Qy
1686		1667	Db
1200	CCTGTGCTCACACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATGAAGACGCACGG		Qy
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1140	CCGATGGGCTTGTGGCTGTTTTCCCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTCC	1081	Qy

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-382-8
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CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 2014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS
FILE REFERENCE: SCH-1811
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                                                CACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGCAGCCG
                                                                              CCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGAGAGAAGGTAGATATG
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                                      HisGlnLeuGlnIleAlaLysLysLeuSerLysGlyIleArgProValLeuGlyGlnPro
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                                                                                                                      ProGlyTyrGlnAlaProGluIleArgProArgIleValTyrAspGluLysValAspMet
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		CCGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCACGCCACACGGCCAACGCT 	ACCTACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCAGCCCCCTCAGGGACATGTTT 1	GAGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACTCCACC 1 	GAGCCCTACATGGCCCCCCCCATGGTTACGTCAGTCGTGTGCAGCTCTGAGGGCAGAGGG 1	AGCAATGGGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCTGGAGATCTGCAGGCGGCTG 1	CAGAACCCCTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTAC 1	TACCTGTGCTCACACACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATGAAGACGCACGG 1	GGCTGTGTTTCCCGTGGTGCGGGGGCACCCCAAAGGACAGCTGCTCC 	TGTTATTAAAAAGAATTCCTACCTGGTCTTAGCGGGGCCT 	CTCAAGGGCATGTGCCCCTTAAACACACCCCAACAGGCCTTGGATACTCCAGCTGTCGTC 1	AGATCCCTGTGGACAGCCACCGAGGACCAGAAAATCTACATCTACACCC 	GAGAAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAGCTGCCAG	TACACCGTGGTGTTTTGGGATGGAAAAGAGGAGTCCAGGAACTACACGGTGGTGAACACA 8 	TTCATGTATGAACTGTGCTGTGGGAAGCAGACAGCCTTCTTCTCATCCCAGGGCCAGGAG 7	GAGAAGCGACCGCTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACC 7
1847	68 82	1560 1807 1620	L500 L787	1440 1767	1380 1747	1320 1727	1260 1707	1200 · 1687	1140 1667	1080 1647	1638	960	900	840 1606	780 1586	720 1566

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	SOFTWARE: Patentin Ver. 2.1
1653 961 1664 1021 1665 1081 1674 1141 1694	E: PatentIn Ver. 2.1  (b) 4  (c) 40  (c) 2040  (c) 2040  (c) 381: Homo sapiens  SSM: Homo sapiens  382-4  Scores:  1.96e-214
1653 961 1664 1021 1665 1081 1674	E: Patentin Ver. 2.1  (0 4) (1 2040) (2 2040) (2 2040) (2 2040) (3 2040) (3 2040) (4 2040) (5 2040) (5 2040) (5 2040) (5 2040) (5 2040) (5 2040) (6 2040) (6 2040) (6 2040) (6 2040) (6 2040) (6 2040) (6 2040) (7 2040) (8 2040) (8 2040) (8 2040) (8 2040) (8 2040) (8 2040) (8 2040) (8 2040) (8 2040) (8 2040) (8 2040) (9
1653 . 961 . 1664 1021 1665	EE: PatentIn Ver. 2.1 (b) 4 (c) 2040 PRT SM: Homo sapiens 382-4 382-4 382-4 382-4 382-4 3574.50 milarity: 94.50% h; 88.09% h; 25
1653 961 1664 1021	IE: PatentIn Ver. 2.1  IO 4  IO 4  II: 2040  PRT  SM: Homo sapiens  382-4  382-4  Scores: 1.96e-214 Length:
1653 961 1664	E: PatentIn Ver. 2.1 (0 4 (10 4 (10 7) (11 7) (12 7) (12 7) (13 7) (13 7) (14 7) (15 7) (15 7) (16 7) (17 7) (17 7) (18 7
1653	E: PatentIn Ver. 10 4 11: 2040 PRT SM: Homo sapiens 382-4 Scores:
Qy 901 CTCCAGGTCCAGAGATCCCTGTGGACAGCCACCGAGGACCAGAAAATCTACATCTACAC	SOFTWARE: PatentIn Ver. EQ ID NO 4 LENGTH: 2040
Qy 841 GAGAAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCTGGGATGAAGGTGAGCTGCCAG	CEC 10 2000 . 60
Qy 781 TACACCGTGGTGTTTTGGGATGGAAAAGAGGAGTCCAGGAACTACACGGTGGTGAACACAC 	R: US/10/132,382 2-04-26
Qy 721 TTCATGTATGAACTGTGCTGTGGGAAGCAGACAGCCTTCTTCTCATCCCAGGGCCAGGAG	PEGG
Qy 661 GAGAAGCGACCGCTGGCCCTGTCGGTGAGCCAGATGAAGGACCCGACTTTTGCCACC	Db 2008 GlualacysThrargLysarg 2014  RESULT 12 INC-10-132-382-4
Qy 601 GAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGACACTAAGCCA	Db 1988 GlyTrpGlyAlaArgGluPheAspIlePheTyrGlnSerTyrGluGluLeuGlyArgLeu 2007  Qy 2161 GAGGCTTGCACTCGCAAGAG 2181
Oy 541 CACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGCAGCCG	Db 1968 AspThValValCysThrPheGluAsnGluAsnThrGluTrpCysLeuAlaValTrpArg 1987  Qy 2101 GGCTGGGGCGCCAGGAGATTTCGACATTTTCTACCAGGAGGTCTACGAGAGCCGGCCG
Qy 481 TTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCTGCACTGGGCCAC	Db 1948 LeuLysAlaArgGluLeuThrProHisGlyValLeuValAspAlaAlaValValAlaLys 1967  Qy 2041 GACACTGTTGTGTGCACCTTTGAAATGAAAATGAAAGGGGTGCTTGGCTGGC
Qy 421 CCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTAGATATG	Oy 1981 TTAAAAGCCGAGAGCTGACTCCGCATGGGTGCTGGTGGATGCTGCCGTGGTGGCAAAG 2040
Qy 361 TCTGACTACGGGATTTCGAGGCAGTCATTCCATGAGGCGCCCCTAGGCGTGGAGGCACT	Db 1908 GİRAİAVƏLLYSTİELEUALAVALARYJASPLEUİLETIPVƏLPROARYGAYGİYĞİYASP 1927  OY 1921 GTTATCGTCATTGGCCTTGGAĞAAĞĞATTCTĞAAĞĞCCĞAĞĞĞĞĞĞĞĞĞĞ
Qy 301 AAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTA	Db 1888 SerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLeu 1907  Oy 1861 CAGGCCGTGAGAGATCCTCAGGACCTCATTTGGGTCCCCAGGCGGTGGAGAT 1920
Qy 241 TACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAAACATCATCTTCTGTGACCTG	Db 1868 SerValProPheSerThrAspCysGluAspSerAspMetLeuH1sThrProGlyAlaAla 1887  Qy 1801 TCCGACAGGTCTGAGCATGACCTGACCCCCATGGACGGGAGACCTTCAGCCAGC
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; APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACID.
FILE REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: PCT/US01/0
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
                                                                   Sequence 38410, Application GENERAL INFORMATION:
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; LOCATION: (1)...(809)
; OTHER INFORMATION: Xaa
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NUMBER OF SEQ ID N
SOFTWARE: Custom
SEQ ID NO 38410
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (223)...(261)
OTHER INFORMATION: Receptor tyrosine kinase clu
OTHER INFORMATION: by eMATRIX, accession number
OTHER INFORMATION: score of 11.56
NAME/KEY: DOMAIN
LOCATION: (103)...(372)
OTHER INFORMATION: Eukaryotic protein kinase du
OTHER INFORMATION: accession name pkinase, E-vu
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                                                                            TTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCCTGCACTGGGCCAC
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                                                              Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                            SOFTWARE: PatentIn
SEQ ID NO 982
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                                                                                                                                                                PRIOR FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 1052
                                                                                                                                                                                  CURRENT APPLICATION NUMBER: PCT/US02/05109
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 09/810,173
                                                                                                                                                                                                                 APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 21272-094-061
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ORGANISM: Homo
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Wang, Zhiwei
Ghosh, Malabika
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Zhang, Jie
Zhao, Qing A.
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Zhou, Ping
Goodrich, Ryle
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Ma, Yunging
Yamazaki, Victoria
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Wang, Dunrui
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; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: Isolated GPCR proteins,
; TITLE OF INVENTION: moelcules encoding GPCR;
; FILE REFERENCE: CL000095
; CURRENT APPLICATION NUMBER: US/60/155,811
; CURRENT FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 1060
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 774
                                                                 GENERAL INFORMATION:
                                                                        Sequence 774, Application
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                                      GluLysIleValCysGlyValPheGlnSerLeuValGlyMetGlyAspAspGluArgCys
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                                                                         TATGAACTGTGCTGTGGGAAG----CAGACAGCCTTCTTCTCATCCCAGGGCCCAGGAGTAC
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                                                                                                       SerIleLeuSerAlaProGluCysIleHisLeuLeuAspValValAlaMetProHisSer
                                                                                                                                         AGCCAGATGAAGGACCCGACTTTTGCCACCTTCATG---
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                                                                                                                                                                                                                                                                                                   SerLeuArgGlnProPheGluGlyHisGlu-----SerIleLysGluCysIleLeuGlu
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1315 CGG 921 Ser 1375 AGA 937 1435 TCC 1435 TCC 1495 ATG 1495 ATG 965 Leu	15 CG 21 Se 75 AG 37 35 TC 46 Se	15 CG 21 Se 75 AG 37	15 C 21 S		1285 901 Val	1237 AACAG ::::: 881 SerAs	1216 861 AlaLe	1195 841 Glu	1156 AC <i>I</i> 821 Phe	1123 CCA 801 Met	1063 CTG 783 Arg	1003 GAT     765 Asp	943 AAAAT :: 747 AsnLe	7 3 3 - 2	707 Pro	S	844 AAG	667 Gly
	TTTCCCGTG    ::: ArqProIleSerValPhe	ACCACCTACCAGCTGTGTGCCCGGTI	100	CTGGAGCCCTACATGGCCCCCTCCATG    ::: LeuGlnSerIleAlaIleAspGluHis	IleSerLysArgIleGluAsnLys	CGGCTCTGAGGTC :         nGluSerHisVal	1LeuCysH1sSerGluGluProAsnLeuIleGluAs	GCACGGCAGAACCCCTACCCA :::     :::	CAGCCAACAGGTCCAAGTTCAGCATCGCGGGATG     :::  heValleuHisalaAlaCysSerValValValA	CCAAAGGACAGCTGCTCCTAC :::   ::::: MetProSerAsnCysAlaPheAlaGluGlyS	GTCTTAGCGGGCCTCGCCGATGGGCTTG     :::    ValalaValGlyThrHisasnGly	ACTCCAGCTGTCGTCACCTGCTTCTTGGCC      ProAsnIleLysSerAlaValIleSer	CTACATCTACACCCTCAAGGGCATG ::::    ::: uHisAlaTyrSerThrSerThrTy	IGAAGGTGAGCTGCCAGGTCCAGAG    ;;             etasnmetLeuCysCysCysLeuValGlyGl	LysThrProGluAsnGlyAlaAsnS	ySerLeuLeuGlnCysAsnSerIleS	GGCCTCATGGAGGTGCAGAGGATGT	${ t GlyLeuGluLeuTrpLeuProSerPheGlyS}$
GINILESERALALEUALAALAHIAEASHISASH GCCCGGTACTTCTGGGGGGTCCCCAGCCCCTCAGGGAC ::	:::::      ESETALALEUALAALAHISA 	GlnIleSerAlaLeuAlaAlaHisAs	ACAAGGCCAACTCCTTGGTGATGTACCA	GTTACGTCAGTCGTGTGCAGCTCTGAGGGC          ValasnLeuIleLysCys	ATCGACTGTGCCTCCCTGGAGATCTGCAGG :::       ::: LeuAspCysSerLysLeuLeuProCysSerGlu	TGGTACAGCAATGGGCCGGGCCTCCTTGTC	GTGAAGGCCATGGAGGTGGTC         ::   GluAspValLysValAlaArgMetCys	euAsnG	TGAAGAC ::: lAspGlyIleTyrGluLeu	erPheValLeuThr	376GCTGTGTTTCCCGTGGTGCGGGGCACC         ArgValPheLeuValAspAlaThrGln	GCCGTGCCTGTTATTAAAAAGAATTCCTAC :::::: SerLeuValTyrMetGluLysIleAla	3TGCCCCTTAAACACACCCCAACAGGCCTTG         	AGATCCCTGTGGACAGCCACCGAGGACCAG :::::    31uAlaIleTrpMetGlyAspValSerGly	gAlaArgSerAlaG	erCysSerProGlnProGlnValAlaPr	– ຄ	${\tt erPheGlySerArgIleAspIleLeuAspCysSerPro}$
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Search completed: April 15, 2003, 07:21:42 Job time: 227 secs

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Maximum Match 100%
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-DB-Pending_Patents_AA_New -OFMT-fastan -SUFFIX-n2p.rapn -MINMATCH-0.1
-LOOPCL-0 -LOOPEXT-0 -CNITS-bits -START-1 -END--1 -MATRIX-blosum62
-TRANS-human40.cd1 -LIST-45 -DOCALLIGN-200 -THR_SCORE-pct -THR_MAX-100
-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTPMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-200000000 -USER-US09836392_@CGN_1_1_59_@runat_08042003_090330_22891
-MCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG
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/cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
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US-10-094-749-1689
US-09-949-016-7789
US-09-949-016-6222
US-10-263-929-188
US-10-363-929-1927
US-10-363-929-192-10-363-929-192-10-363-929-192-10-363-928-56
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US-60-426-964-2
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Sequence 1689, Ap
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	equence 12, App equence 12, App equence 13, App

## ALIGNMENTS

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PCT-US03-01363-170 ; Sequence 170, Application PC/TUS0301363
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; FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: LG:337452.25.orf3:2002JAN18
PCT-US03-01363-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: INCYTE GENOMICS, INC.; JONES, Anissa L.
APPLICANT: DAHL, Christopher R.; GIETZEN, Darryl;
APPLICANT: CHINN, Joyce; DUFOUR, GETATA E.;
"" Timmy Y.;
                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
SEQ ID NO 170
LENGTH: 659
                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/349,413 PRIOR FILING DATE: 2002-01-17
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/349,946 PRIOR FILING DATE: 2002-01-17
                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
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ITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
ILE REFERENCE: PT-1240 PCT
                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US03/01363 FILING DATE: 2003-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHEN, Alice; MARWAHA, Rakesh;
LAN, Ruth Y.; URASHKA, Michael;
R., KRISTNAM, Sreenivasa R.; KOLLURU, Vijaykumar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TUASON, Olivia; YAP, Pletre E.;
AMSHEY, Stefan R.; DAM, Tam C.;
LIU, Tommy F.; GERSTIN Jr., Edward H.;
PERALTA, Careyna H.; LEWIS, Samantha A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JACKSON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jennifer L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YU, Jimmy Y.;
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Best Local Similarity:
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                                                                                                                  TTTGCCACCTTCATGTATGAACTGTGCTGTGGGAAGCAGACAGCCTTCTTCTCATCCCAG
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Indels:
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Matches:
Conservative:
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	643	ValCys	641	Ωb	
	2091	GTGGCAAAGGACACTGTTGTGTGCACCTTTGAAAATGAAAACACAGAGTGGTGCCTGGCC	2032	Qy	
	640	leAlaValLeuLysAlaArgGluLeuThrProHisGlyIleMetProValSerSer	621	ф	
	2031	TGCTG	1972	Qy	
•	620	GlyGlyAspValIleValIleGlyLeuGluLysAspSerGluAlaGlnArgGlyArgVal	601	₽	
	1971	GTGGAGATGTTATCGTCATTGGCCTGGAGAAGGATTCTGAAGCCCAGCGGGGCCGAGT	1912	Qy	
•	600	GlnHisLeuGlnAlaValLysIleLeuAlaValArgAspLeuIleTrpValProArgArg	581	ДĎ	
	1911	CIGCAGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCCAGGC	52	Qy	
	580	GlyAlaAlaSerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSer	561	밁	
	1851	GTGCTGCCTCCGACAGGTCTGAGCATGACCTGACCCCCATGGACGGGGAGACCTTCAG	1792	Qy	
	560	SerSerSerValProPheSerThrAspCysGluAspSerAspMetLeuHisMetPro	541	DЬ	
	1791	PCCAGTGTGCCTTTCTCCACCGACTGCGAGGACTCAGACATGCTACATACGC	32	Qy	
	540	SerSerProProArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAla	521	Db	
	1731	CCTCATCCCCACCCGCCAGGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTCCCCAGC	1672	Qy	
	520	GlyThrGlnIleLeuIleHisGlnGluSerLeuThrAspTyrCysSerMetSerSerTyr	501	ф	
	1671	GCACGCAGATCCTGATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCTA	1612	Qy	
	500	ProLysValProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeu	481	ф	
	1611	CAAAGGTGCCTGAGGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAC	1552	Qy	
	480	AspMetPheProValArgProLeuAspThrGluProProAlaAlaSerHisThrAlaAsn	461	ф	
	1551	ACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCAGC		Qy	
	460	HisSerThrThrTyrGlnLeuCysAlaArgTyrPheCysGlyValProSerProLeuArg	441	Ф	
	1491	ACTCCACCACCTACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCAGCCCCCTCAG	w	Qy	
	440	GlyArgGlyGluGluValValTrpCysLeuAspAspLysAlaAsnSerLeuValMetTyr	421	Db	
	1431	GCAGAGGGGAGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATG	1372	Qy	
	420	ArgArgLeuGluProTyrMetAlaProSerMetValThrSerValValCysSerSerGlu	401	밁	
	1371	GGCGGCTGGAGCCCTACATGGCCCCCTCCATGGTTACGTCAGTCGTGTGCAGCTCTG	1312	Qy	
	400	ValTrpTyrSerAsnGlyProGlyLeuLeuValIleAspCysAlaSerLeuGluIleCys	381	рb	
•	1311	TGGTACAGCAATGGGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCTGGAGATCTG	1252	Qy	
	380	AspAlaArgGlnAsnProTyrProValLysAlaMetGluValValAsnSerGlySerGlu	361	밁	
	1251	acigcacegcagaacccctacccagtgaaggccatggaggtggtcaacagcggctctc	1192	Qy	
	σ	SerCysSerTyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGlu	341	<del>g</del>	
	1191	GCTGCTCCTACCTGTGCTCACACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATG	1132	Qy	
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SOFTWARE: PatentIn Ver. 2.1
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TYPE: PRT
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PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
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PPLICANT: MASCHO, YASUHIKO
ITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
ILE REFERENCE: 084335/0160
URRENT APPLICATION NUMBER: US/10/094,749
URRENT FILING DATE: 2002-03-12
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	328 CTTGAGGTCAAGGACCATCAACCTATCCAAGCTATCCGACTACGGATTTCGAGGCAGTCA	166 AACACCGTGCTGTCCGAGAACGCCAGAGATTCTTCTTATACCCCTGGGACACATGCTC :::       :::	Scores:  1.23e-08  A4.00  Matches:  34.00  Matches:  195  34.09  Conservative: 75  Similarity: 24.62  A.62  Mismatches: 241  Mismatches: 241  Mismatches: 241  Mismatches: 241  Mismatches: 241  Mismatches: 241  Mismatches: 283  38  392-8_COPY_22_2205 (1-2184) x US-09-949-016-7789 (1-885)  CGGCAGGAGGCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGGCCTCATCGGC  [	APPLICATION NUMBER: US/09/949.016 PILICATION NUMBER: 60/241.755— ILING DATE: 2000-04-14 IPPLICATION NUMBER: 60/241.755— ILING DATE: 2000-10-20 PPLICATION NUMBER: 60/237,768 ILING DATE: 2000-10-03 PPLICATION NUMBER: 60/237,768 ILING DATE: 2000-0-06 OF SEQ ID NOS: 207012 E: FastSED for Windows Version 4.0 OF 7789 SCOTES: SM: Human O16-7789 SCOTES:  1.23e-08 Length: 285 Milarity: 34.09% CONSERVATIVE: 75 SM: Human O16-7789 SCOTES: SIMILARITY: 34.09% SIMILARITY: 34.09% SIMILARITY: 34.09% SIMILARITY: 34.09% SIMILARITY: 34.09% SIMILARITY: 34.09% SIMILARITY: 34.09% SIMILARITY: 34.09% SIMILARITY: 34.09% SIMILARITY: 34.09% SIMILARITY: 34.09% SCOTES: SIMILARITY: 34.09% SIMILARITY:

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1105	055 ATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTTGTGGCTGTTTTC	Qy 10	
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604	594 SerAsnGlyGluArgAlaCysTrpAlaTrp	Db 5	
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818	92 GTTTTGGGATGGAAAAGAGGAGT	Qy 7	
433		Db 4	
791	33 CTGTG-CTGTGGGAAGCAGACAGCCTTCTTCTCAT	. Qy 7	
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404	389PheAlaGlnLeuMetAlaAspCysTrpAlaGlnAspProHisArgArg	Db 3	
672	13 TTCCGGCGA	Оу б	
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                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                              TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                          APPLICANT: VENTER, J. Craig et al.
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                                                                                                                                   LeuGluAlaLeuGluAlaGlnValLeuArgGluMetProArgAspSerPheHisSerMet 395
                                                                                                                                                                                                                                                      CTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACCTTCATGTATGAA 732
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lGlmalaSerProGlyLeuAspAr	LeuAspPheLys	496	DЬ
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	GlyThrPheLysArgSerLysLe	476	B 5
lAspArgGluArgProHisValArgArgArg	GluLeuThrLeuLeuLeuGlnGlnV	ı U	, <sub>,</sub> B
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52 CGGC	ignment Scores: ed. No.: 337.5 ore: 34.09 st Local Similarity: 24.62 ery Match: 8.328	ESULT.5  S-10-263-929-188  Sequence 188, Application U GENERAL INFORMATION: APPLICANT: Kim, Jaeseob APPLICANT: Galant, Ron TITLE OF INVENTION: Alzhei FILE REFERENCE: LSD-07417 CURRENT APPLICATION UNMEER CURRENT FILING DATE: 2002 UNMEER OF SEQ ID NOS: 213 SOFTWARE: Patentin version SEQ ID NO 188 LENGTH: 847 TYPE: PRT ORGANISM: Homo Sapiens S-10-263-929-188	Qy 1883 TCAGAGACCTCATTTGGGTCCCCAGGCGCGGTG	1826 CCCCATGGACGG	1766 AGGACTC	1706 CCTCAAGCC	1646 781	1586 T 775 -	1538760 ProLeuGlyLe
GCACGCGCTGCAGCACCCCTGCATCGTG	Length: 847 Matches: 195 Conservative: 75 Mismatches: 241 Indels: 283 Gaps: 38	S/10263929 mer's Disease Linked Genes :: US/10/263,929 -10-03	CCCCAGGCGCGGTGG 1916              AlaGlnAlaProTrp 841	<pre>GGAGACCTTCAGCCAGCACCTGCAGGCCGTGAAGATCCTCGCCG  </pre>	AGACATGCTACATACGCCCGGTGCTGCCTCCGACAGGTCTGAGCATGACCTGA	TCCCCAGCTCCCCAGCAAGTTCTTCCAGTGTGCCTTTCTCCACCGACTGCG          ::::: 	CTGACTACTGCTCCATGTCCTCCTACTCCTCATCCCCACCCCGCCAGGCTGCCAGGTCCC :::	GAGCATCATGTACAGTGAGGAGCTGGGCACGCAGATCCTGATCCACCAGGAATCACTCA	ACCCAAAGGTGCCTG
	,		) <sup>"</sup>	GATCCTCGCCG     	GCATGACCTGA	CACCGACTGCG    ::: roAspSerAsp	TGCCAGGTCCC	GGAATCACTCA	AGGGGGACTCCATCGCGGACG     :::       ::: ArgProSerProLeuArgSer
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1054	1010 CAGCTGTCGTCACCTGCTTCTTGGCCGTGCCTGTTATTAAAAAGA	
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566	S56 SerAsnGlvGluArgArgAlaCvs	B 2
55	36 GluProAlaGluProGlyGlnAlaTrpGlyArgGlnSerProArgArgLeuGluAspSe	Db
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896	879 TGGGATGAAGGTGAGCTG	Q
495	   AlaArgAspGlyGlyGluArgIleSerMetPr	B
878	-GGAGGTGCAGAGGATGTGCTGC	Qy
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455	:::    436 GluGlnLeuArgArgArgGluH1sLeuLeuAlaGlnTrpGluLeuGluValPheGluArg	망
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435	416 GluLeuLeuSerArgGluGluGluLeuThrArgAlaAlaArgGluGlnArgSerGlnAla	Дb
818	818	Qy
415	GluLeuArgAlaLys	멍
818	792 GTTTTGGGAAAAAAGAGGAGTCCAG	Qy
395	376 LeuGluAlaCeuGluAlaGlnValLeuArgGluMetProArgAspSerPheHisSerMet	ф
791	-CTGTGGGAAGCAGACAGCCTTCTTCTCATCCCAGGGCCCAGGAGTA	γQ
375	367ProAspPheAlaSerIleLeuGlnGln	뭥
732	CCGACTTTTGCCACCTTCATGTATG	γQ
366	351PheAlaGlnLeuMetAlaAspCysTrpAlaGlnAspProHisArgArg	문
672	gagtgctgggacactaagccagaga <i>a</i>	Qy
350	335 AlaValAsnLysLeuThrLeuProIleProSerThrCysProGluPro	Db
612	GAA	QY ,
334	γlο	망
558		γQ
314	295 LysAlaSerThrPheSerLysGlySerAspValTrpSerPheGlyValLeuLeuTrpGlu	B
507	္မင္က	γQ
294	275 HisLysThrThrGlnMetSerAlaAlaGlyThrTyrAlaTrpMetAlaProGluValIle	<b>D</b>
447	SCACTCCTGGCTACCAGGCCCCAGAGAT	Qy
274	255 SerAspAspMetGluHisLysThrLeuLysIleThrAspPheGlyLeuAlaArgGluTrp	뭣
387	ACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCA	QΥ
254	::	Db
327	TGTGACCTGAAGTCGGACA	Qy

RESULT 6 US-10-348-119-327

Qy 559AAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGCAGCCAGGAGGAAGTGCAAG 612       :::       :::       :::       335 AlaValAsnLySLeuThrLeuProlleProSerThrCysProGluPro 350	TSERALAALAGIYTHTTYRALATIPMELA TGARGAAGGTAGATATGTTCTCCTATGGAA :::         : : : :       : : :	Oy 280ACATCATCTTCTGTGACCTGAAGACATTCTGGTGTGGG	166 AACACCGTGCTGTCCGAGAACGCCAGAGATTCTTCTTTATACCCCTGGGACACATGCTC :::    :::     202 SerArgAlaLeuAlaGlyArgArg	AGGAGGCCAGCATGC	2-08 Length: 847 50 Matches: 195 38 Conservative: 75 28 Mismatches: 241 Indels: 283 Gaps: 38	
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656 GlyLeuGlyArgAspLeuGlnProProGlyGlyProGlyArgGluArgGlyGluSerPro 675 289 ACTGTGCCTCCTGGAGATCTGCAGGCGGCTGGAGCCCTACATGGCCCCTCCATGGTTA 1348	ACAGGTCCAAGTTCAGCATCGCGATGAAGACGCACGGCAGAACCCCTACCCAGTGAAGG  LII	567 GlyProSerSerProLysProGlyGluAlaGlnAsnGlyArgArgArgSerArgMetAsp 586  1055 ATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTTGTGGCTGTGTTTC 1105	GluProalaGluProGlyGlnAlaTrpGlyArgGlnSarProArgArgLeuGluAspSer ACATCTACACCCTCAAGGGCATGTGCCCCTTAAACACACCCCCAACAGGCCTTGGATACTC ::::::	879 TGGGATGAAGGTGAGCTG	840 854 456 GluLeuThrLeuLeuGlnGlnValAspArg6GluArgProHisValArgArgArgArg 475 855GGAGGTGCAGAGGATCTGCCC 878 476 GlyThrPheLysArgSerLysLeuArgAlaArgAspGlyGlyGluArgIleSerMetPro 495	673 CTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACCTTCATGTATGAA 732  11

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52 CGGCAGGAGGCCAGCATGCACGCGCGCGCACCCCTGCATCGTGGCGCCTCATCGGC 111	6-392-8_COPY_22_2205 (1-2184) x US-10-263-929-192 (1-850)	8.24% Indels: 6 Gaps:	larity: 35,928 imilarity: 25.198	Length:	-929-192	TYPE: PRT ORGANIAN: MUS musculus	PatentIn ver	ENT APPLICATION INTERPORT SECURITY OF SECU	NVENTION:	APPLICANT: Kim, Jaeseob APPLICANT: Galant, Ron	Sequence 192, Application US/10263929 GENERAL INFORMATION:	ULT 7 10-263-929-192	830 aGlnThrLysAspMetGlyAlaGlnAlaProTrp 841	.883 TCAGAGACCTCATTTGGGTCCCCAGGCGCGGTGG 1916	B25 CCCCCATGGACGGGAACCT::CAGCAGCACGGGGGGGGGGGGGAGATCCTGGGG 1882 		AGGACTCAGACATGCTACATACGCCCGGTGCTGCCTCCGACAGGTCTGAGCATGACCTGA	795GlnProAlaProArgArgAlaProTrpThfLeuPheProAspSerAsp 810	PheValSerAla	1646 CTGACTACTCCATGTCCTCCTACTCCTCATCCCCACCCGCCAGGCTGCCAGGTCCC 1705	:::      ArgIleAspProTrpSer	/ou_richenerixhentieserwidrio			CCAGCCCCCTCAGGGACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCA 1	418 CCTTGGTGATGTACCACCTCCACCACCTACCAGCTGTGCCCGGTACTTCTGCGGGGGTCC 1477		1379	694 ProLeuIleCysPheSerLeuLysThrProAspSerProProThrProAlaProLeuLeu 713
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Db 487 ArgAspGly 489	1068 CTTAGCGGGCCTCGCCGATGGGCTTGTGGCTGTGTTTCCCGTGGTGCGGGGCACCCCCAAA	Qy 1017CGTCACCTGCTTCTTGGCCGTGCCTGTTATTAAAAAGAATTCCTACCTGGT 1067	AlaGinTrpGluLeuGluValPheGluArgAspValThrLeuLeuGeuGlnGlnValAsp	Qy 960 CCTCAAGGGCATGTGCCCCTTAAACACACCCCCAACAGGCCTTGGATACTCCAGCTGT 1016	ArgalahlaargGluGlnArgSerGlnAlaGluGlnLeuArgArgArgGluHisLeuLeu	41b	840 AGAGAAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAGCTGCCA	397 GlnGluGlyTrpLysArgGluIleGlnGlyLeuPheAspGluLeuArgAlaLysGlu	792 GTTTTGGGATGGAAAAGAGGAGTCCAGGAACTACACGGTGGTGAACAC		733 CTGTG-CTGTGGGAAGCAGACAGCCTTCTTCTCATCCCAGGGCCAGGAGTACACCGTGGT	QY 6/3 CTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCGACTTTTGCCACCTTCATGTATGAA /3z	352PheAlaGinLeuMetAlaAspCysTrpAlaGlnAspProHisArgArg	613 TTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGACACTAAGCCAAGAGAAGCGACCG	AlaValAsnLysLeuThrLeuProIleProSerThrCysProGluPro	Qy 559AAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGCAGCCGGAGGAAGTGCAG 612	QY 508 TTGCTGTCAGGACAGCGCCCTGCACTGGGCCACCACCAGCTCCAGATTGCC 558	296 LysalaSerThrPheSerLysGlySerAspValTrpSerPheGlyValLeuLeuTrpGlu		QY 300 TECCATGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	256 GlyAspAspMetGluHisLysThrLeuLysIleThrAspPheGlyLeuAlaArgGluTrp	Qy 331GACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTTCGAGGCAGTCA 387	QY 280ARCATCATCTTCTGTGACCTGAAGTCTGGACAACATTCTGGTGGTCCCTT 30 :::                  :::         ::: Db 236 ValProValIleHisArgAspLeuLysSerAsnAsnIleLeuLeuLeuGlnProIleGlu 255	217 ValAsnTrpAlaValGlnIIeAlaArgGlyMetHisTyrLeuHisCysGluAlaLeu	QY 226 ACCCAAAAATAGCCTACCAGATCGCCTCGGGCCTGGGCCTACCTGCACAAGAAA 279	::         ::		112	100 113901100011001100110010000000000000

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SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 656
TYPE: PRT
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                                                                                                               ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 1242491CD1
US-10-311-034-5
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                 Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                                                                RIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,3
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REFERENCE: PI-0125 PCT
ENT APPLICATION NUMBER: US/10/311,034
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OVTZU, Chandra S
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ATGTGCCCCTTAAACACACCCCCAACAGGCCTTGGATACTCCAGCTGTCGTCACCTGCTTC
                             GluSerTrpIleValSerGlyThrGlnSerGlyThrLeuLeuValIleAsnThrGluAsp
                                                           TCCCTGTGG-----ACAGCCACCGAGGACCAGAAAATCTACATCTACACCCTCAAGGGC
                                                                                                                                                     AspArgGlyGlnLeuSerPheLeuAspLeuAsnThrGluGlyTyrThrSerGluGluVal
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                                                                                                                                                                                                                                                   TTCTTCTCATCCCAGGGCCAGGAGTACACCGTGGTGTTTTGGGATGGA-------
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CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: PCT/US00/28066
PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: 60/159,542
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/165,914
PRIOR APPLICATION NUMBER: 60/165,914
PRIOR FILING DATE: 1999-11-17
PRIOR FILING DATE: 1999-13-14
PRIOR FILING DATE: 3000-03-14
NUMBER OF SEQ ID NOS: 34
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LENGTH: 728
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Sequence 82, Application PC/TUS0101435
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 21 human secreted protei
FILE REFERENCE: PS726PCT
CURRENT APPLICATION NUMBER: PCT/US01/01435
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/226, 282
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEO ID NOS: 145
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TYPE: PRT
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PRIOR FILING DATE: 2000-04-12
PRIOR PPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1620
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 1620
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
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GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-01-12
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                                                                                                                                                                                                                         GGGCTTGTGGCTGTTTCCCGTGGTGCGGGGGCACCCCAAAGGACAGCTGCTCCTACCTG
                                                                                                                                                                                                                                                                                         GlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThrProAlaValValThrCys
                                                                                                                                                                                                                                                                                                 GGCATGTGCCCCTTAAACACACCCCCAACAGGCCTTGGATACTCCAGCTGTGGTCACCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ArgProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThrPheMet
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; LENGTH: 706
; TYPE: PRT
; ORGANISM: Homo s
US-09-833-245-1620
                                                                                                                CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: PATENTIN Ver 2.1
SEQ ID NO 1620
LENGTH: 706
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US-09-833-245-1620
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                                     Score:
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                                                                                                                                                                                                                                                           APPLICANT: Human Genome Sciences, Inc
TITLE OF INVENTION: Albumin Fusion Pro
FILE REFERENCE: PF546PCT
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            Similarity:
 8.79e-223
3707.00
100.00%
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91.35%
Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                            Query Match
Best Local Similarity
""" Anas 78; Conserve
                                                                                                                                                                                                             SOFTWARE: CuraSeqList version 0.1

SEQ ID NO 99

LENGTH: 256

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: INFORMATION: Description of Artifical Sequence:
US-10-087-684-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-10-087-684-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  URRENT APPLICATION NUMBER: US/10/087,684
URRENT FILING DATE: 2003-03-10
RIOR APPLICATION NUMBER: 60/253,834
RIOR FILING DATE: 2000-11-29
                     60 SENARDSSFIPLGHMLTQKIAYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIK 119
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89 RRNG-----LLLSEKEAKKIALQILRGLEYLHSRGIVHRDLKPENIL-----LDENGTVK 138
                                                                  29 IKILKKRSLSEKKKRFLREIQILRRLSHPNIVRLLGVFEEDDHLYLVMEYMEGGDLFDYL 88
                                                                                             APPLICATION NUMBER: 60/327,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/264,180 FILING DATE: 2001-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/313,656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/250,926 FILING DATE: 2000-11-30
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INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tchernev, Velizar T. Yernet, Corine A.M. Zerhusen, Bryan D. Malyankar, Uriel M. Guo, Xiaojia
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Stone, David J.
Grosse, William M.
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Millet, Isabelle
                                                                                                                                              Conservative
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                                                                                                                                       Score 271; DB 6; ]
Pred. No. 3.5e-13;
2; Mismatches 93;
                                                                                                                                                                         Length 256;
                                                                                                                                         Indels 28;
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Search completed: April 8, 2003, 10:33:52
Job time: 86 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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DB-Pending_Patents_A_Main -QFWT-fastan -SUFFIX-n2p.rapm -MINMATCH-0.1
LOOPCL-0 -LOOPEXT-0 -UNITS-bits -STARY-1 -END--1 -MATRIX-blosum62
TRANS-human40.cdi -LIST-45 -DCALIGN-200 -THR_SCORE-pct -THR_MAX-100
THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0
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score greater than or equal to the score and is derived by analysis of the total Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, score

# SUMMARIES

Result No.

esult No.	ö	Query Match	Length	DΒ	ID ·	r1pt	
, <u>-</u>	8 8	94.2	728		T-US00-28066-2	ce 21, App	
ມຄ	1 8	94.2	728	22	US-09-836-392-2	Sequence 21, Ap	
<b>.</b> u	20	91.4 91.4	706	<u>_</u>	2 2	e 82, App e 1620. A	
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o	70	Ľ	0		T-US01-01435-59	quence 59, Appl	
7	70	÷	0	, <u>,</u>	T-US01-11988-1	equence 1621, Ap	
· α	3 3	Ë	20	22	S-09-833-245-16	equence 1621,	
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	574.		04	25	-10-132-382-	equence 4, App	
	349.	2	0	-ب	T-US01-08631-38	equence 38410, A	
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	7 0		۵ د ۵ د	) r	S-00-614-150-114	equence 332, Ap	
	54		0	27	S-60-173-464-9298	298	
	64.		30	27	S-60-191-637-115	equence 11516,	
	64		30	27	S-60-191-681-9008	equence 900	
2 2 2	355. 55. 55.	ю ч ю с	26	27	-146-315-749 -146-315-749	nce 11502,	
	48.		2	27	S-60-213-178-79	equence 794,	
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	37.	٠	. 4	21	S-09-791-537-39	391,	
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	ω 5.	٠	$\mathbf{r}$	25	S-10-115-482-4	Sequence 48, A	
	27.	٠	8	27	S-60-139-671-197	equence 197, Ap	
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#### ALIGNMENTS

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Sequence 21, Application PC/TUS0028066
SEQUENCE 11, CENTRAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptide
TITLE OF INVENTION: Antibodies CURRENT APPLICATION NUMBER: PCT/US00/28066 CURRENT FILING DATE: 2000-10-12 PRIOR APPLICATION NUMBER: 60/159,542 PRIOR FILING DATE: 1999-10-15 PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-1 APPLICATION NUMBER: 60/165,914 60/189,027

2000-03-14

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; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 728
; TYPE: PRT
; ORGANISM: Homo sapiens
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# SUMMARIES

Result		Query			•	
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# ALIGNMENTS

RESULT 1 PCT-US00-28066-21

Query Match 100.0%; Score 3822; DB 1; Length 728; Best Local Similarity 100.0%; Pred. No. 0; Matches 728; Conservative 0; Mismatches 0; Indels 0	FILE REFERENCE: PT020PCT CURRENT APPLICATION NUMBER: PCT/US00/28066 CURRENT FILING DATE: 2000-10-12 PRIOR APPLICATION NUMBER: 60/159,542 PRIOR FILING DATE: 1999-10-15 PRIOR APPLICATION NUMBER: 60/165,914 PRIOR APPLICATION NUMBER: 60/189,027 PRIOR FILING DATE: 1999-11-17 PRIOR APPLICATION NUMBER: 60/189,027 PRIOR FILING DATE: 2000-03-14 NUMBER OF SEQ ID NOS: 34 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 21 LENGTH: 728 TYPE: PRT ORGANISM: Homo sapiens	Sequence 21, Application PC/TUS0028066 Sequence 21, Application PC/TUS0028066 GENERAL INFORMATION: APPLICANT: Human Genome Sciences, Inc TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptide TITLE OF INVENTION: Antibodies
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CURRENT APPLICATION NUMBER: US/09/836,392

CURRENT FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: PCT/US00/28066

PRIOR APPLICATION NUMBER: 60/159,542

PRIOR FILING DATE: 1999-10-15

PRIOR FILING DATE: 1999-11-17

PRIOR APPLICATION NUMBER: 60/165,914

PRIOR FILING DATE: 1999-11-17

PRIOR APPLICATION NUMBER: 60/189,027

PRIOR FILING DATE: 1999-11-17

PRIOR APPLICATION NUMBER: 60/189,027

PRIOR FILING DATE: 2000-03-14

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.0

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                                                                                                                                                                                                 Sequence 21, Application US/09836392 GENERAL INFORMATION: APPLICANT: Ruben et al.
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                                                                      Sequence 82, Application PC/TUS0101435
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, In
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Best Local Similarity 100.0%;
Matches 728; Conservative
TITLE OF INVENTION: 21 human secreted pro-
FILE REPERENCE: PS726PCT
CURRENT APPLICATION NUMBER: PCT/USO1/01435
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/226,282
PRIOR FILING DATE: 2000-08-18
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Pred. No. 0;
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RESULT 4

PCT-US01-11988-1620

PCT-US01-11988-1620, Application PC/TUS0111988

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

TITLE OF INVENTION: Albumin Fusion Proteins

FILE REFERENCE: PF546PCT

CURRENT APPLICATION NUMBER: PCT/US01/11988

CURRENT FILING DATE: 2001-01-12

PRIOR APPLICATION NUMBER: 60/229, 358

PRIOR FILING DATE: 2000-04-12

PRIOR APPLICATION NUMBER: 60/256, 931
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Matches 706;
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ENGTH: 706
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Pred. No. 1.1e-312;
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 Sequence 1620, Application US/09833245
GENERAL INFORMATION:
APPLICANY: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Proteins
FILE REFERENCE: PF546PCT
CURRENT APPLICATION NUMBER: US/09/833,245
CURRENT FILING DATE: 2001-04-12
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PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/19
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1620
LENGTH: 706
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Matches 706;
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VYCTFENENTEWCLAVWRGWGAREFDIFYQSYEELGRLEACTRKRR 728
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                                                                        VKILAVRDLIMVPRRGGDVIVIGLEKDSEAQRGRVIAVLKARELTPHGVLVDAAVVAKDT
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PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 38
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2367
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 1620
LENGTH: 706
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US-09-833-245-1620
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Best Local Similarity
Matches 706; Conserv
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TYPE: PRT
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FILING DATE: 2000-04-12
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                                         VYCTFENENTEWCLAVWRGWGAREFDIFYQSYEELGRLEACTRKRR 728
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Sequence 59, Application PC/TUS0101435 GENERAL INFORMATION: APPLICANT: Human Genome Sciences, Inc TITLE OF INVENTION: 21 human secretee

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RESULT 7 PCT-US01-11988-1621

Sequence 1621, Application PC/TUS0111988 GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Albumin Fusion Prot
FILE REFERENCE: PF546PCT

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Best Local Similarity 99.9%;
Matches 705; Conservative
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SEQ ID NO 59
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CURRENT APPLICATION NUMBER: PCT/US01/01435
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/226,282
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 145
COERTIAND DATE: 150
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TYPE: PRT
ORGANISM: Homo sapiens
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VVCTFENENTEWCLAVWRGWGAREFDIFYQSYEELGRLEACTRKRR
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                                               VKILAVRDLIWYPRRGGDVIVIGLEKDSGAQRGRVIAVLKARELTPHGVLVDAAVVAKDT
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Pred. No. 4.3e-312;
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FILE REFERENCE: PF546PCT

OF INVENTION: Albumin Fusion Proteins

Sciences,

APPLICANT: Human Genome

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PRIOR FILING DATE: 2000-04-12
PRIOR PELICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/199, 384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1621
LENGTH: 706
TYPE: PRT
ORGANISM: Homo saplens
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                                              VKILAVRDLIMVPRRGGDVIVIGLEKDSEAQRGRVIAVLKARELTPHGVLVDAAVVAKDT
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          VVCTFENENTEWCLAVWRGWGAREFDIFYQSYEELGRLEACTRKRR
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Pred. No. 4.3e-312;
D; Mismatches 1;
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PRIOR APPLICATION NUMBER: 60/229, 358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256, 931
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-12-21
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 2267
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SEQ ID NO 1621
LENGTH: 706
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                                             RPLDTEPPAASHTANPKVPEGDSIADVSIMYSEELGTQILIHQESLTDYCSMSSYSSSPP
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Pred. No. 4.3e-312;
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Best Local Similarity 94.5%;
Matches 687; Conservative
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TYPE: PRT
ORGANISM: Homo:
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CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTMARE: Patentin Ver. 2.1
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TITLE OF INVENTION: MEMBRANE RECEPTORS
FILE REFERENCE: SCH-1811
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NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
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CURRENT FILING DATE: 2002-04-26
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LENGTH: 2014
TYPE: PRT
ORGANISM: Homo:
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TITLE OF INVENTION: MEMBRANE RECEPTORS FOR
FILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILLING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2:1
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                                        LKARELTPHGVLVDAAVVAKDTVVCTFENENTEWCLAVWRGWGAREFDIFYQSYEELGRL
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                          LKARELTPHGVLVDAAVVAKDTVVCTFENENTEWCLAVWRGWGAREFDIFYQSYEELGRL
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GENERAL INFORMATION:
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CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
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                                                    SDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWVPRRGGDVIVIGLEKDSEAQRGRVIAV
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687; Conservative
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Pred. No. 5.1e
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; OTHER INFORMATION: Xaa - X or * as defined in Table 2
PCT-US01-08631-38410
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CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540, 217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 60736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Eukaryotic protein kinase domain identified by Pram, OTHER INFORMATION: accession name pkinase, E-value-1.8e-44, Pram score of 161.2
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LOCATION: (223).
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Local Similarity 93.3%;
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Pred. No. 1.9e-250;
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nber BL00240E, p-value=7.660e-10,
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PCT-US02-05109-982
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                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.7 Matches 319; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 982
LENGTH: 320
                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Movel Nucleic Acids and
FILE REFERENCE: 21272-094-061
CURRENT APPLICATION NUMBER: PCT/US02/05109
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 09/810,173
PRIOR FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                     469 DKANSLYMYHSTTYQLCARYFCGYPSPLRDMFPYRPLDTEPPAASHTANPKYPEGDSIAD
                                                                181
                                                                                             589
                                                                                                                            121
                                                                                                                                         529 VSIMYSEELGTQILIHQESLTDYCSMSSYSSSPPRQAARSPSSLPSSPASSSSVPFSTDC
                                                                                                                                                                                                                                                             409 MEVVNSGSEVWYSNGPGLLVIDCASLEICRRLEPYMAPSMYTSVVCSSEGRGEEVVWCLD 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    743 HTPGAASDRSEHDLTPMDGETFSQQL
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                                                                                                                                                                                                                                               1 MEVVNSGSEVWYSNGPGLLVIDCASLEICRRLEPYMAPSMVTSVVCSSEGRGEEVVWCLD
EDSDMLHTPGAASDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWVPRRGGDVIVIGLEK 648
                                                                                                                       VSIMYSEELGTQILIHQESLTDYCSMSSYSSSPPRQAARSPSSLPSSPASSSSYPFSTDC
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                                                                                                                                                                                     DKANSLYMYHSTTYQLCARYFCGVPSPLRDMFPVRPLDTEPPAASHTANPKVPEGDSIAD
                                                             EDSDMLHTPGAASDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWVPRRGGDVIVIGLEK
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Wang, Dunrui
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Ghosh, Malabika
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Asundi, Vinod
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Zhou, Ping
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Kamazaki, Victoria
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Pred. No. 1.7e-136;
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 774
LENGTH: 1050
TYPE: PRT
ORGANISM: Drosophila
US-60-155-811-774
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GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Isolated GPCR proteins, nucleic acid
TITLE OF INVENTION: moelcules encoding GPCRs and uses thereof
FILE REFERENCE: CL000095
CURRENT APPLICATION NUMBER: US/60/155,811
CURRENT FILING DATE: 1999-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 SGQRPALGHQLQIAKKLSKGIRPVLGQPEEVQFRR-LQALMMECWDTKPEKRPLALSVV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397 LQH-----SCKAYCTARQELAVLLTLKHPNIVPLVGICIKPLALVLELAPLGGLDALLRH 451
                                              965 LRPISVFRPYENEIKSIITLSKDNVP---LIATIGRRY-RSLISRYVDSAESST----KS
                                                                                                                                                                                      439 RLEPYMAPSMYTSVYCSSEGRGEEVYWCLDDKANSLYMYHSTTYOLCARYFCGVPSPLRD 498
                                                                                                                                                                                                                                                                                                                                   801 MPSNCAFAEGSFVLTEICSGFVLHAACSVVVDGIYELWCGEIAGKINVFPLNENGVSGHQ 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231 SQMKDPTFATFM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 570 SLRQPFEGHE--SIKECILEGSRPALTQ-RETQFPTCCLDLMVLCWHEQPRRRPTASQIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452 YRRSGAH--MGPHTFQTLVLQAARAIEYLHRRRIIYRDLKSENVLVWELPQPHTEDSPRN 509
556 SYSSSPPRQAARS 568
                                                                                        499 MFPV---RPLDTEPPAASHTANPKVPEGDSIADVSIMYSEELGTQILIHQESLTDYCSMS 555
                                                                                                                                            921 SLQSIAIDEHVNLIKC--
                                                                                                                                                                                                                                     861 ALCHSEEPHLIEDYKVARMCSNESHVFSCLYPGCMVYQWDVISKRIENKLDCSKLLPCSE
                                                                                                                                                                                                                                                                                                                                                                                                                               747 NLHAYSTSTYAHLFS--YMLD-PNIKSAVISLVYMEKIA-RVAVGTHNG--RVFLVDATO 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 KIYIYTLKGMCPLNTPQQALDTPAVVTCFLAVPVIKKNSYLVLAGLADGLVAVFPVVRGT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          687 SGSLLQCNSISCSPQPQVAPPKTPENGANSRARSAQRLPKMNMLCCCLVGEAIWMGDVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    627 SILSAPECIHLLDVVAMPHSEKIVCGVFQSLVGMGDDERCGLELWLPSFGSRIDILDCSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 510 LVHIKIADYGISRQTAPSGAKGFGGTEGFMAPEIIRYNGEEEYTEKVDCFSFGMFIYENI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 NARDSSFIPLGHMLTQKIAYQIASGLAYLHKKNIIFCDLKSDNILVWSL------DVKE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LRHLRATDAMKNFSEFRQEASMLHALQHPCIVALIGISIHPLCFALELAPLSSLNTVLSE 61
                                                                                                                                                                                                                                                                                  -VKAMEVVNSGSEVWYSNGPGLLV---
                                                                                                                                                                                                                                                                                                                                                                                --LCSHTANRSKFSIADED----
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                                                                                                                                            QISALAAHNSELY-IGTTWGCLIVAELHT
                                                                                                                                                                                                                                                                                                                                                                                -ARQNPYP-----
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Search completed: April 8, 2003, 10:32:30 Job time: 333 secs

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Minimum DB seq
Maximum DB seq
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein search, using sw model
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3822
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US01_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US01_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US01_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US01_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
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US-10-074-978A-151

US-10-072-012-807

US-10-087-684-99

US-10-087-684-99

US-10-361-942-51

US-10-74-978A-162

US-10-288-798-12

US-10-362-892-12

US-10-310-154-564

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US-10-130-32
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1187, App
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243	243	243.5	244	244	244.5	246.5	247.5	259.5	260	260	260	260	260	260.5	260.5	260.5	260.5	263
6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.5	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.8	6.9
800	455	505	938	938	823	765	922	850	663	610	610	511	511	885	847	847	847	1036
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US-60~438-000-64	US-10-094-749-2477	US-10-099-056-1344	US-09-724-676A-68429	US-09-724-676-68429	US-10-376-564-63	US-10-285-325-2	US-10-263-929-190	US-10-263-929-192	US-09-949-016-7198	US-60-452-680-19069	US-60-443-566-3046	US-09-724-676A-68428	US-09-724-67.6-68428	US-09-949-016-7789	US-10-348-119-327	US-10-263-929-188	US-09-949-016-6222	US-10-354-358-24
Sequence 64, Appl	Sequence 2477, Ap	Sequence 1344, Ap	Sequence 68429, A	Sequence 68429, A	Sequence 63, Appl	Sequence 2, Appl1	Sequence 190, App	Sequence 192, App	Sequence 7198, Ap		Sequence 3046, Ap	Sequence 68428, A	Sequence 68428, A	Sequence 7789, Ap	Sequence 327, App	Sequence 188, App	Sequence 6222, Ap	Sequence 24, Appl

# ALIGNMENTS

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; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: LG:337452.25.orf3:2002JAN18
PCT-US03-01363-170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: SOFTWARE: PERL Program SEQ ID NO 170 LENGTH: 659
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                 Matches 641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/349,946
PRIOR FILING DATE: 2002-01-17
PRIOR APPLICATION NUMBER: US 60/349,413
PRIOR FILING DATE: 2002-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PANESAR, Iqbal S.
TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT FILE REFERENCE: PT-1240 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01363
CURRENT FILING DATE: 2003-01-14
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APPLICANT
APPLICANT
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APPLICANT: DAHL, Christopher R.; GETZEE, Darryl;
APPLICANT: CHIMN, JOyce; DUFOUR, Gerard E.;
APPLICANT: JACKSON, Jennifer L.; YU, Jimmy Y.;
APPLICANT: TUASON, Olivia; YAP, Pierre E.;
APPLICANT: TOMMY F.; GERSTIN Jr., Edward H.;
APPLICANT: LIU, TOMMY F.; GERSTIN Jr., Edward H.;
APPLICANT: LIU, TOMMY F.; GERSTIN Jr., Edward H.;
APPLICANT: PERALTA, Careyna H.; LEWIS, Samantha A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT:
158 VDMFSYGMVLYELLSGQRPALGHHQLQIAKKLSKGIRPVLGQPEEVQFRRLQALMMECWD
                                                                                                                                                                                                     38 ISIHPLCFALELAPLSSLNTVLSENARDSSFIPLGHMLTQKIAYQIASGLAYLHKKNIIF 97
                                                                                                                                                                           1 ISIHPLCFALELAPLSSLNTVLSENARDSSFIPLGHMLTQKIAYQIASGLAYLHKKNIIF
                                                                                                        CDLKSDNILVWSLDVKEHINIKLSDYGISRQSFHEGALGVEGTPGYQAPEIRPRIVYDEK 157
                                                                              CDLKSDNILVWSLDVKEHINIKLSDYGISROSFHEGALGVEGTPGYQAPEIRPRIVYDEK
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94.8%;
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Pred. No. 8e-253;
6; Mismatches 9; Indels 2
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PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILLING DATE: 2002-01-24
PRIOR FILLING DATE: 2001-09-14
PRIOR FILLING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOSTWARE: Patentin Ver. 2.1
SEQ ID NO 1689
LENGTH: 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1689,
                                                                                                                CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
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                                                                                                                                       PPLICANT: MASUHO, YASUHIKO
TILE OF INVENTION: NOVEL FULL-LENGTH CDNA
TILE REFERENCE: 084335/0160
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WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
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IRIE, RYOTARO
TAMECHIKA, ICHIRO
                                                                                                                                                                                                 OTSUKA, MOTOYUKI
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YOSHIKAWA, TSUTOMU
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                                                                                                                                                                                     NAGAHARI, KENJI
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-1689
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Best Local Similarity
Matches 478; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MFSYGMYLYELLSGQRPALGHHQLQIAKKLSKGIRPYLGQPEEVQFRRLQALMMECWDTK
                                                                                                                                                                                                         GEEVVWCLDDKANSLVMYHSTTYQLCARYFCGVPSPLRDMFPVRPLDTEPPAASHTANPK 519
                                                                                                                                                                                                                                                                                                                                                                                                 VTCFLAVPVIKKNSYLVLAGLADGLVAVFPVVRGTPKDSCSYLCSHTANRSKFSIADEDA
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                                                                                                                                     VPEGDSIADVSIMYSEELGTQILIHQESLTDYCSMSSYSSSPPRQAARSPSSLPSSPASS
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SSVPFSTDCEDSDMLHTPGAASDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWVPRR 478
                                      SSVPFSTDCEDSDMLHTPGAASDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWVPRR 637
                                                                                         VPEGDSIADVSIMYSEELGTQILIHQESLTDYCSMSSYSSSPPRQAARSPSSLPSSPASS
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Pred. No. 1.5e-189;
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US-10-311-034-5 GENERAL INFORMATION: Sequence 5, Application US/10311034 APPLICANT APPLICANT PPLICANT PPLICANT PPLICANT PPLICANT PPLICANT PPLICANT PPLICANT: LICANT LICANT ICANT INCYTE GENOMICS, HAFALIA, April ARVIZU, Chandra S. GURURAJAN, Rajagopal TANG, LU, Dyung Aina M. GREENWALD, Sara R. BANDMAN, Olga BOROWSKY, Mari LAL, Preeti GRIFFIN, Jennifer A TRIBOULEY, Catherine AU-YOUNG, Janice O, Terence P THORNTON, Michael BAUGHN, Mariah R. NGUYEN, Danniel B BURFORD, Neil 7AO, Monique G. CHAWLA, Narinder K SANDHI, Ameena R. LU, Yan EARNEY, Liam AMKUMAR, Jayalaxm Ann Tom Shirley A Mark L. :

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PCT-US03-04816-56
; Sequence 56, Application PC/TUS0304816
; GENERAL INFORMATION:
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Best Local :
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APPLICANT: Rosenfeld, Julie Beth
APPLICANT: Silos-Santlago, Inmaculada
TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 99.
TITLE OF INVENTION: 12216, 17719, 41897, 47.774, 33408, 1
TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 211
TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 11
TITLE OF INVENTION: 13424 MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 1242491CD1
-10-311-034-5
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APPLICANT:
APPLICANT:
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                                                                                                                                     APPLICANT: Millennium Pharmaceuticals, APPLICANT: Rosenfeld, Julie Beth
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/311,034
CURRENT FILING DATE: 2002-12-10
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Local Similarity 26.1%;
nes 101; Conservative
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DING, L1
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ISON, Craig H.
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                   PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 6: 12216, 17719, 41897, 47174, 33408, 10002, 1630, 443 27410, 33606, 619, 15985, 69112, 2158, 224, 615, 443 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675,
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Pred. No. 4.8e-17;
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209, 314, 636,
515, 44373,
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PCT-US03-04816-56
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Best Local (
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     454 CSSEGRGEEVVWCLDDKANSLVMYHSTTYQL--
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                                                                                 SGSEVWYSNGPGL
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                                           EGSKQWSSSAPNLGKSPKHTPIAPGFASLNEMEEFAEAEDGGSSVPPSPYSTPSYLSVPL
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PRIOR APPLICATION NUMBER: US 60/370,121
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CURRENT FILING DATE: 2003-02-19
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APPLICATION NUMBER: US 60/360,495
FILING DATE: 2002-02-28
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/373,908
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 60/373,010
                                                                                                                                 APPLICATION NUMBER: US 60/386,879
                                                                                                                                                                                APPLICATION NUMBER: US 60/385,280
                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/382,409
                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/379,949
                                                                                        NG DATE: 2002-06-06
ICATION NUMBER: US 60/387,536
                                                                                                                                                                                                                                                                                                                             CATION NUMBER: US 60/377,717
                                       Application data
                                            removed
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19 QEASMLHALQHPCIVALIGISIHP--LCFALELAPLSSLNTVLSENARDSSFIPLGHMLT 92; Score 289.5; Pred. No. 7. Mismatches 7.8e-14; hes 278; DB 1; Indels 207; Length Gaps 30;

144 QEARLFGALQHPNIIALRGACLNPPHLCLVMEYARGGALSRVLAGRR-----VP-PHVLV -NWAVQVARGMNYLHNDAPVPIIHRDLKSINILI-LLEAIENHNLADTVLKITDFGLARE QKIAYQIASGLAYLHKK----NIIFCDLKSDNILVWSLDVKEHIN-----IKLSDYGISRQ 128 197

---KKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRP-----LALSVVSQ WHKTTKMSAAGTYAWMAPEVIRLSLFSKSSDVWSFGVLLWELLTGEVPYREIDALAVAYG SFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLSGQRPALGHHQLQIA--367 186 232 314

271

SRNYTVVNTEKGLMEVQRMCCPGMKVSCQLQVQRSLWTATEDQKIYIYTLKG-----MCP MPLESFHSLQEDWKLEIQHMFDDLRTKEKELRSREEELLRAAQEQRFQEEQLRRREQELA LCSHTANRSKFSIADEDARQNPYPVK----LNTPQQALDTPAVVTCFLAV----PVI--KKNSYLVLAGLADGLVAVFPVVRGTPKDSCSY LREGSSHISLPSGFEHKITVQASPTLDKRKGSDGASPPASPSIIPRLRAIRLTPVD-----CGGSSSGSSSGGSGTWSRGGP-PKKEELVGGKKKGRTWGPSSTLQKERVGGEERLKGLG -LVIDCASLEICRRL SQEKPRVRKRKGNFKRAVLK -EPYMAPSMVTSVV --- AMEVVN 413 427 381 465 326 453 579 521

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TYPE: PRT
GRGANISM: Homo sapiens
US-10-369-022-56
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Best Local Similarity
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(TLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
(TLE OF INVENTION: PAIN AND PALMEUL DISORDERS USING 99,
(TLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, ...
(TLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 21;
(TLE OF INVENTION: 95431, 2245, 2387, 1658, 55054, 10
(TLE OF INVENTION: 13424 MOLECULES
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  198 - NWAVQVARGMNYLHNDAPVPIIHRDLKSINILI--LEAIENHNLADTVLKITDFGLARE 254
                                                                                             144
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                                            77 QKIAYQIASGLAYLHKK---NIIFCDLKSDNILVWSLDVKEHIN----IKLSDYGISRQ 128
                                                                                                              19 QEASMLHALQHPCIVALIGISIHP--LCFALELAPLSSLNTVLSENARDSSFIPIGHMLT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60/373,010 FILING DATE: 2002-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/387,536
                                                                                    QEARLFGALQHPNIIALRGACLNPPHLCLVMEYARGGALSRVLAGRR-----VP-PHVLV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLICATION NUMBER: US 60/386,879
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                                                                                                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICATION NUMBER: US 60/385,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATION NUMBER: US 60/382,409 G DATE: 2002-05-21
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                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER: US 60/377,717
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                                                                                                                                                                      92,
                                                                                                                                                                  Score 289.5; DB b;
Pred. No. 7.8e-14;
""amatches 278;
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                                                                                                                                                                        Indels 207; Gaps
                                                                                                                                                                                                                Length 953;
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Query Ma Best Loc Matches	RESULT 6 US-60-426-964- Sequence 2, GENERAL INFO APPLICANT: TITLE OF IN TITLE OF IN TITLE REFERE CURRENT APP CURRENT FIL NUMBER OF S SOFTWARE: F SOFTWARE: F SOFTWARE: F TYPE: PRT ORGANISM: US-60-426-964-	Qy 590 Db 807	Qy 544 Db 747	Oy 487	Qy 454 Db 640	Qy 414 Db 580	Qy 382 Db 522	Qy 327 Db 466	Qy 272 Db 428	Qy 233 Db 368	Qy 187 Db 315	Qy 129 Db 255
Match 7.6%; Score 289.5; DB 7; Length 953; Local Similarity 22.6%; Pred. No. 7.8e-14; Local Score 207; Gaps 168; Conservative 92; Mismatches 278; Indels 207; Gaps	SULT 6 -60-426-964-2 GENERAL INFORMATION: APPLICANT: Silos-Santlago, Inmaculada TITLE OF INVENTION: Methods and compositions for treating TITLE OF INVENTION: Methods and compositions for treating TITLE OF INVENTION: Methods and painful disorders using 16314, 1613, 1675 FILE REFERENCE: MPI102-189PIM CURRENT APPLICATION NUMBER: US/60/426,964 CURRENT FILING DATE: 2002-11-15 NUMBER OF SEQ ID NOS: 8 SOPTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2 LENGTH: 953 TYPE: PRT ORGANISM: homo sapiens	DS-DMLHTPGAASDRSEHDLTPMDG 613   T	HQESLTDYCSMSSYSSSPPRQAARSPSSLPSSPASSSSVPFSTDCE 589	RYFCGVPSPLRDMFPVRPLDTEPPAASHTANPKVPEGDSIADVSIMYSEELGTQILI: 543 	CSSEGRGEEVVWCLDDKANSLVMYHSTTYQLCA	SGSEVWYSNGPGLLVIDCASLEICRRLEPYMAPSMVTSVV 453	CCSHTANRSKFSIADEDARQNPYPVK	'LNTPQQALDTPAVVTCFLAVPVIKKNSYLVLAGLADGLVAVFPVVRGTPKDSCSY 381	SRNYTVVNTEKGLMEVQRMCCPGMKVSCQLQVQRSLMTATEDQKIYIYILKGMCP 326	MKDPTFATEMYELCCGKQTAFFSSQGQEYTVVFWDGKEE 271 	KKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQ 232	SFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMYLYELLSGQRPALGHHQLQIA 186 
30;	or 9569		•					•				

19 QEASMLHALQHPCIVALIGISIHP--LCFALELAPLSSLNTVLSENARDSSFIPLGHMLT .76

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US-10-263-929-187

Sequence 187, Application US/10263929

GENERAL INFORMATION:

APPLICANT: Kim, Jaeseob

APPLICANT: Galant, Ron

TITLE OF INVENTION: Alzheimer's Disease Linked Genes

FILE REFERNCE: LSD-07417

CURRENT APPLICATION NUMBER: US/10/263,929

CURRENT FILING DATE: 2002-10-03

NUMBER OF SEQ ID NOS: 213

SOFTWARE: Patentin version 3.2

SEQ ID NO 187

LENGTH: 954
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                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Homo sapiens: US-10-263-929-187
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Best Local Similarity
                                                                                 Best Local Sin
Matches 170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 MPLESFHSLQEDWKLEIQHMFDDLRTKEKELRSREEELLRAAQEQRFQEEQLRRREQELA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 ---KKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRP------LALSVVSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 - NWAVQVARGMNYLHNDAPVPIIHRDLKSINILI - - LEAIENHNLADTVLKITDFGLARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 MKDPTF-------ATFMYELCCGKQTAFFSSQGQEYTVVFWDGKEE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 SFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLSGQRPALGHHQLQIA--
                                  19 QEASMLHALQHPCIVALIGISIHP--LCFALELAPLSSLNTVLSENARDSSFIPLGHMLT 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---RYFCGVPSPLRDMFPVRPLDTEPPAASHTANPKVPEGDSIADVSIMYSEELGTQILI 543
QEARLFGALQHPNIIALRGACLNPPHLCLVMEYARGGALSRVLAGRR-----VP-PHVLV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSLTPTHVTAACAVSRGHRRTPSDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLSSVSDCNSTRSLLRSDSDEAAPAAPSPPPSPPAPTPTPSPSTNPLVDLELESFKKDPR 806
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                                                                                   Conservative
                                                                                                    7.5%;
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                                                                               Score 285; DB 6;
Pred. No. 1.8e-13;
3; Mismatches 275;
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                                                                                                                     Length 954;
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                                                                               208;
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9 DAMKNESEFRQEASMLHALQHPCIVALIGISIHP--LCFALELAPLSSLNTVLSENARDS

99;

257;

Indels

227;

Gaps 66

33;

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NUMBER OF SEQ ID NOS: 213
SOFTWARE: PatentIn version 3.2
SEQ ID NO 193
LENGTH: 1002
TYPE: PRT
ORGANISM: Mus musculus
US-10-263-929-193
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 Query Match 7.4%;
Best Local Similarity 22.8%;
Matches 172; Conservative 9:
                                                                                                                                                                                                                                                                                                     Sequence 193, Application US/10263929 GENERAL INFORMATION:
                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/263,929
CURRENT FILING DATE: 2002-10-03
                                                                                                                                                                                                                               APPLICANT: Kim, Jaeseob
APPLICANT: Galant, Ron
TITLE OF INVENTION: Alzheimer's Disease Linked
FILE REFERENCE: LSD-07417
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GAASDRSE - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEQRRWLDGLFFPRAGRFP-RGL--SPPARPHGRREDVGPGLGLAP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLNTPQQALDTPAVVTCFLAV---PVI--KKNSYLVLAGLADGLVAVFPVVRGTPKDSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EREMDIVERELHLL --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MPLESTHSLQEDWKLEIQHMFDDLRTKEKELRSREEELLRAAQEQRFQEEQLRRREQELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKDPTF - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VAMNKLTLPIPSTCPEP----FAR---LLEECWDPDPHGRPDFGSILKRLEVIEQSALFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---KKLSKGIRPVLGOPEEVQFRRLQALMMECWDTKPEKRP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WHKTTKMSAAGTYAWMAPEVIRLSLFSKSSDVWSFGVLLWELLTGEVPYREIDALAVAYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IHQESLTDYCSMSSYSSSPPRQAA-RSPSSLPSSPASSSSVPFST----DCEDSDMLHTP
                                                                                                                                                                                                                                                                                                                                                                                                                                            -HDLTPMDG 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LVIDCASLEICRRL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----MCQL------SQEKPRVRKRKGNFKRSRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---ATFMYELCCGKQTAFFSSQGQEYTVVFWDGKEE---
Score 283.5; DB
Pred. No. 2.5e-13
99; Mismatches 28
                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------EPYMAPSMVTSV 452
                                                                                                                                                                                                                                                   Genes
                                    Length
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PCT-US02-39126-13
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                                                                                                                                                                                                      PPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        792 KEESSLGNARDLCGPTTLTPDPGSAAPESGCELIP 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        522 DSGLCSPPGSPLMLPRLRAIQLTSDENNKTRGRNMVFRQEDFE----DVKRSFKKKGCTW 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 334 LDTPAVVTCFLAVPVIKKNSYLVLAG---LADGLVAVFP-----VVRGTP-----KDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 LM----EVORMCCPGMKVSCQLQ------VQRSLWTATEDQKIYIYTLKGMCPLNTPQQA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480 TTYQLCARYFCGVPSPLRDMFPV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 INI-----KLSDYGISRQSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMYLYEL
                                                                                                                                                                                                                                                                                                                                                                                             LICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 LSGQRPALGHHQLQIA-----KKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 DDICNKTLKITDEGLAREWHRTTRMSAAGTYAWMAPEVIRSSLESKGSDIWSYGVLLWEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206 R--APGPRRARRIPPQVLVNWAVQIARGMLYLHEEAVVPILHRDLKSSNILL--LEKIEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 DAAAAAESVRREARLFAMLRHPNIIQLRGVCLRQPHLCLVLEFARGGALNRALAAAASDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKKEEGALQPASRCQSSPSSLLRQPSAGRAPSGGSTLLLPSAPSHSSKSSLSMKCLLQAG 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----QESLTDYCSMSSYSSSPPRQ--AARSPSS-----LPSSPASSSSVPFSTDC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SREEGSPKGSPVNNYGAPMLRKKTESALCECGMLLASMALGLDVRKLHGAQAPAKPSPKM 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KTTPL-ASLFVDQPGSCEEQKLVPEGLEHRKPKQTKFPGQAHVGLPLCKDSQREDSSEAE 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPGLLVIDCASLEICRRLEPYMAPSMVTSVVCSSEGRGEEVVWCLDD---KANSLVMYHS 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSYLCSHTAN-----RSKFSIADED-----ARQNPYPVKAMEVVNSGSEVWYSN 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LRSREEELSRAALQQKSQELLLRRREQQLAEREIDVLERELNVLIFQLS------QEA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----PEGDSIADVS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SFIPLGHMLTQKI-----AYQIASGLAYLHKK---NIIFCDLKSDNILVWSLDVKEH 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LTGEVPYRGIDGLAVAYGVAVNKLTLPIPSTCPEP----FAKLMKECWEQDPHIR--
                                                                                                                                                                                                                                                                                                                                                                                                       INCYTE GENOMICS,
                                                                                                                                                                                                                                        GORVAD, Ann E.
HAFALIA, April J.A.
EMERLING, Brooke M.
                                                                                                                                                                                                                                                                                                               WILSON, Amy D.
SWARNAKAR, Anita
       HAWKINS, Phillip R.
                                                          KHARE,
                                                                                                                          BAUGHN, Mariah R.
                                                                                                                                                GRIFFIN, Jennifer A. MARQUIS, Joseph P.
                                                                                                                                                                                                                       RAMKUMAR, Jayalaxmi
                                                                                                                                                                                                                                                                                                                                                                CHIEN, David
                                                                              CHAWLA, Narinder K.
LEHR-MASON, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PSFALILQQLTAIEEAVLTNMPQESFHSMQEDWKLEIQQMFSELRTKEKE 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---PHVKKRKGRFRRGRLRLKDGHRISLPSDFQHKITVQASPTLDKRRSS 521
                                                          Reena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----PGAASDRSEHDLTP 610
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; OTHER INFORMATION: Incyte ID No: 3810039CD1
PCT-US02-39126-13
                                                                                                                                                                                                                                                                                                                                                        Sequence 130, Applic
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.2
Best Local Similarity 31.3
Matches 78; Conservative
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                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/340,235
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/343,007
PRIOR FILING DATE: 2001-12-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: PCT/US02/39126
CURRENT FILING DATE: 2002-12-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLICANT: SPRAGUE, William W.
PPLICANT: ZEBARJADIAN, Yeganeh
UTLE OF INVENTION: KINASES AND PHOSPHATASES
LLE REFERENCE: PF-1315 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 SFTNILDQL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 -DVKEHINIKLSDYGISRQSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 RHDPDEDISQTIENVRQEAKLFAMLKHPNIIALRGVCLKEPNLCLVMEFARGGPLNRVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 LALSVVSQM 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 LLSGQRPALGHHQLQIA-----KKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 GDLSNKI-LKITDFGLAREWHRTTKMSAAGTYAWMAPEVIRASMFSKGSDVWSYGVLLWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ENARDSSFIPLGHMLTQKI----AYQIASGLAYLHKK---NIIFCDLKSDNILVWSL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 2002-02-04
APPLICATION NUMBER: US 60/357,675
FILING DATE: 2002-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/354,388 FILING DATE: 2002-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/343,546 FILING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHLRATDAMKNFSEFRQEASMLHALQHPCIVALIGISIHP--LCFALELAPLSSLNTVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLTGEVPFRGIDGLAVAYGVAMNKLALPIPSTCPEP-----FAKLMEDCWNPDPHSRP
                                                                                                                                                                                                        Kekuda, Ramesh
Miller, Charles E.
Rieger, Daniel K.
Pena, Carol E.A.
                                                                                                                                                                                                                                                                                                                             erhusen, Bryan D.
                                                                                                              Berghs, Constance
Zhong, Mei
                                         Boldog, Ferenc L.
                                                                                            Casman,
                                                                                                                                                                                     Shimkets, Richard A.
                                                                                                                                                                                                                                                                                                     Patturajan, Meera
                   adigaru,
                                                               Casman, Stacie J.
Voss, Edward Z.
                                                                                                                                                                                                                                                                                                                                                                          Application US/10210130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -GKRIPPDILVNWAVQIARGMNYLHDEAIVPIIHRDLKSSNILILQKVEN
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Muralidhara
Glennda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.2%; Score 273.5; DB 1; 31.3%; Pred. No. 1.7e-12; tive 41; Mismatches 93;
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Indels Length 1081;

Gaps 60

8

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394

341 169

õ

Gorman, Linda Vernet, Corine A.M.

Anderson,

Kimberly A.

David W.

Xiaojia Sasha

Mario

Ji, Weizhen

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                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: HOMO
US-10-210-130-130
                                                                                                                 Query Match
Best Local S
Matches 78
                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 369
SOFTWARE: CuraSeqList version
SEQ ID NO 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRENT FILING DATE:
                                                        152 RHDPDEDISQTIENVRQEAKLFAMLKHPNITALRGVCLKEPNLCLVMEFARGGPLNRVLS 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ICANT
                            61 ENARDSSFIPLGHMLTQKI----AYQIASGLAYLHKK---NIIFCDLKSDNILVWSL--- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ICANT
                                                                           3 RHLRATDAMKNESEERQEASMLHALQHPCIVALIGISIHP--LCFALELAPLSSLNTVLS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2001-08
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/311,979 FILING DATE: 2001-08-13
                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2002-05-16
APPLICATION NUMBER: 60/3
FILING DATE: 2001-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/316,508
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/381,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/354,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPLICATION NUMBER: 60/310,291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WI: Shenoy, Suresh G.
FINVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING FERENCE: 21402-416C (Cura-716 SMT)
APPLICATION NUMBER: US/10/210,130
                                                                                                                                                                                                                           1096
                                                                                                                                                                                                                                                                                                                                                                                                                                          PLICATION NUMBER: 60/310,951
                                                                                                                                                                                                                                                                                                                                                                                                               PLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LING DATE: 2002-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ING DATE:
                                                                                                                    18; Conser
                                                                                                                                                                                                                                                                                                                                                                                             ING DATE: 2001-09-2
                                                                                                                                                                                                                                                                                                                                                                                                                           ING DATE:
                                                                                                                                                                                                                                                                                  Prior Application data removed -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATION NUMBER: 60/383,887
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Catterton, Elina
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Spaderna, Steven
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angolli, Esha A.
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                                                                                                                 Conservative
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-GKRIPPDILVNWAVQIARGMNYLHDEAIVPIIHRDLKSSNILILQKVEN 260
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                                                                                                                                  Score 273.5;
Pred. No. 1.
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                                                                                                                    Mismatches
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                                            SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 42
SERGIH: 251
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zerhusen, Bryan D.
TITLE OF INVENTION: PROTEINS, POLINUCLEOTII
TITLE OF INVENTION: USING THE SAME
FILE REFERENCE: 21402-250 (CURA-550)
CURRENT APPLICATION NUMBER: US/10/052,648A
CURRENT FILING DATE: 2002-12-09
                                                                                                                                  NUMBER OF SEQ ID NOS: 97
                                                                                                                                                                   PRIOR FILING DATE: 2001-02-2
FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         PLICATION NUMBER: 60/272,920 CLING DATE: 2001-03-02 PLICATION NUMBER: 60/284,549 LING DATE: 2001-04-18
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Rothenberg, Mark
Shimkets, Richard
Smithson, Glennda
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Gerlach, Valerie
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Mehraban, Fuad
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 Description of Artificial Sequence: Protein kinase domain sequence
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                 pkinase,
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US-10-074-978A-151
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                                                                               CURRENT APPLICATION NUMBER: US/10/074,978A
CURRENT FILING DATE: 2003-01-07
PRIOR APPLICATION UNDERE: 60/268,221
PRIOR FILING DATE: 2001-02-12
                                                                                                                                                                                                     PPLICANT:
                                                                                                                              PPLICANT: Smithson, Glennda
ITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
ILE REFERENCE: 21402-269
                                                                                                                                                                                                                                                     PLICANT
                                                                                                                                                                                                                                                                                                                       PLICANT
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                                                                                                                                                                                                                                                                                      PLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 IADFGLARKLESSSYEKLTTFVGTPEYMAPEVLEGRGYSSKVDVWSLGVILYELLTGKLP
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                         APPLICATION NUMBER: 60/312,284
                                                              APPLICATION NUMBER: 60/335,109
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Boldog, Ferenc
Patturajan, Meera
Blalock, Angela
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Gunther, Erik
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Peyman, John
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Malyankar, Uriel M
Gusev, Vladimir
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60/268,496
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Pred. No. 3.4e-13;
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; OTHER INFORMATION: Protein kinase domain sequence
US-10-074-978A-151
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SEQ ID NO 151
LENGTH: 254
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                                                                                                                                                                                     120 LSDYGISRQ---SFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLSGQRP 176
252 N 252
                                     231 S 231
                                                                                                              177 ALGHHOLQIAKKLSKGIRPVLGQP-----EEVQFRRLQALMMECWDTKPEKRPLALSVV
                                                                                                                                                      139 IADFGLARKLESSSYEKLTTFVGTPEYMAPEVLEGRGYSSKVDVWSLGVILYELLTGKLP
                                                                        199 FPGIDPLEELFRIKE--RPRLRLPLPPNCSEE-----LKDLIKKCLNKDPEKRPTAKEIL 251
                                                                                                                                                                                                                                     89 RRNG-----LLLSEKEAKKIALQILRGLEYLHSRGIVHRDLKPENIL-----LDENGTVK 138
                                                                                                                                                                                                                                                                      60 SENARDSSFIPLGHMLTQKIAYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIK 119
                                                                                                                                                                                                                                                                                                                  29 IKILKKRSLSEKKKRFLREIQILRRLSHPNIVRLLGVFEEDDHLYLVMEYMEGGDLFDYL
                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 32.4 les 78; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/280,899
FILING DATE: 2001-04-02
APPLICATION NUMBER: 60/310,797
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Pred. No. 3.5e-13;
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RESULT 13 US-10-072-012-800 **SPEICANT** PPLICANT PPLICANT PPLICANT LICAN JICANT Grosse, William M Spytek, Kimberly Colman, Steven D. Wolenc, Adam R. Pena, Carol E. A Gerlach, Valerie Taupier Jr, Raymond Gusev, Vladimir Y. Furtak, Katarzyna Padigaru; Gangolli, Esha Shimkets, Richard erhusen, Bryan Patturajan, Meera Application US/10072012 astelli, Luca iller, Charles E. Velizar David W Muralidhara

LICANT: Burgess, Catherine E. Licantine E. L

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Alsobrook II, John P

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                                                    RESULT 14
US-10-072-012-857
; Sequence 857, Applicat
; GENERAL INFORMATION:
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SEQ ID NO 800
SEQ TH: 256
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                    120 LSDYGISRQ---SFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLSGQRP 176
                                                                                                                                                                  252 N
                                                                                                                                                                                                                                                                          177 ALGHHQLQIAKKLSKGIRPVLGQP-----
                                                                                                                                                                                                                                                                                                                   139 IADFGLARKLESSSYEKLTTFVGTPEYMAPEVLEGRGYSSKVDVWSLGVILYELLTGKLP
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1 Similarity 32.48;
78; Conservation
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             Tchernev, Velizar
Spytek, Kimberly
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Zerhusen, Bryan
                                                                     Application US/10072012
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Pred. No. 3.
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SEQ ID NO 857
LENGTH: 256
                                                                                                                                                                                                                                                                         Matches
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RIOR APPLICATION NUMBER: 60/265,514
RIOR FILING DATE: 2001-01-31
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RIOR APPLICATION NUMBER: 60/2
PRIOR APPLICATION NUMBER: 60/2
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URRENT FILING DATE: 2002-01-31
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177 ALGHHQLQIAKKLSKGIRPVLGQP---
                                                                                        120 LSDYGISRQ---SFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLSGQRP 176
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                                                                                                                           89 RRNG-----LLLSEKEAKKIALQILRGLEYLHSRGIVHRDLKPENIL-----LDENGTVK 138
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APPLICATION NUMBER: 60/265,412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/267,459
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                                                      IADFGLARKLESSSYEKLTTFVGTPEYMAPEVLEGRGYSSKVDVWSLGVILYELLTGKLP
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INVENTION: Proteins and Nucleic Acids Encoding Same
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                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prior
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Rieger, Daniel K.
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Wolenc, Adam R.
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                                                                                                                                                                                                                                                                                          Score 271;
Pred. No. 3
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                  EEVQFRRLQALMMECWDTKPEKRPLALSVV 230
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PRIOR APPLICATION UNMBER: 08/232,545
PRIOR FILING DATE: 1994-04-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 2770
TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
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OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte; OTHER INFORMATION: kinase 3
US-09-977-261-5
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CURRENT APPLICATION NUMBER: US/09/977,261
CURRENT FILING DATE: 2001-10-16
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LOCATION: (366)..(1880)
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                                                                                                                                                                                                                                                                                                         1449
                                                                                                                                                                                                                                                                                                                                                                                             1401 GAGTCTCGGAACTACATTCACAGAGATCTGGCTGCCAGAAATGTCCTC---
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                                                                                                                                                                                                                    1506 GTAGATAAIGAAGACATCTATGAATCTAGACACGAAATAAAGCTGCCGGTGAAGTGGACT
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180. HisHisGlnLeuGlnIleAlaLysLysLeuSerLysGlyIleArgProValLeuGlyGln 199
                                                                                                                                                                           141
                                                                                                                                                                                                                                                                                                                                                111 AspValLysGluHisIleAsnIleLysLeuSerAspTyrGlyIleSerArg------
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LICANT: SURES, IRMINGARD
LE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
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                                          TGGTCATTTGGAATCCTTCTTTATGAAATCATTACTTATGGCAAAATGCCTTACAGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTTATGCTGTTTGCACTTTAGAAGATCCAATTTATATTATTACAGAGTTGATGAGACAT 1298
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                                                                                   PheSerTyrGlyMetValLeuTyrGluLeuLeuSer---GlyGlnArgProAlaLeuGly
                                                                                                                                                                                                                                                                                                         ---GTTGGTGAACATAATATCTACAAAGTAGCAGATTTTTGGACTTGCCAGAGTTTTTAAG 1505
                                                                                                                                                                    ProGlyTyrGlnAlaProGluIleArgProArgILeValTyrAspGluLysValAspMet 160
                                                                                                                              -GCGCCCGAAGCCATTCGTAGTAATAAATTCAGCATTAAGTCCGATGTA 1613
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Db 2108 TTAAGCACACTAAACCAAGTTATTTTTCTT 2137
Qy 348 ValileLysLysAsnSerTyrLeuValLeu 357
Db 2048 TTGACTGGGCAACACTGCAGGACAGTCAAGGTCATATATAT
Qy 328 AsnThrProGlnGlnAlaLeuAspThrProAlaValThrCysPheLeuAlaValPro 347
Db 1988 TATTCAAGTGATAAGGTAAAAGTTGGCCATGTATTATGAAAAAAGATTATTTGTGCATTTTA
Qy 309 ThrAlaThrGluAspGlnLysIleTyrTleTyrThrLeuLysGlyMetCysProLeu
Db 1961CAACTGCACAATCAGTTTATCCTGACA 1987
Qy 289 ArgMetCysCysProGlyMetLysValSerCysGlnLeuGlnValGlnArgSerLeuTrp 308
Db 1928 AAATAATCCATTCCAAAATACAATGTTATCAAC196
Qy 271 GluSerArgAsnTyrThrValValAsnTh
Db 1868 TAACTTCATAAGATGAACACTGGAGAAGAATATCAAATAATAAAGTAGCAAAACAAATTC 1927
Qy 255SerSerGlnGlyGlnGluTyrTh
Db 1809 ACACTGCGTTGGAAACTTGAAGACTATTTTGAAACAGA-CTCTTCATATTCAGATGCAAA 1867
Qy 240 ThrPheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhePhe
Db 1785 CCTAAGGAACGA
Qy 220 ProGluLysArgProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAla 239
Db 1728 CCATCCAACTGTCCACAGCAATTTTACAACATCATGTTGGAGTGCTGGAATGCAGAG
Oy 200 proGluGluValGlnPheArgArgLeuGlnAlaL
Db 1674 ATGACAGGTGCCCAGGTAATCCAGATGTTGGCTCAAAACTATAGACTTCCGCAA 1727

Search completed: April 15, 2003, 09:55:51 Job time: 175 secs

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US-09-977-260-5
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US-09-977-260-5
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Best Local Similarity:
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SEQ ID NO 5
LENGTH: 2770
TYPE: DNA
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publication No. US20020192790A1
GENERAL IMPORMATION:
APPLICANT: ULLRICH, AXEL
APPLICANT: GISHIZKY, MIXHAIL
APPLICANT: SURES, IRMINGARD
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
FILE REFERENCE: 038602/1260
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PRIOR FILING DATE: 1994-04-22
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                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: CDS
LOCATION: (366)..(1880)
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                                                                  SerGluPheArgGlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAla
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2108 TTAAGCACACTAAACCAAGTTATTTTCTT 2137
                                                                                                                                                                   1988 TATTCAAGTGATAAGGATAAAGTTGGCCATGTATTATGAAAAAAGATTATTTGTGCATTTTA
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                                     348 ValileLysLysAsnSerTyrLeuValLeu 357
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                                                                                TTGACTGGGCAACACTGCAGGACAGTCAAGGTCATATATAATTGCTCACTGCCTGGAAAA
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US-09-938-842A-903
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US-09-938-842A-903
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EQ ID NO 903
LENGTH: 1638
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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APPLICANT: Kreps, Joel
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NPPLICANT: Zhu, Tong
NPLICANT: Zhu, Tong
NPLITLE OF INVENTION: STRESS-REGULATED GENES OF
NPLITLE OF INVENTION: SAME, AND METHODS OF USE:
TLE REFERENCE: SCRIP1300-3
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                     ValTyrAspGluLysValAspMetPheSerTyrGlyMetValLeuTyrGluLeuLeuSer 172
                                                           GTTATGACAGCTGAAACTGGAACATATCGCTGGATGGCTCCAGAGGTGATAGAACACAAG 1344
                                                                                                   AlaLeuGlyValGlu---GlyThrProGlyTyrGlnAlaProGluIleArgProArgIle 152
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                                                                                                                                           GAAAATGAGGTGGTTAAGGTTGCAGACTTTGGGGTGGCTAGAGTGAAAGCACAAACTGGA
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1577
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NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1577
LENGTH: 2211
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/264,647 PRIOR FILING DATE: 2001-01-16 PRIOR APPLICATION NUMBER: US 60/300,111
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IleProLeuGlyHisMetLeuThrGlnLysIleAlaTyrGlnIleAlaSerGlyLeuAla
                                                                                                                            TATATGCCAAGAGGGAGTCTCTTCAAAATACTTCATAATACGAATCAG------
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278	4 ValPheTrpAspGlyLysGluGluSerArgAsnTyrThrValVal	Оу 26	
17	03 GACGAGCTGCGAGCCAAGGAAAAGGAACTACTGAGCCGCGAGGAGGAGCTGACGCGA	Db 170	
26	4 GluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGluTyr	Оу 24	
170	:::    :::CGCGGGACTCCTTCCATTCCATGCAGGAAGGCTGGAAGCGCGAGATCCAGGGT	Db 164	
243	4 LysaspProThrPheAlaThrPheMetTy	0у 23	
164	3 GACTTCGCCTCCATCCTGCAGCAGTTGGAGGCGCTGGAGGCACAGGTCCTACGGC	Db 158	
233	5LeuAlaLeuS	Оу 22	
158	2TTCGCACAGCTTATGGCCGA	Db 153	
224	5 PheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysProGluLysArgPr	Оу 20	
153	CACCTGCCCC	Db 148	_
204	7LysLysLeuSerLysGlyIleArgProValLeuGlyG	Ωу 18	_
4		Db 142	
185	4 AAGGCCTCCACCTTCTCTAAGGGCAGTGACGTCTGGAGTTTTGGGGTGCTGCTGGGG	DB 136	
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136	4 CACAAAACCACAAATGAGTGCCGCGGGCACCTACGCCTGGATGGCTCCTGAGGTTATC	Db 130	_
149	0 PheHisGluGlyAlaLeu	Оу 13	
130		_ _	
129	LeuAspValLysGluHisIleAsnIleLysLeuSerAspTyrGlyIleSerArqGlnS	11	_
109	4ASNILEILEPHECYSABLEULTYSSETABDASHILELEUVALTTPSer :::	Οy 9 118	
, -	GTCAACTGGGCTGTGCAGATTGCCCGTGGGATGCACTACCTGCACTGCGAGGCCCTG	112	_
93	6 ThrGlnLysIleAlaTyrGlnIleAlaSerGlyLeuAlaTyrLeuHisLysLys	Qy 7	_
112	HI:::III AGCCGAGCTCTGGCCGGGCGCGC	108	_
75	AsnAlaArqAspSerSerPhe	Oy 5	_
55 108	8 IleSerIleHisProLeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeu :::	Qy 3 Db 102	
1024	CCGGCTCTTCGCCATGCTGGCACACCCCAACATCATTGCCCT	Db 96	-
37	rgGlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleVal	Qy 1	_
	6-392-21 (1-728) x US-10-143-133-1 (1-3558)	US-09-83	_
	t Scores: 9.1e-19 Length: 3558 260.50 Matches: 151 Similarity: 35.76% Conservative: 90 al Similarity: 22.40% Mismatches: 236 tch: 6.82% Indels: 199 Gaps: 29	Alignment So Pred. No.: Score: Percent Simi Best Local Source Match DB:	
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600	584 eSerThrAspCysGluAspSerAspMetLeuHisThrProGlyAlaAl	Qy
2538	564 nAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSerSerSerValProPn	Db Qy
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564	544 sGlnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSerProProArgGl	Qy
2464	524 pserIleAlaAspValSerIleMetTyrSerGluGiuLeuGlyThrGinileLeuileHi :::	pb Qq
- 4-	59 TGTCCCCGCAGAGCGCGGTAGCAGCTCTGGGACGCCCAAGCTGATCCAGCGGG	В
24	euAspThrGluProProAlaAlaSerHisThrAlaAsnProLysValProGluGlyAs	Qy
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485 2310	465 pCysLeuAspAspLysAlaAsnSerLeuValMetTyrH1sSerThrThrTyrGlnLeuCy	P (2
2250	2191 CCCCAAGCCTGGGGAAGCCCAGAATGGGAGGAGGAGGTCCCGCATGGACGAAGCCACATG	В
465	GlyGluGluValValTr	Qy
2190	CAAGCAATG	DЪ
458	erGluGly	Qy
2143	2129	Db .
450	TyrMetAlaProSerMetValTh	Qγ
2128	2089 GCCTGCAGAGCCAGGCCAGGCATGGGGCCGCCAGTCCCCC	B
430	SerGluValTrpTyrSerAsnGlyProGlyLeuLeuValIleAs	Qy
2088		D 1
410	391 sPheSerIleAlaAspGluAspAlaArgGlnAsnProTyrProValLysAlaMetGl	Q <sub>V</sub>
391 2028	371 largGlyThrProLysAspSerCysSerTyrLeuCysSerHisThrAlaAsnArgSerLy   :::	ος VQ
1992		В
371	Va	Qy
1941	TGCGCCGCCGCGGG-ACATTCAAGCGCAGCAAGCTCCGGGCGCGCGA	Ф
358	laValProValIleLysLysAsnSerTyrLeuValLeuAl	Qy
1889	1889	Db
338	318 eTyrThrLeuLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThrProAl	ν
1889	AGGTGGACCGCGAGCGACCGC	В
318	ysGlnLeuGlnValGlnArgSerLeuTrpThrAlaThrGluAspGlnLysIleTyrIl	Qy
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298	uMetGluValGlnArg-MetCysCysProGlyMetLysValSe	Qy
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PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 882
LENGTH: 1428
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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
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CURRENT FILLING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILLING DATE: 2000-08-24
PRIOR FILLING DATE: 2000-08-24
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                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/143,133
CURRENT FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: 60/290,555
PRIOR FILING DATE: 2001-05-10
                                                                                                                                                                                                                                                         APPLICANT: Delaney, Allen TITLE OF INVENTION: Cancer Associated FILE REFERENCE: KINE-023
                                                                                 NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version
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438 ArgArgLeuGluProTyrMetAlaProSerMetValThrSerValValCysSerSerGlu 457	Qy	Db 1209 ATCAAGTCTTCCTTTTTTCTAAGGGAAGCGACATCTGGAGCTATGGAGTGCTGCTGTGG 1268
428 Val	Qy VQ	149 ArgProArgIleValTyrAspGluLysValAspMetPheSerTyrGlyMetValLeuTyr
408 AlaMetGluValValAsnSerGlySerGluValTrpTyrSerAsnGlyProGlyLeuLeu 427 ::::::         :::         :::	ОУ	Qy 129 SerPheHisGluGlyAlaLeuGlyValGluGlyThrProGlyTyrGlnAlaProGluIle 148 :::         :::
0 3	dy vy	Oy 114 GluHisIleAsnIleLysLeuSerAspTyrGlyIleSerArgGln 128
	o da	Qy 94 AsnIleIlePheCysAspLeuLysSerAspAsnIleLeuValTrpSerLeuAspValLys 113
	. ob	Qy 77 GlnLysIleAlaTyrGlnIleAlaSerGlyLeuAlaTyrLeuHisLysLys 93
335 AspfirProAlaValValThrCysPheLeulalaValProValIleLysLysAsnSerTyr	o da Qy	Qy 64
	Ωy	Qy 47 LeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAla 63
07	Qy Db	
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270 GluGluSerArgAsnTyrThrValValAsnThrGluLysGly	Qy Db	7.05% Indels: 12 Gaps: 8) x US-10-014-882-3 (1-3518)
263ValvalPheTrpAspGlyLys ::: 1668 GAGCGCGAGATCGACGTGCTGGAGCGGGAACTTAACATTCTGATATTCCAGCTAAACCAG	Qy Db	Pred. No.: 8.64e-20 Length: 3518  Pred. No.: 269.50 Matches: 177  Percent Similarity: 36.668 Conservative: 102  Best Local Similarity: 32.268 Mismarches: 258
262	Qy Db	; ORGANISM: homo sapiens US-10-014-882-3
253 Phe	Оу	RE: Fast NO 3 H: 3518 DNA
233 MetLysAspProThrPheAlaThrPheMetTyrGluLeuCysCysGlyLysGlnThrAla     :::    :::    11   1488 ATGCCTCAAGAATCTTTTCATTCCATGCAAGATGACTGGAAACTAGAAATTCAACAAATG	Qy	
224 ProLeuAlaleu	Encoding t Db	APPLICANT: DONOHO, Gregory  APPLICANT: DONOHO, Gregory  TITLE OF INVENTION: No. US20020107384A1e1 Human Kinase and Polynucleotides E  FILE REFERENCE: LEX-0279-USA  CURRENT APPLICATION UNMBER: US/10/014.882
204 GlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysProGluLysArg	Qy Db	INFORMATION
187LysLysLeuSerLysGlyIleArgProValLeuGlyGlnProGluGluVal 203       ::     1329 GTAGCAGTCAATAAACTCACTTTGCCCATTCCATCCACCTGCCCTGAGCCG 137	Оy	SULT 9 -10-014-882-3 Sequence 3. Application US/10014882
169 GluLeuLeuSerGlyGlnArgProAlaLeuGlyHisHisGlnLeuGlnIleAla 186 	Qy	Qy 595HisThrProGlyAlaAlaSerAspArgSerGluHisAspLeuThrPro 610

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	270 GluGluSerArgAsnTyrThrValValAsnThrGluLysGly 283     ::: ::           1465 GAGAAGCCCAAGGTAAAGAAGAGGGCAAGGTTTAAGAGAAGTCGT 1512			Phe		ProLeualaLeu	luLysArg     ATATTCGT					114 GluHisileAsnile			64	47 LeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAla 63	29 HisProCysIleValAlaLeuIleGlyIleSerIleHisProLeuCysPheAla 46	
Qy 59 Db 244	Qy 574 Db 2383	Oy 56	Oy 54 Db 221	Оу 5: Db 22(	Оу 5: рь 21:	Оу 49 ДБ 208	Оу 47 ББ 201	Oy 45 Db 190	0y 4: Db 19:	Db 1873	Oy 408 Db 1837	Оу 389 Дъ 1783	Oy 369 Db 1741	Oy 355 Db 1693	Qy 335 Db 1636		Qy 295 Db 1573	ш
590AspSerAspMetLeu 594  [1]	574 SerSerProAlaSerSerSerSerValProPheSerThrAspCysGlu 589	560 SerProProArgGlnAlaAlaArgSerProSerSerLeuPro 573	545GlnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSer 559 :::   ::	537 LeuGlyThrGlnIleLeuIleHis	517 AsnProLysValProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGlu 536	497 gAspMetPheProValArgProLeu-Asp-ThrGluProProAlaAlaSerHisThrAla 516	477 rHisSerThrThrTyrGlnLeuCysAlaArgTyrPheCysGlyValProSerProLeuAr 497 ::::	458 GlyArgGlyGluGluValValTrp-CysLeuAspAspLysAlaAsnSerLeuValMetTy 477	438 ArgArgLeuGluProTyrMetAlaProSerMetValThrSerValValCy8SerSerGlu 457	428 Val	408 AlaMetGluValValAsnSerGlySerGluValTrpTyrSerAsnGlyProGlyLeuLeu 427 ::::::         ::       ::   ::	389 ArgSerLysPheSerIleAlaAspGluAspAlaArgGlnAsnProTyrProValLys 407 :::	369 ProValValArgGlyThrProLysAspSerCysSerTyrLeuCysSerHisThrAlaAsn 388	355 LeuValLeuAlaGlyLeuAlaAspGlyLeuValAlaValPhe	335 AspThrProAlaValValThrCysPheLeuAlaValProValIleLysLysAsnSerTyr 354 :::   :::::       :::::         :::::	LysileTyrIleTyrThrLeuLysGlyMetCysProLeuAsnThrProglnGlnAlaLeu :::::   TCCAGTCCCCCG	MetLysv :::::: GTGCAG	

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US-09-938-842A-1014
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
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SEQ ID NO 1014
SEQTH: 1662
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PPLICANT: Kreps, Joel
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                                            SerLeuAsnThrValLeuSerGluAsnAlaArgAspSerSerPheIleProLeuGlyHis 73
                                                                                                                                                                  GluPheArgGlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAlaLeu
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                 AGCATTTATGATTTCCTTCACAAACAC-
                                                                           ATTGGTGCATGTACACGATCACCAAACCTCTGCATTGTGACAGAGTTCATGACTCGGGGG 1065
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                                                                                                                                                                                                                                                                               SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/254,744 PRIOR FILING DATE: 2000-12-11
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/014,882
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TITLE OF INVENTION: No. US20020107384A1el Human Kinase and Polynucleotides Encoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hu, Yi
APPLICANT: Kieke, James
APPLICANT: Donoho, Greg
                                                                                                                                                                                                    LENGTH: 3111
TYPE: DNA
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
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                                                                                                    ArgTyrPheCysGlyValProSerProLeuArgAspMetPheProVa 502
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	400 5498	1 TyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaArg	y 38 b 543	D D
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	360 5378	ThrCysPheLeuAlaValProValIleLysLysAsnSerTyrLeuValLe	53 34	₽ Q
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	320 5351	SerLeuTrpThrAlaThrGluA             CCCTGTGGACAGCCACCGAG-	30 531	β δ
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	120 4775	euValTrpSerLeuAspValLysGluHisIleAsnIleLysLeu 	10 471	B 5
	4715	ACATCATCTTCTGTGACCTG	465	문 .

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Sequence 226, Application US/09969347

Patent No. US20020115085A1

GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
TITLE OF INVENTION: Cancer Gene Determination TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-69

CURRENT APPLICATION NUMBER: US/09/969,347

CURRENT FILING DATE: 2001-10-02

PRIOR APPLICATION NUMBER: US/60/237,598

PRIOR APPLICATION NUMBER: US/60/237,598

PRIOR APPLICATION NUMBER: US/60/237,604

PRIOR APPLICATION NUMBER: US/60/237,604

PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                                                                               SEQ ID NO 3
LENGTH: 7307
TYPE: DNA
ORGANISM: Home
                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/10132382 Publication No. US20030045699A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MEMBRANE RECEPTORS FOR FILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                  APPLICANT: WEISS, BERTRAM
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; sequence 7, Application US/10132382
; publication No. US20030045699A1
; GENERAL INFORMATION:
   APPLICANT: WEISS, BERTRAM
   TITLE OF INVENTION: MEMBRANE RECEPTORS FOR S
   FILE REFERENCE: SCH-1811
; CURRENT APPLICATION NUMBER: US/10/132,382
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 7229
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; TYPE: DNA
; ORGANISM: Homo s
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                                                                                                                                                                                                                                  Sequence 1, Application US/10132382 Publication No. US20030045699A1 GENERAL INFORMATION:
                                                                                                                                                     SEQ ID NO 1
LENGTH: 7
                                                                                                                                                                     TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS FILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
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TYPE: DNA
ORGANISM: Homo sapiens
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publication No. US20030045699A1
GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS
FILE REFERENCE: SCH-1811
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GluProTyrMetAlaProSerMetValThrSerValValCysSerSerGluGlyArgGly
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                                            ProvalargProLeuAspThrGluProProAlaAlaSerH1sThrAlaAsnProLysVal
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                                   {\tt LeuLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThrProAlaValVal}
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Qy 661 LeuLysalaargGluLeuThrProHisGlyValLeuValAspalaalaValValAalaLys 680	301 LeuGlnValGlnArgSerLeuTrpThrAlaThrGluAspGlnLysIleTyrIleTyrThr 3	
1942 GTTATCGTCATTGGCCTGGAGAAAGGATTCTGAAGCCCAGCGGGGCCGAGTCATTGCCGTC 2	Qy 281 GluLysGlyLeuMetGluValGlnArgMetCysCysFroGlyMetLysValSerCysGln 300	
THE CONTROL OF THE	Qy 261 TyrThrValValPheTrpAspGlyLysGluGluSerArgAsnTyrThrValValAsnThr 280	
601 SeraspargSerGluH:saspLeuThrProMetAspGlyGluThrPheSerGlnHisLeu	Qy 241 PheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGlu 260	
581 SerVallroPheSerThrAspCysGluAspSerAspMetLeuHisThrProGlyAlaAla 	Qy 221 GluLysArgProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAlaThr 240	
561 ProProArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSerSer	Qy 201 GluGluValGlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysPro 220	
42	Qy 181 HisGinLeuGinIleAlaLysLysLeuSerLysGlyIleArgProValLeuGlyGlnPro 200	
21 ProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGln 5	Qy 161 PheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeuGlyH1s 180	
501 ProValargProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProLysVal	AlaProGluIleArgProArgIleValTyrAspGluLysValAspMet 1 	
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461 GLUGALVALVALTEPCYSLEGASPASPLYSALAASGETLEUVALMETTYFHISSETTHT	Qy 101 LysSerAspAsnIleLeuValTrpSerLeuAspValLysGluHisIleAsnIleLysLeu 120	
441 GluproTyrMetalaProSerMetValThrSerValValCysSerSerGluGlyArgGly	Qy 81 TyrGlnIleAlaSerGlyLeuAlaTyrLeuH1sLysLysAsnIleIlePheCysAspLeu 100	
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Qy 341 ThrCysPheLeuAlaValProValILeLysLysAshSerTyrLeuValLeuAlaGlyLeu 360	Macch: 100.00% Indets: 9 Gaps: 836-392-21 (1-728) x US-09-836-392-8 (1-3496)	
321 LeuLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThrProAlaValVal 	Pred. No.: 0 Length: 3496 Score: 3822.00 Matches: 728 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0	

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Minimum DB
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Sequence 1, Appli Sequence 25, Appl Sequence 106, App Sequence 3, Appli Sequence 58, Appl Sequence 647, App	quence 10/9, equence 1246 equence 3688 quence 14, Apquence 3, Appquence 1085, 4 quence 342, 4 quence 1559, equence 262,	equence 16, Ap equence 128, A equence 1354, Sequence 1, Ap Sequence 16, A Sequence 908,	Sequence 5, App Sequence 1631, Sequence 19, App Sequence 6, App Sequence 170, App Sequence 1, App Sequence 1, App Sequence 1, App	Sequence 3, Appl1 Sequence 226, App Sequence 1014, Ap Sequence 1, Appl1 Sequence 3, Appl1 Sequence 882, Appl1 Sequence 1, Appl1 Sequence 103, App Sequence 903, App Sequence 5, Appl1 Sequence 5, Appl1 Sequence 5, Appl1

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## ALIGNMENTS

US-09-836**-**392-8

US-09-836-392-8 Sequence 8, Application US/09836392
Patent No. US20020173458A1
GENERAL INFORMATION: SOFTWARE: PRIOR FILING DATE: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PCT/US00/28066 PRIOR FILING DATE: 2000-10-11 LENGTH: 3496
TYPE: DNA
ORGANISM: Homo sapiens PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 60/159,542 URRENT APPLICATION NUMBER: US/09/836,392
URRENT FILING DATE: 2001-04-18 ITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptic of INVENTION: Antibodies ILE REFERENCE: PT020P1 FILING DATE: 1999-10-15 ID NOS: -03-14 60/189,027 60/165,914

Alignment Scores

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NUMBER
SOFTWARE: Patentli VC.
SOFTWARE: Patentli VC.
SEQ ID NO 6
LENGTH: 1365
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LCCATION: (1)...(1365)
US-09-163-115-6
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Best Local Similarity:
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                                301 GAGATGGATATGGATCACATTATGACCTGG-----GCCACTGATGTAGCCAAAGGAATG
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AlaTyrLeuH1sLysLys---
                                                          PholieProLouGlyHisMetLouThrGlnLysIleAlaTyrGlnIleAlaSerGlyLou
                                                                                                GAATATGCTTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGA-----
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                                 244 GluLeuCys 246
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Search completed: April 15, 2003, 08:59:00 Job time: 84 secs

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; LOCATION: (1)..(1365)
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CURRENT FILING DATE: 1998-12-28
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                                       IleAla---LysLysLeuSerLysGlyIleArgProValLeuGlyGlnProGluGluVal 203
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                                                                                                                                                                                                            AlaProGluIleArgProArgIleValTyrAspGluLysValAspMetPheSerTyrGly 164
                                                                                  GTGGTTCTCTGGGAGATGCTAACAAGGGAGGTCCCCTTTAAAGGTTTGGAAGGATTACAA
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LENGTH: 1365
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EARLIER APPLICATION NUMBER: US 09/163,115
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
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LOCATION: (1)..(1365)
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Best Local Similarity:
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GENERAL INFORMATION:
APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC
FILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/221,236
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
                                                                                                 Sequence 6, Application US/09221236 Patent No. 6146841
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NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver
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LENGTH: 1365
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ORGANISM: Homo
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; NAME/KEY: CDS
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US-09-221-928-6
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US-09-221-928-6
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APPLICANT: Acton, Susan
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TYPE: DNA
ORGANISM: Homo s
                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/221,928
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
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SOFTWARE: Patentin Ver. 2.0
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US-09-221-527-6
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Patent No. 614683
                                                                                                                SEQ ID NO 6
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/221,527
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE:
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC
FILE REFERENCE: MNI-050
                                                                            TYPE: DNA
NAME/KEY: CDS
LOCATION: (1)..(1365)
                                       FEATURE:
                                                       ORGANISM: Homo
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FILING DATE: 04-APR-1994 ATTORNEY/AGENT INFORMATION: Ò,

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Pred. No.: 5.65e-13
Score: 243.50
Percent Similarity: 45.38%
Best Local Similarity: 27.73%
Query Match: 6.37%
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 19:
                                                            2013
                                                                                                                                                                                                           2127
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LENGTH: 7607 bases
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TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                              2067 ATGACAGGTGCCCAGGTAATCCAGATGTTGGCTCAAAACTATAGA-----CTTCCGCAA 2014
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220 ProGluLysArgProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAla 239
                                                                                         200 ProGluGluValGlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLys 219
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                                                                                                                                                                                                                                    161 PheSerTyrGlyMetValLeuTyrGluLeuLeuSer---GlyGlnArgProAlaLeuGly 179
                                                                                                                                                                                                                                                                                                                141 ProGlyTyrGlnAlaProGluIleArgProArgIleValTyrAspGluLysValAspMet 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 AspValLysGluH1sIleAsnIleLysLeuSerAspTyrGlyIleSerArg------ 127
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                                                      CATCCAACTGTCCA---CAGCAATTTTACAACATCATGTTGGAGTGCTGGAATGCAGAG 1957
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                                                                                                                                                             HisHisGlnLeuGlnIleAlaLysLysLeuSerLysGlyIleArgProValLeuGlyGln 199
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NUMBER OF NUMBER OF CORRESPONDING STREET CITY: STATE: COUNTR ZIP: COMPUTER MEDIUM COMPUTER MEDIUM COMPUTER APPLICO FILING FILING CLASSI PRIOR APPLICO APPLICO	RESULT 8 PCT-US95-04 Sequence GERAL APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC APPLIC	Oy 328 Db 1693	Db 1780 Qy 309 Db 1753	Qy 271 Db 1813 Qy 289	Qy 255 Db 1873	Qy 240 Db 1932	Qy 220 Db 1956	Qy 200 Db 2013	Qy 180 Db 2067	Qy 161 Db 2127	Db 2175
NUMBER OF SEQUENCES: 45 CORRESPONDENCE ADDRESS; ADDRESSE: Genentech, Inc. STREET: 460 Point San Bruno Blvd CITY: South San Francisco STATE: California COUNTRY: USA ZIP: 94080 COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patin (Genentech) CURRENT APPLICATION DATA: APPLICATION UMBER: PCT/US95/04228 FILING DATE: CLASSIFICATION DATA: APPLICATION UMBER: PCT/US95/04228 PRIOR APPLICATION DATA: APPLICATION UMBER: PCT/US95/04228	1228-19/c 19, Application INFORMATION: INFORMATION: Genentech, ANT: Genentet, BANT: Genddel, DANT: Gedddel, Lee, James ANT: Lee, James ANT: Tsai, Siac ANT: Tsai, Siac ANT: Wood, Will OF INVENTION:	ASnThrProGlnGlnAlaLeuASpThrProAlaValValThrCysPheLeu 344	ThralaThrGluAspGlnLysIleTyrThrLeuLysGlyMetCysProLeu 327	GluSerArgAsnTyrThrValValAsnThrGluLysGlyLeuMetGluValGln 288 :::	SerSerGlnGlyGlnGluTyrThrValValPheTrpAspGlyLysGlu 270 :::    :::      :::::: TAACTTCATAAGATGAACACTGGAGAAGAATATCAAATAAAGTAGCAAAACAAATTC 1814	ThrPheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhePhe	ProGluLysargProLeuAlaLeuSerValValSerGlnMetLysAspProThrPheAla 239    ::::::	ProGluGluValGlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLys 219	HisHisGinLeuGinIleAlaLysLysLeuSerLysGlyIleArgProValLeuGlyGin 199    :::     :::::         ATGACAGGTGCCCAGGTAATCCAGATGTTGGCTCAAAACTATAGACTTCCGCAA 2014	PheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeuGly 179 :::  :::  :::   :::	

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US-09-836-392-21 (1-728) x US-08-222-616-19 (1-7607)
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7607 bases
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

MEDIUM TYPE: 5.00 compatible
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: patin (Genen CURRENT APPLICATION DATA:
                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                            2442 GGAAGTCTGCAAGAATATCTC---CAAAATGACACTGGATCAAAAATC----
                                                                                                                     2502 CTTTATGCTGTTTGCACTTTAGAAGATCCAATTTATATTATTACAGAGTTGATGAGACAT 2443
                                                                                          53
                                                                                                                                                 35 LeuIleGlyIleSerIle-----HisProLeuCysPheAlaLeuGluLeuAlaProLeu 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 4-APR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                          SerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSerSerPheIleProLeuGly 72
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T: 460 Point San Bruno Blvd
South San Francisco
California
                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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Wood, William I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       patin (Genentech)
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Matthews, William
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22-JAN-1992
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27.73%
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Matches:
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· ·	APPLICANT: TSA1, SIAO PING APPLICANT: WOOD, WILLIAM I TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES NUMBER OF SEQUENCES: 45	APPI APPI TITI NUME	
	Genertech, Bennett, B; Goeddel, Da Lee, James Matthews, V	APPI APPI APPI APPI	
	19, Application U 19, Application U 6331302 DEFORMATION:	SUL Seq Pat Pat	RE:
	TTGACTGGGCAACACTGCAGGACAGTCAAGGTGATATAATTTCCTC 1646	1693	ф
	AsnThrProGlnGlnAlaLeuAspThrProAlaValThrCysPheLeu 344	328	Qy
1694	:::::::: TATTCAAGTGATAG	1753	. של
327	) ThrAlaThrGluAspGlnLysIleTyrIleTyrThrLeuLysGlyMetCysProLeu	309	Ωy
1754		1780	qq
308	$oldsymbol{ArgMetCysCysProGlyMetLysValSerCysGlnLeuGlnValGlnArgSerLeuTrp$	289	Qγ
1781	AAATAATCCATTCCAAAATACAATGTTATCAAC	1813	da
288	•	271	Qy
1814	TAACTTCATAAG	1873	ДD
270	SerSerGlnGlyGlnGluTyrT	255	Qy
1874		. 1932	Db
254	ThrPheMetTyrGluLeuCysCysGlyLysGl	. 240	Qy
1933	CCTAAGGAACGACCTACATTTGAG	1956	, Db
239	ProGluLysArgProLeuAlaLeuSerValValSerGlnMetLysAspP	220	γo
1957		2013	망
219		200	γO
2014	ATGACAGGTGCCCAGGTAATCCAGATGTTGGCTCAAAACTATAGACTTCCGCAA	2067	Db
199	I	180	γQ
2068	TGGTCATTTGGAATCCTTCTTTATGAAATCATTACTTATGGCAAAATGCCTTACAGTGGT	2127	말.
179		161	Qy
2128		2175	Db.
160	ProGlyTyrGlnAlaProGluIleArgProArgIleValTyrAspGluLysValAspMe	141	Qy
2176	GTAGATAATGAAGACATCTATGAATCTAGACACGAAATAAAGCTGCCGGTGAAGTGGACT	2235	Db
140	1	128	δĀ
2236	:	2292	망
127	Asp	111	Qy
2293	GAGTCTCGGAACTACATTCACAGAGATCTGGCTGCCAGAAATGTCCTC	2340	Db
110	HisLysLysAsnIleIlePheCysAspLeuLysSerAspAsnIle	91	Qy

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Best Local Similarity:
Query Match:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, Laura A.
REGISTRATION UNMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
                                                              1239 CTTTATGCTGTTTGCACTTTAGAAGATCCAATTTATATTATTACAGAGTTGATGAGACAT 1298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2108 TTAAGCACACTAAACCAAGTTATTTTCTT 2137
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LENGTH: 2770 base pair
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URRENT APPLICATION DATA:
APPLICATION NUMBER: PC:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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ZIP: 10036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                             LeuIleGlyIleSerIle-----HisProLeuCysPheAlaLeuGluLeuAlaProLeu 52
                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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1155 Avenue of the Americas
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Redwood City, California 94063-4720
United States of America
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Munchen 80539
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24-APR-1995
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                                                                                                                                                                                                                                                                                                                                                     unknown
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44.32%
26.76%
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-616-19/c = 19, Application US/08222616 No. 5635177	: :	ValIleLysLysAsnSerTyrLeuValLeu 357		AsnThrProGlnGlnAlaLeuAspThrProAlaValValThrCysPheLeuAlaValPro 3	Thralathroluaspolinlysiletyriletyrthrieulysoly - Metcysbroieu 3 Thralathroluaspolinlysiletyriletyrthrieulysoly - Metcysbroieu 1	ATCCTGACA	<pre>gMetCysCysProGlyMetLysValSerCysGlnLeuGlnValGlnArgSerLeuTrp  </pre>	AAATAATCCATTCCAAAATACAATGTTATCAAC	AsnThrGluLysGlyLeuMetGluValGln		SerSerGlnGlyGlnGluTyrThrValValPheTrpAspGlyLysGlu 2	ATATTCAGATGCAAA	ThrPheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhePhe 2	CCTAAGGAACGACCTACATTTGAG ]	roLeuAlaLeuSerValValSerGlnMetLysA	CCATCCAACTGTCCACAGCAATTTTACAACATCATGTTGGAGTGCTGGAATGCAGAG		ATGACAGGTGCCCAGGTAATCCAGATGTTGGCTCAAAACTATAGACTTCCGCAA	roValLeuGlyGln	TGGTCATTTGGAATCCTTCTTATGAAATCATTACTTATGGCAAAATGCCTTACAGTGGT 1				GTAGATAATGAAGACATCTATGAATCTAGACACGAAATAAAGCTGCCGGTGAAGTGGACT 1		GTTGGTGAACATAATATCTACAAAGTAGCAGATTTTGGACTTGCCAGAGTTTTTAAG 1			alTrpSerLeu	catctgactcaacaggtagacatggcggcacaggttggctttggaatggcctatctg		GGAAGTCTGCAAGAATATCTCCAAAATGACACTGGATCAAAAAATC 1	erGl
			2107	47	2047	1987	308	1960	288	1927	270 .	1867	254	1808	239	1784	219	1727	199	1673	179	1613	160	1565	140	1505	27	1448	110	1400	90	343	

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US-09-836-392-21 (1-728) x US-08-426-509A-5 (1-2770)
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US-08-426-509A-5
                                                                                                                                      Alignment Scores:
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2770 bass
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2178 -----GGGTCCCAGCACTTGACCCCCATCTGCACTGCTGTACAGGGCTGCCGTCACCCGA 2231
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                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       660 ValLeuLysAlaArgGluLeuThrProHisGlyValLeuValAspAlaAlaValValAla 679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          640 AspValIleValIleGlyLeuGluLysAspSerGluAlaGlnArgGlyArgValIleAla 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          620 LeuGlnAlaValLysIleLeuAlaValArgAspLeuIleTrpValProArgArgGlyGly 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT: Sures,, Irman G.

ITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN

ITLE OF INVENTION: TYROSINE KINASES
                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: unkno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     RAME: Coruzzi, Laura A EGISTRATION NUMBER: 30,742
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                                                                                                                                                                                                                                                                                                                       ELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       OR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASSIFICATION: 435
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1155 Avenue of the Americas
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Gishizsky,, Mikhail
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Mismatches:
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Qy 328 AsnThri	Qy 309 ThrAlaT:::: Db 1988 TATTCAA	Qy 289 ArgMet( Db 1961	Qy 271 Glu ::: Db 1928 AAATAAT	QY 255 Db 1868 TAACTTC	Qy 240 ThrPheN     Db 1809 ACACTGO	Qy 220 ProGluI    :::: Db 1785 CCTAAGO	Qy 200 ProGluc     Db 1728 CCATCC	Qy 180 Hishiso Db 1674 ATGACAC	Qy 161 PheSerT:::   : :::   : Db 1614 TGGTCAT	Qy 141 ProGlyT Db 1566	Oy 128 Db 1506 GTAGAT <i>I</i>	Qy 111 ASPVall     Db 1449GTTC	Qy 91 HisLysI Db 1401 GAGTCTC	Qy 73 HismetI     73 HismetI   73 HismetI	Qy 53 SerSerLe	Qy 35 Leuileo	Qy 15 SerGlur :::::  Db 1179 AATGACT
roGlnGlnAlaLeuAspTh;      GCAACACTGCAGGACAGTO	hre	gMetCysCysProGlyMetLysVa	SerargasnTyrThrValValasn        :::     CCATTCCAPAATACPATGTTATCAAC	ATAAGATGAAC	etTyrGluLeu :::::    GTTGGAAACTT	OGluLysArgProLeuAlaLeuSerVa  :::::    TAAGGAACGA	roGluGluValGlnPheArgArgLeuGlnAlaI 	HisHisGlnLeuGlnIleAlaLysLysLeuSer     :::     ::: argacaggrgcccaggraarccagargrrggcr	YrGlyMetValLeuTyrGluLeuLe ;:   :::::          TTGGAATCCTTCTTTATGAAATCAT	yrGlnAlaProGluI         GCGCCCGAAG		ySGluHiSIleAsnIleLy:         GTGAACATAATATCTACAA	ysAsnIleIlePheCysAsj 	MetLeuThrGlnLysIleAlaTy            arcTgAcTcAACAGGTAGACATGGCGGC	euAsnThrValleuSe 	ilyIleSerIleH1; ;;; ;CTGTTTGCACTTTAGAAGA;	heArgGlnGluAlaSerMet    :::      ::  TCCTGAGGGAGGCACAGATI
ThrProGlnGlnAlaLeuAspThrProAlaValThrCysPhe	lluaspGlnLysIleTyrIleTyrThrLeuLysGlyMetCysP: ::	LysValSerCysGlnLeuGlnValGlnArgSerLeuTrp 	ThrGluLys	GlnGlyGlnGlüTyrThrvalValPheTrpAspGlyLySGlu    :::      	lyLysGlnThrAlaPhePhe :::     ATTTTGAAACAGA-CTCTTCAT	lValSerGlnMetLysAsı	JGlnAlaLeuMetMetGluCys :::   :::      !TACAACATCATGTTGGAGTGC	LysGlyIleArgPr ::: CAAAACTATAGA	uSerGl ::::    TACTTATGG	.gProArgIleValTyrAspGl ; ; ; !TCGTAGTAATAAATTCAGCAT	InSerPheHisGluGlyAlaLeuGlyValGluG::           ::	pVallysGluHisIleAsnIleLysLeuSerAspTyrGlyIleSerArg- 	isLysLysAsnIleIlePheCysAspLeuLysSerAspAsnIleLeuValTrpSe	-AlaTyrGlnIleAlaSerGlyLeuAl 	rGluAsnAlaArgAspSerSerPheIlePr 	LeulleGlylleSerIleHisProLeuCysPheAlaLeuGluLeuAlaProLeu 	SerGluPheArgGlnGluAlaSerMetLeuHisAlaLeuGlnHisProCysIleValAla :::::    :::     :::       AATGACTTCCTGAGGGAGGCACAGATAATGAAGAACCTAAGACATCCAAAGCTTATCCAG
eLeuAlaValPro     ACTGCCTGGAAAA	-MetCysProLeu           TTTGTGCATTTTA	nArgSerLeuTrp       GTTTATCCTGACA	GlyLeuMetGluValGln	paspGlyLysGlu      CAAAACAAATTC	ATTCAGATGCAAA	ב ג	sTrpAspThrLys     ::: CTGGAATGCAGAG	oValLeuGlyGln         CTTCCGCAA	yGlnArgProAlaLeuGly  :::          caaaaTGCCTTACAGTGGT	pGluLysValAspMet        ::: CATTAAGTCCGATGTA	yValGluGlyThr    :::      GGTGAAGTGGACT	rarg :    cagagttttaag	uValTrpSerLeu   	yLeuAlaTyrLeu  :::         AATGGCCTATCTG	elleProLeuGly	uLeuAlaProLeu       TTGATGAGACAT	OCYSIleValAla   ::::: AAAGCTTATCCAG
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266 pAspGlyLysGluGluSerArgAsnTyrThrValValAsnThrGluLysGlyLeuMetGl	1281 GAAAAGATTAAGTCAGAAGGGACCTGTCTGCACCGCCTAGAAGAGGAACTGGTGATGAGG	260GluTyrThrValValPhe-Tr	JPOINTH ALECTRIC FROM SELECTION OF THE S	מהנה השהיה   הפלימה המינה במינה המונים המינה במינה המונים במינה במינה במינה במינה במינה במינה במינה במינה במ   מחולה במינה במינה במינה במינה במינה במינה במינה במינה במינה במינה במינה במינה במינה במינה במינה במינה במינה ב		1134 TGCTGGAATAGCAAACCACGAAATCGCCCATCATTCCGACAGATCCTGCTGCATCTGGAC			<b>ArgArgLeuGlnAlaLeuMetMetGl</b> u	ATCTGGGGTGTGGGAAGCAACAGTCTCCATCTGATCTGGGGTGTGGGAAGCAACAGTCTCCATCTG		ValleuryTGluLeuLeuSerGlyGlnArgPro	CCIVAGGIGATCCGCAATGAACCTGIGTCTGAGAAGGTCGACATCTGGTCCTTTGGCGTG		AAGGAGCTGAGTGACAAGAAGCACCAAGATGTCCTTTGCAGGGACAGTAGCCTGGATGGCC	AIGGINSETPHENSGINGLYALBLENGLYVALGLUGLYTNTPTOGLYTYTGINALA	WICKCINCHAUGHIGIG	ValTrpSerLeuAspValLysGluHisIleAsnIleLysLeuSerAspTyrGlyIleSer	ATGAACTACCTGCACCTGCACAAGATTATCCACAGGGATCTCAAGTCACCCCAACATGCTA	LeuAlaTyrLeuHisLysLysAsnIleIlePheCysAspLeuLysSerAspAsnIleLeu	CCTGTCACCCCCTCCTTACTGGTTGACTGGTCCATGGGCATCGCTGGTGGC	SerPheIleProLeuGlyHisMetLeuThrGlnLysIleAlaTyrGlnIleAlaSorGly	ATGGAGTTCTGCGCCCAGGGCCAGCTGTATGAGGTACTGCGGGCTGGCCGC	47 LeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAlaArgAspSer 66	606 CACCCCAACATCATCACTTTCAAGGGTGTGCGCACCCCAGGCTCCCTGCTACTGCATCCTC	SerIleHisProLeuCy		erMetLeuHisAlaLeuGln	-836-392-21 (1-728) x US-08-395-580-1 (1-3389)	6.74% Indels:	257.50 t Similarity: 32.14% ocal Similarity: 21.16%	Scores: 6.51e-15 Length:	US-08-395-580-1
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	equence 1, Appl	equence 34,	equence 3, Appl	equence 5,	equence 1, Appl	equence 14,	equence 14, App	equence 16, App	equence 1, Appl	equence	1	Sequence 1, Appli	e 1, Appl	equence 1,	equence 104, Ap	e 77	equence 1, Appl	Ф ~	Sequence 4, Appl1	e 4	equence 4,	е 4-	equence 4, App	e 4, App	Sequence 4, Appli	e 4, App	e 4, App	e 6, Appl	equence 6, Appl	equence 6, Appl	equence 6, Appl	equenc	, Appl

## ALIGNMENTS

JS-09-387-212-10

APPLICANT: ROBISON

Patent No.

10, Application US/09387212A 5, 6309849

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US-09-836-392-21 (1-728) x US-09-387-212-10 (1-526)
                                                         Percent Similarity:
Best Local Similarity:
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                                         Query Match:
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                                                                                                                                                                                                                                       SOFTWARE:
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                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID
                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                         LENGTH: 526
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AspLeuLysSerAspAsnIleLeuValTrpSerLeuAspValLysGluHisIleAsnIle 118

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TITLE OF INVENTION: NUCLEIC ACID MOLECULES E
TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES
FILE REFERENCE: MNI-090
CURRENT APPLICATION NUMBER: US/09/948,802
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 09/387,212
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 10
LENGTH: 526
TYPE: DNA
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139 GlyThrProGlyTyrGlnAlaProGluIleArgProArgIleValTyrAspGluLysVal 158
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                                                                                                                                 TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch disk, 720

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS
                                                                                                                                                              NAME: Rebecca L. Ralph (formerly Gaumond)
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: CH-0488
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                          APPLICATION NUMBER: 08/20 FILING DATE: 01-MAR-1994 ATTORNEY/AGENT INFORMATION: NAME: Rebecca L. Ralph ()
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
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ADDRESSEE: Woodcock
STREET: One Liberty
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                            FEATURE:
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                                      Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PMO&t2=PMO-MTO202-
090501-013-hil&t3=2001-05-09&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 477.
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Rua Prof. Antonio Prudente 109, 4 an
                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
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                                                                                             nGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSerFroProArgGlnAl 565
                                                                                                                                                                                AspThrGluProProAlaAlaSerHisThrAlaAsnProLysValProGluGlyAspSer 525
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                                                                                   GGAATCACTCACTGACTACTGCTCCATGTCCTCCTACTCCTCATCCCCACCCCGCCAGGC
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                                Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 707)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                  AZ358773 707 bp DNA linear GSS 0: IM0101P17F Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0101P17 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                             967
plasmid inserts
Unpublished (2000)
                                                                                                                                                              Eukaryota; Metazoa;
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CCTGTGGCACGGGGCACCCCAAAAGAAGCTGCTCCTACCTGTGCTCCCACACAGCCAAC
                  ProValValArgGlyThrProLysAspSerCysSerTyrLeuCysSerHisThrAlaAsn
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                                                                   CCCCCACAGAACTCCTTCCTGGTGCTGGCAGGCCTGGCTGACGGACTCGTGGCTGTTTT
                                                                                       AlaValValThrCysPheLeuAlaVal-----
                                                                                                                                       TCTGTGGTTTCTCTCTCGCATGTGTGACATGAAAGAATATTGTGTGTCCCTGTCCCTTC
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0
Plate: 0101 row: P column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                           IleTyrThrLeuLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThrPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor ollgonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwm12 (gi14732114|gb)AF1290721), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XIIO-Gold (Stratagene) cells and selected for ampicillin resistance."
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/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0101P17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                            AAGATCATGTGACCACTTGAGGCACATAGAGAG----ATGAGTCTGGTG
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AACTCCTTCCTGGTGCTGGCAGGCCTGACGGACTCGTGGCTGTTTTCCTGTGGCA
                                                                               CAGGCCCTGGACACCCCAGCTGTCGCACCTGTTTCTTGGCAGTACCTGTTATCAAAAAG
                                                                                                     GlnAlaLeuAspThrProAlaValValThrCysPheLeuAlaValProValIleLysLys
                        AsnSerTyrLeuValLeuAlaGlyLeuAlaAspGlyLeuValAlaValPheProValVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sug
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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primer adapter of sequence [5,
GAGAGAGAGTTCTCGGTTAATTAATTCCCCCCCCCCCC 3,]
was cloned into the XhoI and BamHI sites. Vector: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by
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prepared and sequenced in Mouse Genome Encyclopedia
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/dev_stage="16 days
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/clone="C130082A22"
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/strain="C57BL/6J"
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Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Fujiwake,S., Inhlawa,T., Ozawa,K., Tanaka,T., Matsuura
1,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
/note="s1+- "
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BM469840
                                                                                                                                                                                                                    High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae 1 (bases 1 to 996)
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                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information ca
/Clone_lib="NIH_MCC_85"
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/tissue_type="lymphoma, cell line"
/lab_host="PHHOB (phage resistant)"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
                                                                                                                                     /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"IMAGE:5552973"
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.

Query Score Match Length DB

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Description

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39.3	39.3	39.3	39.3	39.3	39.3	39.3	42.8	42.8	43.1	49.8	49.8	. 88.7	88.7	88.7	88.7	97.6	99.9	100.0	100.0	100.0
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 8	Sequence
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FILE REFERENCE: PT0020CT
CURRENT APPLICATION NUMBER: PCT/US00/28066
CURRENT FILING DATE: 2000-10-12
PRIOR PPPLICATION NUMBER: 60/159,542
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/165,914
PRIOR FILING DATE: 1999-11-17
PRIOR FILING DATE: 1999-11-17
PRIOR FILING DATE: 1999-13-17
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 34
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PCT-US00-28066-8
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; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US00-28066-8
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PRIOR FILI
NUMBER OF
SOFTWARE:
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Human Geneme Sciences, Inc.
TITLE OF INVENTION: Protein Tyrosine Kinase
TITLE OF INVENTION: Antibodies
FILE REFERENCE: PT020PCT
                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 2184; Conservative 0
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US-10-092-399-38919

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US-09-902-919-4

US-09-342-216A-400

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US-09-362-510A-61416

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US-09-99-489-036-7225

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Sequence 4, Appli
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Sequence 400, App
Sequence 400, App
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Sequence 1275, Ap
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Sequence 10, Appl
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Sequence 10, Appl
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Sequence 51416, A
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RESULT 2
US-09-836-392-8
; Sequence 8, Application US/09836392
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Protein Tyrosine Kinase Rec; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: PT020P1
; CURRENT APPLICATION NUMBER: US/09/836,392
; CURRENT FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: PCT/US00/28066
; PRIOR FILING DATE: 2000-10-11
; PRIOR APPLICATION NUMBER: 60/159,542
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PRIOR APPLICATION NUMBER: 60/16:
PRIOR APPLICATION NUMBER: 60/18:
PRIOR APPLICATION NUMBER: 60/18:
PRIOR FILING DATE: 2000-03-14
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
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ORGANISM: Homo
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SOFTWARE: PatentIn V
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Best Local :
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CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/226,282
PRIOR FILING DATE: 2000-08-18
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ORGANISM: Homo
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                                 TCTGACTACGGGATTTCGAGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACT
                                           TCTGACTACGGGATTTCGAGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACT
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(GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: 21 human secreted protei
FILE REFERENCE: PS726PCT
CURRENT APPLICATION NUMBER: PCT/US01/01435
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/226,282
PRIOR FILING DATE: 2000-08-18
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 3564
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; TYPE: DNA
; ORGANISM: Homo s
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Best Loc
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Local Similarity
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ATGCTGAGGCACCTGCGGGCCACCGATGCCATGAAGAACTTCTCCGGAGTTCCGGCAGGAG
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PCT-US01-08631-8042

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APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR REFERENCE: 21272-049
CURRENT APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NO 8042
LENGTH: 2652
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FRATURE:
NAME/KEY: SIMILAR
LOCATION: (136)..(1515)
OTHER INFORMATION: 29% homologous to Caenorhabditis elegans contains similarity
OTHER INFORMATION: to protein kinases (Pfam:pkinase.hmm, score: 149.36),accession
OTHER INFORMATION: number AF098504, Smith-Waterman Score-427.
-USO1-08631-8042
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TYPE: DNA
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Sequence 5, Application US/10132382

Sequence 5, Application US/10132382

GENERAL INFORMATION:

APPLICANT: WEISS, BERTRAM

TITLE OF INVENTION: MEMBRANE RECEPTORS FOR ST

FILE REFERENCE: SCH-1811

CURRENT APPLICATION NUMBER: US/10/132,382

CURRENT FILING DATE: 2002-04-26

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 7015

TYPE: DNA

ORGANISM: Homo sapiens

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RESULT 7
US-10-132-382-1
VS-10-132-382-1
Sequence 1, Application US/10132382
GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS FOR S
FILE REFERENCE SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 7093
TYPE: DNA
ORGANISM: Homo sapiens
US-10-132-382-1
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Best Local Similarity

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RESULT 8
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US-10-132-382-7
Sequence 7, Application US/10132382
GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS FOR S
FILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 7
SEQ ID NO 7
LENGTH: 7229
TYPE: DNA
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                                                       ATCCTGATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCTACTCCTCATCC
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RESULT 9
US-10-132-382-3
; Sequence 3, Application US/10132382
; GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STI
FILE REFERENCE: SCH-1811
; FILE REFERENCE: SCH-1811
; CURRENT APPLICATION NUMBER: US/10/132,382
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
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LENGTH: 7307
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ORGANISM: Homo:
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RESULT 10 PCT-US02-05109-456 Sequence 456, Applicat GENERAL INFORMATION:
APPLICANT: HySeq Inc.
APPLICANT: Tang, Tom APPLICANT: APPLICANT: APPLICANT: APPLICANT: PPLICANT: PPLICANT: PPLICANT: Yang, Long Ma, Yunging Pi, Victoria Goodrich, Ryle Asundi, Vinod Zhang, Jie Zhao, Qing A. Ren, xue, Application PC/TUS0205109 , Felyan , Aldong J. g, Yonghong יי Ping א. Ryle אי Tom Y.

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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (872)..(1834)~
CT-USO2-05109-456
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Best Local Similarity
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SEQ ID NO 456
LENGTH: 2839
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TITLE OF INVENTION: Novel Nucleic Acids and
FILE REFERENCE: 2127-094-061
CURRENT APPLICATION NUMBER: PCT/US02/05109
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 09/810,173
PRIOR FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 1052
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GGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTCCCCAGCTAGTTCTTCCAGTGTGCCTTT
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Wang, Dunrui
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Ghosh, Malabika
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0; Mismatches 33;
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                                                           FILE REFERENCE: 804
CURRENT APPLICATION NUMBER: US/09/810,173
CURRENT FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 526
SOFTWARE: Pt_fl_genes Version 2.0
SEQ ID NO 456
LENGTH: 2839
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 456, Application GENERAL INFORMATION:
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FEATURE:
NAME/KEY: CDS
LOCATION: (872)..(1831)
                                   TYPE: DNA
ORGANISM: Homo
                                                                                                                                                 APPLICANT: Drmanac, Radoje T.
ITLE OF INVENTION: Novel Nucleic
ITLE OF INVENTION: Polypeptides
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Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
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Goodrich, Ryle
Asundi, Vinod
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Wang, Zhiwei
Yamazaki, Victoria
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Wehrman, Tom
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EARLIER APPLICATION NUMBER:
EARLIER FILING DATE: 1999-12-16
NUMBER OF SEQ ID NOS: 10451
SOFTWARE: pt_CT_genes Version 1.0
SEQ ID NO 7370
LENGTH: 995
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (298)...(811)
OTHER INFORMATION: Similar to g1530
OTHER INFORMATION: Run with FASTXY
US-09-471-275-7370
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EARLIER APPLICATION NUMBER: US/09/471,275

CURRENT FILING DATE: 1999-12-23

EARLIER APPLICATION NUMBER: US 09/235,076

EARLIER FILING DATE: 1999-01-20

EARLIER APPLICATION NUMBER: US 09/240,371

EARLIER FILING DATE: 1999-01-29

EARLIER FILING DATE: 1999-01-29

EARLIER APPLICATION NUMBER: US 09/277,227

EARLIER APPLICATION NUMBER: US 09/277,227

EARLIER APPLICATION NUMBER: US 09/271,490

EARLIER FILING DATE: 1999-03-18

EARLIER APPLICATION NUMBER: US 09/271,490

EARLIER APPLICATION NUMBER: US 09/293,972

EARLIER APPLICATION NUMBER: US 09/274,861

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FILE REFERENCE: 782
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APPLICATION NUMBER: US 09/399,720
FILING DATE: 1999-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 60/125,453
FILING DATE: 1999-03-19
APPLICATION NUMBER: US 60/126,605
FILING DATE: 1999-03-26
APPLICATION NUMBER: US 09/306,350
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Search completed: April 15, 2003, 06:31:19
Job time: 3391 secs

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RESULT 13
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Culpepper, Janice A
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; SOFTWARE: FastSI
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US-09-637-890-9034
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Best Local Similarity
Matches 937; Conserv
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CURRENT APPLICATION NUMBER: US/09/637,890
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/147,939
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 10217
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                                                                         GAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGACACTAAGCCA
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US-09-644-869-9514
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SOFTWARE: FastSEQ fo:
SEQ ID NO 9514
LENGTH: 1912
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Best Local Similarity
Matches 937; Conserv
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TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 1600.1182-001
CURRENT APPLICATION NUMBER: US/09/644,869
CURRENT FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: 60/51,062
PRIOR FILING DATE: 1999-08-27
PRIOR FILING DATE: 1999-08-27
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                                                 TCTGACTACGGGATTTCGAGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACT
                                                                   TCTGACTACGGGATTTCGAGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACT
                                                                                                             AAGTCGGACAACATTCTGGTGGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTA
                                                                                                                                 AAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTA
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Holtzman, Douglas A.
Monahan, John
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Pred. No. 2.9e-182;
0; Mismatches 4;
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PCT-US01-01354-25701
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GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, I
TITLE OF INVENTION: Nucleic Acids,
FILE REFERENCE: PC004PCT
                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
SEQ ID NO 25701
LENGTH: 18286
                                                                                                                                                                                                                                                                                                 Matches
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Best Local Similarity
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                                   TGGTCAACAGCGGCTCTGAGGTCTGGTACAGCAATGGGCCGGGCCTCCTTGTCATCGACT
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ilarity 96.0%;
Conservative
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2001-03-17
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Pred. No. 1.7e-166;
0; Mismatches 37;
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Proteins, and
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Searched:
Database :
                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                        Perfect score:
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2184
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5386.053 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2.5						. 2	N	2:8	2.9	3.0	3.1	3.1	ω. 1	3.1	4.9	6.2	8.2	13.0	13.1	15.8	84.2	87.6	Match I
3364		3285	3285	83	3113	1427	1329	1069	1497	381	1878	2506	3138	3138	601	361	1330	500	288	352	3112	4120	Length
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Sequence 20993, A		-Segmence 20991. A	Sequence 20991, A	Sequence 46691, A	Sequence 1766, Ap	Sequence 6444, Ap	Sequence 55, Appl	Sequence 43167, A	Sequence 4356, Ap	Sequence 2993, A	Sequence 25817, A	Sequence 1475, Ap	Sequence 7097, A	Sequence 1806, A	Sequence 15716, A	Sequence 46466, A	Sequence 18122, A	Sequence 231260,	Sequence 16014, A	Sequence 127829,	Sequence 50, Appl	Sequence 66, Appl	Description

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δ	σ	6	σ	o	σ	σ	თ	σ	o,	σ	σ	σ	σ	თ	6	σ	o,	σ	σ	σ	σ	σ
US-09-724-676A-22322	US-09-724-676-22322	US-09-724-676A-22316	US-09-724-676-22316	US-09-724-676A-22326	.US-09-724-676-22326	US-09-724-676A-22368	US-09-724-676-22368	US-09-724-676A-22356	US-09-724-676-22356	US-09-724-676A-22376	US-09-724-676-22376	US-09-724-676A-22319	US-09-724-676-22319	US-09-724-676A-22328	US-09-724-676-22328	US-09-724-676A-22370	US-09-724-676-22370	-724	US-09-724-676-20992	US-09-724-676A-20990	US-09-724-676-20990	US-09-724-676A-20993
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Query Match 87.6
Best Local Similarity 93.3
Matches 2073; Conservative
                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Program
SEQ ID NO 66
LENGTH: 4120
                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: PT-1240 PCT
CURRENT APPLICATION NUMBER: PCT/US03/01363
                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/349,413
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/349,946 PRIOR FILING DATE: 2002-01-17
                                                                                                                                                                                NAME/KEY: misc_feat
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT: PANESAR, IQDal S.
ITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INCYTE GENOMICS, INC.; JONES, Anissa L.;
DAHL, Christopher R.; GIETZEN, Darryl;
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TUASON, Olivia; YI
AMSHEY, Stefan R.
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                                                                                                                                                                                                _feature
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                                                                                                                                                                                Incyte ID No: LG:337452.25:2002JAN18
                  87.6%;
93.3%;
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                                                                                                g, or other
                    Score 1913.8;
Pred. No. 0;
Mismatches
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                                       DB 1; Length 4120;
  2;
  Indels 148; Gaps
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results. These databases were split into to two parts to reduce the time needed to update the databases daily. The split freed up more machine time for processing searches Pending Nucleic Acid and/or Pending Amino Acid database searches now generate two sets of

extensions, .rnpm and .rnpn Searches run against the Nucleic Acid Pending database produce two sets of results, with the

extensions, .rapm and .rapn Searches run against the Amino Acid Pending database produce two sets of results, with the

contain data that is confidential. The Pending database search results should not be left in the case because they

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APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: US/10/4381
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 50,
LENGTH: 3112
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; ORGANISM: Homo sapiens US-10-094-749-50
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Best Local Similarity
Matches 1851; Conserv
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APPLICANT: SUGIYA
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OTSURA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
YOSHIKAWA, TSUTOMU
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                                                                                                                             NAME/REY: misc_feature
LOCATION: (331). (351)
OTHER INFORMATION: n is equal to a,t,g, or
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PRIOR FILING DATE: 1993-08-09
PRIOR APPLICATION NUMBER: 09/249,651
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: 08/104,507
PRIOR FILING DATE: 1993-08-09
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                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                     FEATURE:
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1740 CAGTGTGCCTTTCTCCACCGACTGCGAGGACTCAGACATGCTACATACGCCCGGTGCTGC 1799
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                                                                                                                                                                                                                                         PE: DNA
                                                                                                                                                                                                                                                       NO 127829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/196,363
FILING DATE: 1994-02-15
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                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/813,155
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LING DATE: 2001-05-18
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NG DATE: 1994-03-31
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llarity 99.1%;
Conservative
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                                                     Score 345.2; DB 6;
Pred. No. 2.2e-68;
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; LOCATION: 192, 263
; OTHER INFORMATION:
US-10-349-781-16014
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Seilhamer, Jeffrey J.; Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.; Stuve, Laura L.
APPLICANT: Mullahy, Sara J.; Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIV
FILE REFERENCE: PD-1028-2 CON
                                                                                                                                                                                                                                                                                                Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 61458
SOFTWARE: PERL Program
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PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 08/92,868
PRIOR FILING DATE: 1997-12-11
PRIOR APPLICATION NUMBER: 60/032,838
PRIOR FILING DATE: 1996-12-13
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                                                                                                                                                                                                          ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                      NAME/KEY: misc_feature OTHER INFORMATION: Inc
                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/772,783 FILING DATE: 1996-12-23
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/008,794
FILING DATE: 1995-12-14
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SEQ ID NO 231260
LENGTH: 500
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2001-03-2:
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PRIOR FILING DATE: 1993-08-09
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                                                                                                                                                                        OTHER INFORMATION: n is
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OTHER INFORMATION: n is
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             NAME/KEY: misc_feature
OCATION: (222)..(222)
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LOCATION: (120)..(120)
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OCATION: (22)..(22)
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INFORMATION: n
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Best Local S
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LOCATION: (437)..(437)
OTHER INFORMATION: n is
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LOCATION: (341)...(341)
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LOCATION: (470)..(470)
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LOCATION: (450)..(450)
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                                                            CTGCCCTGGGATGAAGGTGAGCTGCCAGCTCCAGGTCCAGAGATCCCTGTGGACAGCCAC 932
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                                                                                                      GTCCAGGAACTACACGGTGGTGAACACAGAGAAGGGCCTCATGGAGGTGCAGAGGATGTN
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US-10-144-771-18122
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SEQ ID NO 18122
LENGTH: 1330
TYPE: DNA
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CURRENT FILING DATE: 2002-05-15
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                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/912,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: CL001321
                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1993-08-09
                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/103,744
                                                                                                                                                                                                                                                                                                                                                    (TLE OF INVENTION: Human Genes, Sequences,
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                                                                                                                                                                                                                                                                                                                                   REFERENCE: PO-100
                                                                                                                                                                                                                APPLICATION NUMBER: 09/249,651 FILING DATE: 1999-02-12
                                                                                                                                                   FILING DATE: 1993-08-09
APPLICATION NUMBER: 08/196,363
APPLICATION NUMBER: 08/220,691
                                        APPLICATION NUMBER: 08/221,623
                                                              FILING DATE:
                                                                              APPLICATION NUMBER:
                                                                                                                   APPLICATION NUMBER: 09/859,490
                                                                                                                                       FILING DATE: 1994-02-
                                                                                                                                                                                              APPLICATION NUMBER: 08/104,507
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HUMAN GENOME DISCOVERY
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Pred. No. 1.5e-30;
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US-09-947-907-15716

Sequence 15716, Application US/09947907
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
COLLECTION OF CODING REGION SINGLE
TITLE OF INVENTION:
NUCLECTIOE POLYMORPHISM (CSNPS) LOC
TITLE OF INVENTION:
CHROMOSOMES, METHODS OF DETECTION,

LOCATED

EACH OF THE HUMAN

CURRENT APPLICATION NUMBER: US/09/947,907

FILE REFERENCE:

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Best Local S
Matches 137
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Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 244538
SEQ ID NO 46466
LENGTH: 361
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LOCATION: (307)..(307)
OTHER INFORMATION: n i
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LOCATION: (162)..(162)
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OTHER INFORMATION: n
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les 137; Conserv
                          CTTGCACTCGCAAGAGAAGG, 2184
                                                                              GGGGCGCCAGGGAGTTCGACATTTTCTACCAGTCCTACGAGGAGCTGGGCCCGGCTGGAGG 2164
                                                                                                        CTGTTGTGTGCACCTTTGAAAATGAAAACACAGAGTGGTGCCTGGCCGTCTGGAGGGGCT
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CTTGCACTCGCAAGAAAAGG 140
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03

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RESULT 10
US-60-452-680-7097
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JS-60-455-444-1806
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SEQ ID NO 15716
LENGTH: 601
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-09-947-907-15716
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CURRENT FILING DATE: 2003-03-18
NUMBER OF SEQ ID NOS: 50986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CARGILL, Michele APPLICANT: BEGOVICH, Ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
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                                                                                                                                                                                                                              1786
                                                                                                                                                                                                                                                                                                                                                                               1675 AAATCGCTATCGGCCTSTTCTTCCTTCACAATCAGGGCATCATCTACAGGGACCTGAAGC 1734
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                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 55.3 es 156; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                         TGGACAATGTGATGCTG----
                                                                                                                                                                                                                                                                                                                              CGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACCATCAAGCTATCTG 364
                                                                                                                                                                                                                              GCATGTGTAAGGAGAACGTCTTCCCCGGGACGACAACCCGCACCTTCTGCGGGACCCCGG
                                                                                                                CCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCC 527
                                                                                                                                                     ACTACATAGCCCCGGAGATCATTGCCTACCCAGCCCTATGGGAAGTCTGTCGATTGGTGGT
                                                                                                                                                                                        GCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTAGATATGTTCT 484
                                                                                                                                                                                                                                                                   ACTACGGGATTTCGAGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.1%;
                                                                                                                                                                                                                                                                                                         -----GATGCTGAGGGACACATCAAGATCACTGACTTYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107.6; DB 7, Pred. No. 1.7e-14; 1; Mismatches 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 68.6; DB 10;
Pred. No. 1.9e-05;
2; Mismatches 116;
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GENERAL INFORMATION

Sequence 7097

Application US/60452680

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305 CGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTATCTG

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LENGTH: 3138
; TYPE: DIA
ORGANISM: Homo sapiens
US-60-452-680-7097
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                                                                                                                                                                                              ; ORGANISM: Human US-09-949-016-1475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1475, Application US/09949UL6
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS
                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1475
LENGTH: 2506
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Best Local Similarity 55.1%;
Matches 156; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
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APPLICANT: GRUPE, Andrew
                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/237,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/241,755 PRIOR FILING DATE: 2000-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1846 ACTACATAGCCCCGGAGATCATTGCCTACCAGCCCTATGGGAAGTCTGTCGATTGGTGGT 1905
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                                           245 AGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTGAAGT 304
                                                                                            Local Similarity
nes 157; Conserv
AAATCGCTATCGGCCTCTTCTTCCTTCACAATCAGGGCATCATCTACAGGGACCTGAAGC 1642
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                                                                                               Conservative
                                                                                                                   3.1%;
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Pred. No. 1.9e-05;
                                                                                                                 Score 67.8; DB 7;
Pred. No. 2.7e-05;
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                                                                                               Mismatches 117;
                                                                                                                                          Length 2506;
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US-10-282-122A-25817
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SEQ ID NO 25817
LENGTH: 1878
TYPE: DNA
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                                                                                       Query Match
Best Local Similarity
                                                                                                                                            ORGANISM: Mycobacterium avium -10-282-122A-25817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                                   Remaining Prior Application data NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        485 CCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCC 527
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166 TTCCGGCGCGAGGCGCAAAACGCCGCCGCGCTCAACCACCCGTCCATCGTCGCCGTCTAC 225
                                 49 TTCCGGCAGGAGGCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATC 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/207,727
FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/206,848 FILING DATE: 2000-05-23
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                                                                                                                                                                                                                                                                                                         ICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATION NUMBER: 60/3
                                                                                                                                                                                                                                                                                                                            ATION NUMBER: 60/267,636
DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATION NUMBER: 60/230,347
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Malone, Cheryl
Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                  DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                           TION NUMBER: 60/257,931
DATE: 2000-12-22
                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                ION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ON NUMBER: 60/242,578
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                                                               Score 67.4; DB 9; Length 1 Pred. No. 3.1e-05; 0; Mismatches 361; Indels
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                                                                                                                                                                                                                                                                  See File Wrapper
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                                                                                                      Length 1878;
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                                                                                                                                                       : NAME/KEY: misc_feature
: LOCATION: (226)..(372)
: OTHER INFORMATION: n=unknown
US-60-422-176-2993
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                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
SEQ ID NO 2993
LENGTH: 381
                                                                          Query Match 3.0%;
Best Local Similarity 54.8%;
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2993,
                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 3114
                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/60/422,176
CURRENT FILING DATE: 2002-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 01040_PR
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DIFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE POLYPEPT TITLE OF INVENTION: ENCODED THEREBY, AND METHODS OF USING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pharmacia Corporation APPLICANT: Bourner, Maureen J.
                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: homo sapiens
                                                                                                                                                                                                                                       FEATURE:
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                      245 AGATCGCCTCGGGCCTGGCCTGCACCAAGAAAAACATCATCTTCTGTGACCTGAAGT 304
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AAATCGCTATCGGCCTCTTCTTCCTTCACAATCAGGGCATCATCTACAGGGACCTGAAGC 124
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                                                                                               Score 65.8;
Pred. No. 4
                                                                            Mismatches 119;
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                                                                                                                 DB 11;
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                                                                                                                 Length 381;
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US-10-156-761-4356
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Best Local Similarity 43.4%;
Matches 294; Conservative
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SEQ ID NO 4356
LENGTH: 1497
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SAKAKÍ, YOSHÍYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
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CURRENT FILING DATE: 2002-05-29
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464
                                                                                                                                                                                                                                                                                                                    83 AGCACCCCTGCATCGTGGCGCTCATCGGCATCCACCCGCTCTGCTTCGCCCTGG 142
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                                                                                                 CCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGT
                                                                                                                                         CCGAGGCCCCGGGGCCCGAGCAGGCGTTGATCATCGTCTCCGGGGGTGCTGGAGGCGCTGG
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GGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGC
                                                                    CCTACTCGCACCAGCACGGCATCGTGCACCGCGACATCAAGCCGGCCAACGTCATCATCA
                                                                                                                                                                          TTATACCCCTGGGACACATGCTCACCCAAAAAATAGCCTACCAGATCGCCTCGGGCCTGG
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HORIKAWA, HIROSHI
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 64.2; DB 8;
Pred. No. 0.00015;
0; Mismatches 383;
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NUMBER OF SEQ ID NOS: 47374; SEQ ID NO 43167; LENGTH: 1069; TYPE: DNA; ORGANISM: MYXOCOCCUS XANTHUS US-10-369-493-43167
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Best Local Similarity 45.9%;
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                                             346 GCGCACTTCCGCCACATCATCCACCGCGACCTCAAGCCCGCCAACGTCATGCTCACCAAG 405
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                                                                                                                                                                                                                           148 GCGCCGCTCAGCAGCCTCAACACCGTGCTGTCCGAGAACGCCAGAGATTCTTCCTTTATA 207
                                                                                                                                                                                                                                                                                                                 181 CAGAACATCGTGACGCTCTACGACATGGTGGAGAAGGGTGÄGAGCCTCTTCATGGTGATG
                                                                                      268 CTGCACAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGGTCC
                                                                                                                                  286 CCGCTGCCCGCGGATGTCACCGGCGTCATCGCCGCGCGCATCGCCAGCGCGCTGGACCAC
                                                                                                                                                                             208 CCCCTGGGACACATGCTCACCCAAAAAATAGCCTACCAGATCGCCTCGGGCCTGGCCTAC
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13-NOV-2000;
                                                                                                                                                   prions, infections caused by bacteria, interiors caused by bacteria, interiors caused by bacteria, interiors are useful dysfunction, mood disorders, attention disorders, cognition disorders, hypotension, hypertension, psychotic disorders, dyskinesias, and organ transplant rejection. Kinase inhibitors are useful for treating diseases and disorders
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                                                                                                                                                                                                                                                             of tissues and cancers of hematopoietic origin), immune-related discand disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g. Alzheimer's disease, parkinson's disease, multiple
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Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis; development; hepatitis; cardiovascular; hypertension; drug screening; myocardial infarction; Goodpasture's syndrome; lipid disorder; growth; fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;

US-09-836-392-21 (1-728) x AAD38851 (1-7093)

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Percent Similarity:
Best Local Similarit
Query Match:
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                                                                                                                                                                                                                     Treating and preventing cancer, an immune system disorder (e.g., 2 acquired immune deficiency syndrome (AIDS), Addisorder (e.g., 2 affecting and preventing cancer, an immune system disorder (e.g., 2 affecting growth and development (e.g., arteriosclerosis, cirrhosis, 2 affecting growth and development (e.g., hypertension, myocardial) infarction, Goodpasture's syndrome), and a lipid disorder (e.g., fatty 2 liver, Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia, Obesity), and for assessing the effects of exogenous compounds. Anti-PKIN antibody is useful in a diagnostic test for a 2 condition or a disease associated with the expression of PKIN in a biological sample. A composition comprising PKIN or an agonist of a condition decreased or increased expression of functional PKIN. 2 associated with decreased or increased expression of unctional PKIN. 2 condition is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN DNA is useful for creating and in somatic or germline gene therapy. The present sequence is human for many and in somatic or germline gene therapy. The present sequence is human contains to many and the sequence is human contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains and contains a
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27-OCT-2000;
03-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human kinase polypeptide, for diagnosing, preventing and treating cancer, immune system disorders, growth and development disorders, cardiovascular disorders and lipid disorders
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                                                                                                          NO . :
                                                                                                                                                                       Sequence 7093
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Rosen CA, Barash SC, Ruben SM;

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 25701; 3071pp + Sequence Listing; English

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and care treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased cexample, they may be used to treat disorders associated with decreased cexample, they may be used to treat disorders associated with decreased cexample, they may be used to produce the nactive proteins or to supplement the patients own production of (I). Additionally, (I) concepts and send be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent; and cancer metastases of haematopoletic acids: AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK54942 to AAK5590 and AAM82169 represent sequences used in the exemplification of the present invention AAK54951 to AAK64702 encode the human immune/haematopoietic antigen amino acid sequences given in AAM82170 to AAM91921. (I) have cytost

Sequence 18286 BP; 4372 A; 4856 C; 4941 G; 4117 T; 0 other;

US-09-836-392-21 (1-728) x AAK70889 (1-18286)

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밁 13685 405 ProValLysAlaMetGluValValAsnSerGlySerGluValTrpTyrSerAsnGlyPro 424 CCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTACAGCAATGGGCCG 13744

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.505 LeuAspThrGluProProAlaAlaSerHisThrAlaAsnProLysValProGluGlyAsp 524
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GAGCACGGCTACCGACAAATCGCTTCCCCTTCTGGGTTTTTGGTTGCTTAGGCGCGGTGGA
                                                                                                                                                                                           TGGGAATGGAAGCGATCGCTTTAGCAAATCTAAGAGTGGCCGCACAAAAGCTTATTGCCT 14583
                                                                                                                                                                                                                                                                                          CATCCAGGGCACGCCCACTGCTCCTGCTCTGGGGACAGAGGGGGAAGCCCCCTGGCT 14463
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                                              AAACTGCATGTCTGTTGCCTCCCTCCCGCACCTTTCTGCACACCGGCTTCACTCCCCGGA
                                                                                             TGAGAAAATTCTCCTCTGCTTTGAAGTCTGTCCCCCTCCCCATAACTTAATCCCTTAGCAG
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05-SEP-2000;
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cytostatic; gene therapy; vacci
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vaccine; metastasis; ds.
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2000US-0251988.
2000US-0256719.
2000US-0251479.
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2000US-0251989
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                                                                                                            SCI INC
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Rosen ÇĄ, Barash SC, Ruben ;MS

2001-483426/52.

Nucleic acids encoding useful for preventing, metastasis human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and

Disclosure; SEQ Ħ ö 38916; 3071pp + Sequence Listing; English.

amino acid sequences given in AAM82170 to AAM891221. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) controlled treatment of diseases may be used in the prevention, diagnosis and controlled treatment of diseases associated with inappropriate (I) expression. For controlled the activity of the controlled treatment of a patient's genome controlled the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) controlled tides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, controlled acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, controlled acancer metastases of heematopoletic derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK84942 to AAK54950 and AAM82169 contents a sequences incoming the account invention. AAK54951 to AAK64702 represent sequences used in the exemplification of the encode the human immune/haematopoietic antigen present invention and

Sequence 18286 BP; 4372 A; 4856 C; 4941 G; 4117 T; 0 other;

US-09-836-392-21 (1-728) x AAK84104 (1-18286)	DB:	Best Local Similarity:	Percent Similarity:	Score:	Pred. No.:	Alignment Scores:
) x AAK84104	22	67.73%	68.15%	1560.50	1.27e-113	
(1-18286)	Gaps:	Mismatches:	Conservative:	Matches:	Length:	
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밁 S 13505 346 ValProVal---IleLysLysAsnSerTyrLeuValLeuAlaGlyLeuAlaAspGlyLeu :::|||||||
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ATCCCTGTCTCCTTCCTTCAGAATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTT 13564

QΥ ₽ Ş 13565 385 365 HisThralaasnargSerLysPheSerIlealaaspGluaspalaargGlnasnProTyr 404

CACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATGAAGACGCACGGCAGAACCCCTAC 13684

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                                                                                          TGGGAATGGAAGCGATCGCTTTAGCAAATCTAAGAGTGGCCGCACAAAAGCTTATTGCCT
                                                                                                                      TCCTTACAGGTCATGTGGGGAGGCAGGTGCTGCTTCTTCCAAGAGGGTTTGGTTTCCTCCAT
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                                                              GCCAGAGAGCTTAAGGTGCCACACAAGGAAAGCCACAGTCAACTGTGACTCAGTTTCCAC
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                                   TGAGAAAATTCTCCTCTGCTTTGAAGTCTGTCCCCCTCCCCATAACTTAATCCCTTAGCAG
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24-FEB-2000;
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2001WO-US01354.

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           Human; immune;
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haematopoietic; immune/haematopoietic ne therapy; vaccine; metastasis; ds.
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              cancer;
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2000US-0251868.
2000US-0251869.
2000US-0251989.
2000US-0251990.
2000US-0254097.
2001US-0259678.
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2000US-0249297
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Ruben MS

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis

Disclosure; SEQ ID NO 25704; 3071pp + Sequence Listing; English

AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAM62170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to provent, diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic-derived cells. AAK64703 concers and cancer metastases of haematopoletic antigen genomic sequences from the present invention. AAK84942 to AAK84950 and AAM82169 crepresent sequences used in the exemplification of the present invention.

Sequence 18287 BP; 4371 A; 4858 C; 4942 G; 4116 T; 0 other;

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Pred. No.:	1.27e-113	Length:	18287
Score:	1560.50	Matches:	319
Percent Similarity:	68.15%	Conservative:	N
Best Local Similarity: 67.73%	67.73%	Mismatches:	4
Query Match:	40.83%	Indels:	147
DB:	.22	Gaps:	N
US-09-836-392-21 (1-728) x AAK70892 (1-18287)	) x AAK70892	(1-18287)	
Qy 346 ValProValIleLysLysAsnSerTyrLeuValLeuAlaGlyLeuAlaAsp	leLysLysAsnSe	rTyrLeuValLeuAlaG	lyLeuAlaAspo
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13506 ATCCCTGTCTCCTTCAGAATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTT 13565
                                                           GlyLeu
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13686

405

13626

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14824 639 14764

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GlnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSerProProArgGln
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                  TGAGAAAATTCTCCTCTGCTTTGAAGTCTGTCCCCTCCCCATAACTTAATCCCTTAGCAG
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                                                                                      GCCAGAGAGCTTAAGGTGCCACACAAGGAAAGCCACAGTCAACTGTGACTCAGTTTCCAC
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RESULT 10

AAK84107

ID AAK84107

AC AAK84

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2000US-0209467.
2000US-0214886.
2000US-0215135.
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2000US-0205515
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antigen; cancer;

SEQ 당

NO:38919

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05-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000; 08-SEP-2000; 08-SEP-2000;

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                                                                US-09-836-392-21 (1-728) x AAK84107 (1-18287)
                                                                                                           Query
                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                               Pred. No.:
                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                  amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic concers and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For cexample, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to complement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent. (C) classome and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic actived cells. AAK64703 to AAK97694 represent human immune/haematopoietic actived cells. AAK64703 to AAK97694 represent invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
346 ValProVal---IleLysLysAsnSerTyrLeuValLeuAlaGlyLeuAlaAspGlyLeu 364
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13506 ATCCCTGTCCTTCCTTCAGAATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTT 13565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                                                                                                            Sequence 18287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN
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2000US-0254097.
2001US-0259678.
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                                                                                              1.27e-113
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68.15%
67.73%
40.83%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human immune/hematopoietic diagnosing and/or treating
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                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
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2000US-0246611 2000US-0246613

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14644	GCCAGAGAGCTTAAGGTGCCACACAAGGAAAGCCACAGTCAACTGTGACTCAGTTTCCAC	14585	Db
635		635	Qy
14584	TGGGAATGGAAGCGATCGCTTTAGCAAATCTAAGAGTGGCCGCACAAAAGCTTATTGCCT	14525	밁
635		635	ρ
14524	TCCTTACAGGTCATGTGGGGAGGCAGGTGCTGTTCTTCCAAGAGGGTTGGTT	14465	밁
635		635	Q
14464	TCCAGGGCACGCCCACTGCTCCTGCTCTGGGGACAGAGCAAGGGGAAGCCCC	14405	문
635		635	γQ
4	CCCCAGGTACGTTTCCCGAGGTGAGGGCA	4	문 5
23.2	Nalargasi.euTleTrnValDro	625	ş
624 14345	GluHisaspLeuThrProMetaspGlyGluThrPheSerGlnHisLeuGlnAlaValLys 	605 14286	B 6
14285	CCACCGACTGCGAGGACTCAGACATGCTACATACGCCCGGTGCTGCCTCCGACAG	14226	밁
604	SerThrAspCysGluAspSerAspMetLeuHisThrProGlyAlaAlaSerAspArgSer	585	VQ.
584 14225	AlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSerSerValProPhe	565 14166	B 8
4		0	용.
σ.	<pre>lnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSerProProArgGln</pre>	545	Ş
544 14105	SerileAlaAspyalSerileMetTyzSerGluGluLeuGlyThrGlnTleLeuIleHis	525 14046	g S
14045	GGAACCCCCGGCAGCCAGCCACGGCCAACCCAAAGGTGCCTGAGGGG		타
524	spThrGluProProAlaAlaSerHisThrAlaAsnProLysValProGluGlyAsp	505	Q
504 13985	CysAlaArgTyrPheCysGlyValProSerProLeuArgAspMetPheProValArgPro	485 13926	₽ <i>Q</i>
	TGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACTCCACCACCTACCAGCTG	13866	물 5
• 6	() () () () () () () () () () () () () (	, (	? !
464 13865	AlaProSerMetValThrSerValValCysSerSerGluGlyArgGlyGluGluValVal 	4.45 13806	B 5
13805	GIVENIEURA ILEAS PCYSALASELIEUGIOLIECYSAIGAIGLEGOAGCCCTACAIG GCCTCCTTGTCATCGACTGTGCCTCCCTGGAGATCTGCAGGCGGCTGGAGCCCCTACAIG	13746	B. 12
13/45	GTGAAGGCCATGGAGGTGGTCAACAGCGCTCTGAGGTCTGGTACAGCAATGGGCCG	). č	8
24	ProValLysAlaMetGluValValAsnSerGlySerGluValTrpTyrSerAsnGlyPro	6	, 1 <sub>0</sub>
404 13685	HisThralaAsnArgSerLysPheSerTleAlaAspGluAspAlaArgGlnAsnProTyr 	385 13626	g 44
13625	GCTGTGTTTCCCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTCCTACCTGTGCTC	Ō	밁
4	ValAlaValPheProValValArgGlyThrProLysAspSerCysSerTyrLeuCysSer	36	2

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RESULT 11
AAS17057
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       The invention relates to identifying a compound which binds to a Kinase (cencoded by a nucleotide sequence of 1868, 403, 545, 361, 473, 3001, 526, 683 or 1448 base pair (bp) as given in the specification) comprising contacting the kinase with a test compound under suitable conditions for binding, and detecting binding of the compound to the Kinase. The method is useful for identifying a compound which binds to the kinase and also for isolating compounds which modify the activity of the kinase. The identified compounds are useful for treating a subject having a clisorder characterised by aberrant kinase activity where the disorder includes cellular growth related disorders which includes a disorder, clisease, or condition characterised by a deregulation, e.g. and compound the to deregulation of cellular growth, Cellular growth ceregulation due to deregulation of cellular proliferation, cell cycle progression, cellular differentiation and/or cellular hypertrophy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14765 GAGCACGGCTACCGACAAATCGCTTCCCCTTCTGGGTTTTGGTTGCTTAGGCGCGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14705 AAACTGCATGTCTGCTTGCCTCCCGCACCTTTCTGCACACCGGCTTCACTCCCCGGA 1476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14645 TGAGAAAATTCTCCTCTGCTTTGAAGTCTGTCCCCTCCCCATAACTTAATCCCTTAGCAG 14704
                                                                                                                                                                                                                                                                                               Identifying compound which binds to a Kinase, useful for treating diseases e.g. cancer, by contacting kinase with test compound and detecting its binding to the kinase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ss; protein kinase; mine32641human_s1; cytostatic; antianginal; hypotensive; cardiant; cardiovascular disorder; heart failure; hypertension; attrial fibrillation; dilated cardiomyopathy; idiopathic cardiomyopathy; angina; proliferative disorder; cancer; melanoma; prostate cancer; cervical cancer; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-FEB-2002
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                                                                                                                                                                                                                                                               Claim 1; Fig 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6309849-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         colon sarcoma;
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                                                                                                                                                                                                                                                                                                                                                                                                            Robison KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-AUG-1999;
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RESULT 12
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ID ABL09494
AX ABL09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prostate cancer, cervical, breast, colon sarcoma). The kinases and antibodies raised against them are useful in one or more method such as screening assays, predictive medicine and methods of treatment. The nucleic acid molecules are useful for expressing kinase and phosphatase protein (e.g. in gene therapy applications), to detect kinase and phosphatase mRNA or a genetic alteration in a Kinase and phosphatase gene and to modulate kinase and phosphatase activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cardiovascular disorders such as heart failure, hypertension, fibrillation, dilated cardiomyopathy, idiopathic cardiomyopath anginal, proliferative disorders such as cancer (including melanginal)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 526
                                                          Drosophila melanogaster expressed
                                                                                                                                                    ABL09494 standard;
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:
                             Drosophila;
                                                                                          26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                    199 GlnProGluGluValGlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 GATATGTTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCTGCACTG
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                                                                                                                                                                                                              eAlaThrPheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhePhe-SerSerGlnG
                                                                                                                                                                                                                                                                                                                                         AAGCCAGAGAAGCGACCACTGGCCCTGTCGGTGGAAGCCAGATGAAGGACCCGACTTT
                                                                                                                                                                                                                                                                                                                                                       LysProGluLysArgProLeuAlaLeuSerValVal-SerGlnMetLysAspProThrPh
                                                                                                                                                                                                                                                                                                                                                                                                    CAGCCGGAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AspMetPheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCACTCCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to modulate kinase and is a cDNA for a human
                           developmental biology; cell signalling; insecticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP;
                                                                                       (first entry)
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856.00
97.69%
97.69%
22.40%
                                                                                                                                                    cDNA; 9947
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- Matches:
Conservative:
                                                          polynucleotide SEQ ID NO
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                                                                                                                                                                                                                                             268
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169
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Best Local Similarity:
Query Match:
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Alignment Scores:

No . .

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Conservative: Mismatches: Indels:

Length: Matches:

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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, the
                                                                                                                                                                                           New isolated nucleic acid genes from Drosophila and interactions -
                                                                      discloses genomic DNA sequences (ABL16 sequences (ABL01840-ABL16175) and the
                                                                                                                                                                      Claim 1; SEQ ID NO 22964; 21pp + Sequence Listing; English
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
Sequence 9947
                                                                                                                                             The invention relates to an
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                                                            (ABB57737-ABB72072)
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DB; ABB65391.
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	134	115 HisileAsnIleLysLeuSerAspTyrGlyIleSerArgGlnSerPheHisGluGlyAla 134		δ
	7148		7089	밁
	114	102 SerAspAsnIleLeuValTrpSerLeu		δõ
	7088	7029 CAGGCGGCTCGAGCAATCGAGTATTTGCATCGCAGAAGAATCATCTACCGCGATCTAAAG		Дd
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•	7028	CCGCATACTTTCCAGACCCTTGTCCTG		В
	18	62 AsnAlaArgAspSerSerPheIleProLeuGlyH1sMetLeuThrGlnLysIleAlaTyr 81		δÃ
	6974	6915 CCATTAGCTCTGGTTCTGGAACTAGCTCCTCTAGGCGGTTTGGACGCTTTGCTCCGGCAT 6974		В
	19	uCysPheAlaI '		δĀ
	6914	55 GCAGTACTTCTAACTCTCAAGCATCCAAACATTGTACCCTTGGTCGGGATCTGCATTAAA 6914	6855	₽
	41.	22 SerMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIleHis		Qy
	6854	CTGCAGCACTCTTGCAAGGCCTACTGCACTGCGCGTCAGGAATTG	6810	뫄
	21	LeuArgAlaThrAspAlaMetLysAsnPheSerGluPheArgGlnGluAla	•	γQ

364	351 sAsnSerTyrLeuValLeu	, QV
8210	8151 GCCGCTTGTTCCGTTGTTGTGGATGGGTAAGCTGACAAATCTATAACCAAATATTTACTT	dg.
351	alProVal	Qγ
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343	339ValValThrCysPh	Qγ
338 8090	320 ThrLeuLysGlyMet-CysProLeuAsnThrProGlnGlnAlaLeuAspThrProAla	og dg
8039	7980 ATTAAGTCAGCTGTGATCAGTCTAGTCTACATGGAGAAAATAGCTCGCGTGGCTGTCGGA	В
319	319	Qy
7979	7920 CTGCACGCCTATAGCACATCCACCTATGCCCCACCTGTTTTCCTACATGCTCGATCCCAAC	ర్జ
319	316 IleTyrIleTyr	Qy
7919	7860 AACATGTTGTGCTGCCTGGTGGGTGAAGCCATCTGGATGGGCGACGTTTCCGGCAAT	В
315	llSerCysGlnLeuGlnValGlnArgSerLe	γQ
7859		밁
295	293ProGlyMet	Q V
7799	7740 GGCAGCCTACTGCAGTGCAACAGCATCAGTTGTTCTCCGCAGCCACAGGTTGCTCCGCCC	ДЬ
292	LeuMetG	QY
7	O CITGAACTGTGGCTACCCTCCTTCGGCTCTCGCATTGACATTCTAGACTGCTCACCCTCG	문 .
282	ValValPheTrpAspGlyLysGluGluSerArgAsnTyrThrValValAsnThrGluLys	Q
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262	YsGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGluTyrThr	Ωy
7619	7560 ATACTAAGTGCACCGGAGTGCATCCACCTCCTGGATGTCGTTGCCATGCCGCATAGCGAG	Дb
243		γQ
7559	212 MetMetGlucystrpAsptnrlysProGlulysArgProLeuAlaLeuSerValValSer	B 5
4	AGTCGCCCGGCTTTGACTCAAAGGGAAACCCAGTTTCCCACCTGCTGTTTGGATCTT	B
211	roGluGluValGlnPheArgArgLeuGlnAlaLeu	Q
7442	9 TTACGACAACCTTTCGAAGGCCACGAGTCTATTAAAGAGTGCATCTTGGAGGGT	₽.
192	gProAlaLeuGlyHisHisGlnLeuGlnIleAlaLysLysLeuSerLysGly	δ
7388	н —	g
172	Ser	Qγ
7328	GTATGTTTATTTATTTACTTCTCATAAATCATATGGCTTATC	Ş
157	AspGluLys	γQ
7268	9 AAAGGATTTGGTGGCACCGAGGGTTTTATGGCTCCGGAGATCATACGCTACAATGGTGAG	밁
151	5 LeuGlyValGluGlyThrProGlyTyrGlnAlaProGluIle····-ArgProArg	δ V
7208	7149 CTTGTGCACATAAAGATTGCCGACTACGGAATTAGCCGGCAAACTGCTCCAAGTGGAGCT	당

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ABLO9495;  ABLO9495;  26-MAR-2002 (first entry)  Drosophila melanogaster expressed polynucleotide SEQ ID NO 22967.  Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.  Drosophila melanogaster.  WO200171042-A2.  23-MAR-2000; 2000WS-191637P.  11-JUL-2000; 2000WS-0614150.	53 881	518 oLysValProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGl 53 :::    ::::   ::      8772 CCACGATCGGAAGACGATATCGCTCTCTGATCTCTCGATATGTGG 88	514HisthralbasnPr 518 8712 CTATTCCCTTACAGATCAAATCTATAATAACCCTTTCTAAAGACAATGTTCCGCTGATCG 877	503 gProLeuAspThrGluProProAlaAlaSer513	486 aArgTyrPheCysGlyValProSerProLeuArgAspMetPheProValAr 503	466 sLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThrThrTyrGlnLeuCysAl 48 :::::::    ::::::    8545CAGATTTCGGCACTGGCGCTCACAATTCAGAACTGTATATTGGGAC 85	446 OSERMETVALTHISERVALVALCYSSERSERGLUGLYARGGLYGLUGLUVALVALTRPCY 46	429IleAspCysAlaSerLeuGluIleCysArgArgLeuGluProTyrMetAlaPr 44	420 rSerAsnGlyProGlyLeuLeuVal	400 gGlnAsnProTyrProValLysAlaMetGluValValAsnSerGlySerGluValTrpTy 420	380 rTyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaAr 400	364 uValAlaValPheProValValArgGlyThrProLysAspSerCysSe 380 :::         :::         8271 GATAAATGTTTTTCCGTTGAACGAGAATGGAGTTTCCGGACAT	ATCTATGAATTGTGGTGCGGCGAAATTGCAGGAAA 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental blology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511).
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P-PSDB; ABB65392.
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                                                                                                                                              GlnIleAlaSerGlyLeuAlaTyrLeuHisLysLysAsnIleIlePheCysAspLeuLys 101
                                                                                                                                                                                                                        TCTGAAAATGTCTTGGTTTTGGGAGCTTCCACAACCACACGGAAGACAGTCCCCGCAAC 5388
                                                                                                                                                                                                                                                              SerAspAsnIleLeuValTrpSerLeu-----
                                                                                                                                                                                                                                                                                                      CAGGCGGCTCGAGCAATCGAGTATTTGCATCGCAGAAGAATCATCTACCGCGATCTAAAG 5328
                                                                                                                                                                                                                                                                                                                                                                                   TACCGACGCAGCGGAGCCCAC-----ATGGGACCGCATACTTTCCAGACCCTTGTCCTG 5268
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                                                                        AAAGGATTTGGTGGCACCGAGGGTTTTATGGCTCCGGAGATC
                                                                                            LeuGlyValGluGlyThrProGlyTyrGlnAlaProGluIleArgProArgIleValTyr 154
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428 6500	421 rasnGlyProGlyLeuLeuVal	₽. ¥
421 6440	401 nAsnProTyrProValLysAlaMetGluValValAsnSerGlySerGluValTrpTyrSe	ου 2γ
401 6393	381 rLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaArgGl	₩ ¥
381 6356	SerTy CAGGC	₩ ¥
365 6311	lyLeuVa    :: GAAAGAT	8 8
345 6252	339ValValThrCysPheLeuAl	95 34
338 6192	322 LysGlyMet-CysProLeuAsnThrProGlnGlnAlaLeuAspThrProAla	8 8
321 6141	GGAG	8 8
319	318 IleTyr	8 8
317	AspGlnLysIleTyr ::::: TCCGGCAATCTGCAC	8 8
297 5961	-ProGlyMetLysVal         :::  GCCCAAGATGAACATG	₽ ₹
292 5901	284 LeuMetGluValGlnArgMetCysCys	.₽ ₹
283 5841	265 PheTrpAspGlyLysGluGluSerArgAsnTyrThrValValAsnThrGluLysGly	8 8
26 <b>4</b> 5781	246 CysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGluTyrThrValVal	8 8
245 5721	234 LysaspProThrPheAlaThrPheMetTyrGluLeu.	₽ ₹
233 5661	214 GluCysTrpAspThrLysProGluLysArgProLeuAlaLeuSerValValSerGlnMet	₽ ₹
213 5601	195 ProValLeuGlyGlnProGluGluValGlnPheArgArgLeuGlnAlaLeuMetMet	¥ ¥
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              23-JUN-2000;
30-JUN-2000;
07-JUL-2000;
13-JUL-2000;
                                                                                                                                                                                                                                                                                                                 Human; kinase; pKIN-5; cancer; leukaemia; adenocarcinoma; osteoarthritis; immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease; Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia; allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoporosis; Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris; cardovascular disease; hypotremsion; vasculitis; myocarditis; obesity; congestive heart failure; ischaemic heart disease; lung tumour; gout;
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                                                                                                                                                                                                                                                                                                     liver; Niemann-Pick's disease; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -CAGATTTCGGCACTGGCGGCTCACAATTCAGAACTGTAT - - - ATTGGGACGAC
2000US-212073P.
2000US-213467P.
2000US-215651P.
2000US-216605P.
2000US-218372P.
2000US-228056P.
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Gandhi AR, Tribou
Ramkumar J, Griff.
Baughn MR, He A,
Lo TP, Khan F. Re
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Gandhi
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                                                                                                                                                                                                                                                                P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald Si
Griffin JA, Kearney L, Burford N, Nguyen DB, Tang 1
He A, Thornton M, Hafalla A, Patterson C, Gururajan
F, Recipon SA, Azimzai Y, Policky JL, Ding L;
Ellicht VG Theometry T, Policky JL, Ding L;
                                                                                                                                                                                                                                                                                                               INC
                                                                                                                                                                                                                                                             Thangavelu K,
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                                                                                                                                                                                                                                                              Ison CH;
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2002-090207/12. DB; AAE16559.

New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, diseases such as cancer, comprise human kinase polypeptides New polypeptides, useful for diagnosing, disorders of growth and development, car and

Claim 5; Page 178-179; 197pp; English.

The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition containing PKIN agonist is useful for CC corresponding cDNAs. A composition containing PKIN agonist is useful for PKIN and a disease or condition associated with decreased expression of PKIN and a composition comprising PKIN antagonist is useful for treating CC disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, CC myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes ce continuous, multiple sclerosis, Good pasture's syndrome, Graves' disease, contendative, multiple sclerosis, Good pasture's syndrome, Graves' disease, contendative, multiple sclerosis, Good pasture's syndrome, Graves' disease, contendative, multiple sclerosis, Good pasture's syndrome, Graves' disease, contendative, and development disorders syndrome, vestis, ulcerative colitis, contendative, and development disorders (arteriosclerosis, cirrhosis, hepatitis, contendative heart failure, angina pectoris, myocarditis, cardio contendative heart disease, chronic bronchitis, lung tumours); lipid conscity of a test compound and in gene therapy. The present sequence is human PKIN-5 cDNA.

Sequence 2693 BP; 857 Þ 475 ü 550 <u>و</u>; 811 Ŧ; 0 other;

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Percent Similarity:
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Pred. No.:
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                           64
                                                                       CysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAla ::::!!! ::::::
                                                                                                              CTTTGCCACCTCCACCCCAGTTTGATATCTTTGCTGGCAGCTGGGATTCGTCCCCGG
                                                                                                                                      LeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIleHisProLeu
                                                                                                                                                                   GCTGTGAAGATTTTTAATAAACATACATCACTCAGGCTGTTAAGACAAGAGCTTGTGGTG
                                                                                                                                                                                                                                                                                                                                        Scores:
                                                       ATGTTGGTGATGGAGTTAGCCTCCAAGGGTTCCTTGGATCGCCTGCTTCAGCAGGACAAA
                          ArgAspSerSerPheIleProLeuGlyHisMetLeuThrGlnLysIleAlaTyrGlnIle
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330.50
47.34%
27.34%
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 -CTCACTAGAACCCTACAGCACAGGATTGCACTCCACGTA
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84

AlaSerGlyLeuAlaTyrLeuH1sLysLysAsnIleIlePheCysAspLeuLysSerAsp

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 Human; protein kinase;
                           Polynucleotide sequence encoding human protein kinase #54.
                                                            12-SEP-2001
                                                                                         AAS06754;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlnAlaProGluIle---ArgProArgIleValTyrAspGluLysValAspMetPheSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlyIleSerArgGlnSerPhèHisGluGlyAlaLeuGlyValGluGlyThrProGlyTyr
                                                                                                                                                                           TTTTCTTTTGGTTGGAACCGCTGATGGCAAGTTAGCAATTTTT
                                                                                                                                                                                                                                                                rProAlaValValThrCysPheLeuAlaValProValIleLys-----LysAsnSerTy
                                                                                                                                                                                                                                                                                                CCTGGTCATCAATACCGAAGATGGGAAAAAGAGACATACCCTAGAAAAGATGACTGATTC
                                                                                                                                                                                                                                                                                                                           eTyrIleTyrThrLeuLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspTh
                                                                                                                                                                                                                                                                                                                                                                                    rCysGlnLeuGlnValGlnArgSerLeuTrp...-ThrAlaThrGluAspGlnLysIl
                                                                                                                                                                                                                                                                                                                                                                                                                   AGGATACACTTCTGAGGAAGTTGCTGATAGTAGAATATTGTGCTTAGCCTTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                             uLysGlyLeuMetGluVal-----GlnArgMetCysCysProGlyMetLysValSe
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 PTK;
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STK;
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cancer;
cardiovascular disease;
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Homo sapiens.
                                                                                  metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder; gene therapy; ss.
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WO200138503-A2

31-MAY-2001

22-NOV-2000; 2000WO-US32085

24-NOV-1999; 99US-0167482

(SUGE-) SUGEN INC

Plowman GD, Flanagan P, Whyte Clary ۵۵ Manning ė Sudarsanam Ś Martinez

2001-343950/36. DB; AAU03554.

Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections

Example 1; Figure 1; 433pp; English.

cc novel protein kinases have been identified as members of the tyrosine cc or serine/threonine kinase (PTK and STK) families. The polynucleotides cc encoding protein kinase (PTK and STK) families. The polynucleotides cc encoding protein kinase and the polypetides may be used in the cc inappropriate kinase expression. For example, they may be used to treat cc cancers (especially cancers of haematopoietic origin), cardiovascular cc disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), cc immune related diseases (e.g. rheumatold arthritis), neurological cc disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. cc.) earkinson's disease), inflammatory disorders (e.g. asthma), infectious cc disease (e.g. HIV) and reproductive disorders (e.g. asthma), infectious cc disease (e.g. hIV) and reproductive disorders (e.g. infertility). cc Additionally, polynucleotides encoding protein kinases may be cused for gene therapy and as DNA probes in diagnostic assays. The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify condulators of protein kinase expression and activity. 

Sequence 2730 BP; 821 A; 516 C; 602 G; 791 T; 0 other;

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US-09-836-392-21 (1-728) x AAS06754 (1-2730)	DB:	Query Match:	Best Local Similarity:		Score:	Pred. No.:	Alignment Scores:
) x AAS06754		8.65%	27.348	47.348	330.50	1.56e-16	
(1-2730)	Gaps:	Indels:	Mismatches:	Conservative:	Matches:	Length:	
	14	59	150	79	108	2730	
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1479	1435 GCCAGCCTCACTAGAACCCTACAGCACAGGATTGCACTCCACGTA 1479	1435	Дb
83	64 ArgAspSerSerPheIleProLeuGlyHisMetLeuThrGlnLysIleAlaTyrGlnIle 83	64	Qγ
1434	1375 ATGTTGGTGATGGAGTTAGCCTCCAAGGGTTCCTTGGATCGCCTGCTTCAGCAGGACAAA 1434	1375	당
63	44 CysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsnAla 63	44	Qy .
1374	1315 CTTTGCCACCTCCACCACCCCAGTTTGATATCTTTGCTGGCAGCTGGGATTCGTCCCCGG 1374	1315	뮍
43	24 LeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIleHisProLeu 43	24	ν
1314	1255 GCTGTGAAGATTTTTAATAAACATACATCACTCAGGCTGTTAAGACAAGAGCTTGTGGTG 1314	1255	Дb
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-DB-EST -QFMT-fastap -SUFFIX-p2n.rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-blts -START=1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdl -LIST-45
-DOCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
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-USER-US09836392_GCGN_1_1_1456_grunat_08042003_090540_23413 -NCDU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -MAIT -LONGLOG -DEV_TIMEOUT-120
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Emmail: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA.Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: Baylor College of Medicine Human
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Contact: villalon@bcm..tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S.,
A.M., Holloway, M., Telford, B. Hodgson, A., Bouck,
Muzny,D.M., Gunaratne, PT., Yoon, V., Kowis, C., Mar
Lawrence, S., Richards, S., Gibbs,R.A.
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/db_xref="taxon:9606"
/clone="IMAGE:3463102"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Consc
DNA Sequencing by: Incyte Genomics, Inc.
                                                           Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 863)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 863)
                                                                                                                                              5', mRNA sequence.
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                                              Unpublished (1999)
Contact: Robert Strausberg,
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                                                                                                                     house mouse
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Rodentia;
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/clone="IMAGE:5042011"
/clone_1b="NGI_CGAP_Kid14"
/clone_1b="NGI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1:
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1:
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1:
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc;
Clone distribution: MGC clone distribution information
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Mammalia; Eutheria; Primates; Catarrhini;
1 (bases 1 to 611)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5193448"
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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Exploration Research Group,
Laboratory for Genome Exploration Research Group,
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (I
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Tel: 81-45-503-9216
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Arakawa, T., et al. 2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Sakto, T., Kiyosawa, H., Yamanaka, I., Aizav, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Su
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URL:http://genome.gsc.riken.go.jp/
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'e mouse tissues
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/dev_stage="0 day neonate"
/lab_host="DH10B"
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/clone="4832415J17"
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                                                                                                                               Tissue Procurement: Louis Staudt, M.D., Ph.D.

Tissue Procurement: Louis Staudt, M.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                  1 (bases 1 to 1066)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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602259046F1 NIH_MGC_85 Homo sapiens
                                                                                    http://image.llnl.gov
http://image.llnl.gov
Plate: LLAM957 row: k column:
Plate: LLAM957 row: k column:
                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/clone="IMAGE:4342403"
/clone_lib="NIH_MGC_85"
                                                                         Location/Qualifiers
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                                                                                                                                          CCAACAGCTTCCGATTGCCAAGAGGTGTC--CAAGGCATCCGCCCGGTACTGAGGACAGC
                                                                                                                                                                                              tPheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeuGlyHi
                                                                                                                                                                                                                                                                    USETASPTYTG1Y11eSetArgGlnSetPheHisGluG1yAlaLeuG1yValGluG1yTh
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                                                                                                    CGGAAGGAACTGCAATCCGGCGATGCATGGCTCA-TTATTGAGATGCTGGGAAACT
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DB:
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ArgSerProSerSerLeuProSerSerProAlaSerSerSerSerValProPheSerThr
                                                                                                        AspLeuThrProMetAspGlyGluThrPheSerGlnHisLeuGlnAlaValLysIleLeu
                                                                                                                                                                       GACTGCGAGGACTCAGACATGCTACATACGCCCGGTGCTGCCTCCGACAGGTCTGAGCAT
                                                                                                                                                                                         AspCysGluAspSerAspMetLeuHisThrProGlyAlaAlaSerAspArgSerGluHis
                                                                                                                                                                                                                                                                                                                                                              SerLeuThrAspTyrCysSerMetSerSerTyrSerSerSerProProArgGlnAlaAla
                                                                                    GACCTGACCCCCATGGACGGGGAGACCTTCAGCCAGCACCTGCAGGCCGTGAAGATCCTC
                                                                                                                                                                                                                                                        AGGTCCCCCTCAAGCCTCCCCAGCTCCCCAGCAAGTTCTTCCAGTGTGCCTTTCTCCACC
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1. 1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Becksttom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley.C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC Project URL: http://mgc.nci.nih.gov
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(bases 1 to 18
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/tlssue_type="Muscle, rhabdomyosarcoma"
/clone_tlb="NHH_MGC_17"
/lab_host="DH10B-R"
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/db_xref="taxon:9606"
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Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 562)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                            Single pass sequencing, Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore and _minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus
                                                                                                                                                                                                                                     FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 82 row: F column: 5
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                    Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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MARC 4BOV Bos taurus cDNA 5', mRNA
                                                                           ρ
                                                                                                                                  /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_llb="MARC 4BOV"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                           /note-"Vector: pCMV SPORT6; Site
Library made from pooled tissue
embryos." 156 c 175 g 100 t
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                                                                                                                                                                                                                                                                                BJ042551 631 bp
BJ042551 NIBB Mochii normalized
laevis cDNA clone XL032a19 5', r
BJ042551 51:17392727
                              1111 Yata, Mishima, Tel: 81-559-81-6856 Fax: 81-559-81-6855
                                                          Center For Genetic Resource Information National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540,
                                                                                                     Expressed genes in X. laevis embryo Unpublished (2001) Contact: Tadasu Shin-1
                                                                                                                                                               Xenopodinae: Xenopus.
1 (bases 1 to 631)
Kitayama,A., Terasaka
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea
                                                                                                                                                                                                                                        Xenopus laevis
   Email: tshini@genes.nig.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                     African clawed frog
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Xenopus neurula library Xenopus
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Pipidae;
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                                                                                                                  ArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysProGluLysArgProLeuAla
                                                                                                                                                  CTGTATGAGCTATTGTCAGGCCAGGAGACCATCTTTGGGCCAGCACCAGGTGCAGAATTTCC
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/db_xref-"taxon:8355"
/clone-"%1032a19"
/clone_lib-"NIBB Mochii normalized
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                                                                                                                               AsnThrGluLysGlyLeuMetGluValGlnArgMetCysCysProGlyMetLysValSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone (DKFZp686M2317) is available at the RZPD in please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 737)
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DKFZp686M2317 5', mRNA sequence
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Unpublished (1999)
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198 c 212 g · 166 +
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/tissue_type="human skeletal muscl
/dev_stage="adult"
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/db_xref="taxon:9606"
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Pred. No.: 2.21e-77 Length: 939	Scores:	ORIGIN	24	Note: Organ: sativaty grand; vector: powy sector, site_i. Noti; Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.3 kb. Constructed by Life		/db_xref="faxon:10090" /clone="IMAE:4164981" /clone_lib="NCI_CGAP_SG2"			Plate: LLAM9451 row: j column: 22 High cuality secuence stor: 575	CLONE distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:	Technologies, Inc. M.A.G.E. Consortium (LLNL) ics, Inc.	Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D.	AL Unpublished (1999)  Contact: Robert Strausberg, Ph.D.	RIPHERICE I (Dases 1 to 939)  RIPHORS NIH-MGC http://mgc.nci.nih.gov/.  TITLE National Institutes of Health, Mammalian Gene Collection (MGC)	Eukaryota; Mammalia;	e.	_		Old by mount linear per ol. Nov.	Db 723 TCCAAGTTCAGCATC 737	Qy 390 SerLysPheSerIle 394	Oy 370 ValValArgGlyThrProLysAspSerCysSerTyyTLeuCysSerHisThrAlaAsnArg 389	603 CTTCAGAATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTTGTGGCTGTGTTTCCC	352AsnSerTyrLeuValleuAlaGlyLeuAlaAspGlyLeuValAlaValPhePro	Db 543 ACTCTGTGTCTCTTGGAATGTGTGAAAIGGAAGGATGTGACACATCCCTGTCTCCTTC 602	Оу 351 351	Db 483 GAGGCGCACTGGTGGAAAGTGACTGCCCGCCTGGTGTGGGTGCAGATGAGTCCAGTGCCT 542	351	423 GGAGTCAGAGCTGCACTTCTTTAGGAGTAGCCCCGGCCTTTCTAAGAGATTTACTGCCCT	AAA	Db 363 GTCGTCACCTGCTTCTTGGCCGTGCCTGTTATTAAAAAGGGATGGTAGATATGGCTCTGC 422	
RESULT 11		887 AAAACACAAACACAAACCCA	Qy 577 laSerSerSerValPro 583	Y-00-00-00-00-00-00-00-00-00-00-00-00-00	, , ,	Qy 537 euglyThrGlnILeLeuILeHisGlnGluSerLeuThrAspTyrCysSerMetSerSerT 55/	752 CACAACAAAGGGCACTCCCGGCGCTTATGAACCCCACCCA	523 lyAspSerIleAlaAspValSerIleMetTyrSerGluGluL	Db 695 GACCTGAAGAAACCCCACGGGCGGCACCAAGACCAACCTTCACAACGGGGCCAGGCG 751	Qy 503 rgProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProLysValProGluG 523	Qy 487 rgTyrPheCysGLYValProSerProLeuArgAsp	576 TOGACGAGAACGGCCCATCGCTAACTGATGTACCAATCAGCACCTAACAGCTCCG-TGCC	467 euAspAspLysAlaAsnSerLeuValMetTyrHlsSerThrThrTyrGlnLeuCysAlaA 	516 CATGGTCACTTGTGTGCAGCTCAGACTGCAGAGGAGGAGGAGGACTGGTCTGCCA	Qy 447 rMetValThrSerValValCysSerSerGluGlyArgGlyGluGluValValTrpCys-L 467	Db 456 CGTCATCGACCATCCTGGACATCAGCAGGCGGCTGGAGCCCTACGCAGCTCCGTC 515	370 UGCANA LAGANA LAGA TONGO LAGA LAGA LAGA LAGA LAGA LAGA LAGA LA	Qy 407 sAlaMetGluValValAsnSerGlySerGluValTrpTyrSerAsnGlyProGlyLeuLe 427	336 CAACAGGTCCAAGTTCTGCATCCCCGACGAAGATGCACGGCAGAACCCTTACCCAAGTGAA			TGTTATCAAAAAGAACTCCTTCCTGGTGCTGGCAGGCCTGACCGACC	Qy 347 oVallleLysLysAsnSerTyrLeuValLeuAlaGlyLeuAlaAspGlyLeuValAlaVa 367	ANGCGTGCCCCAGCAGCCCTGGACACCCCAGCTGTCGTCGTCTTTCTT	307 Macamhaccanodandanahanahanahanahanahanahanahanahanah	Qy 30/ UTTPINTALATICALMASPALADAAAAATTATATATATATATATATATATATATATATA	olorgentianulianulianilianilianilianilianilianil	N	-392-21 (1-728) x BF301427 (1-939)	12 Gaps:	/ Match: 23.01% Indels:	Best Local Similarity: 60.71% Mismatches: 60

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                                                                                                     GlyLeuLeuVallleAspCysAlaSerLeuGluIleCysArgArgLeuGluProTyrMet
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Plate: LLAM9815 row: 1 column:
High quality sequence stop: 630.
Location/Qualifiers
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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National Institutes of Health, Mammalian
Unpublished (1999)
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Mammalia; Eutheria;
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Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new
                                                                                           Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Rese
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, K
Tel: 81-45-503-9216
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Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Arakawa,T., et al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001060; Cdc15_Fes_CIP4.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000980; SH2.
InterPro; IPR001245; Tyr_pkinase:
Pfam; PF00017; SH2; 1.
Pfam; PF00069; gkinase: 1.
Pfam; PF00611; FCH; 1.
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BINDING
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VARIANT
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770 REQVERGYRMSAPQHCPEDI-----SKIMMKCWDYKPENRP 805
                                                                                                                                                       Genew; HGNC:3655; FER. MIM; 176942; -.
                                     186 AKKLSKGIRPVLGQ--PEEVQFRRLQALMMECWDTKPEKRP 224
                                                                          712 --GVYSSSGLKQIPIKWTAPEALNYGRYSSESDVWSFGILLWETFSLGVCPYPGMTNQQA 769
                                                                                                                                                                                                                                      604 KFLQEAKILKQYDHPNIVKLIGVCTQRQPVYIIMELVSGGDFLTFL---RRKKDELKLKQ 660
                                                                                                              134 ALGVEGTPG-----YQAPEIRPRIVYDEKVDMFSYGMVLYELLS-GQRPALGHHQLQI 185
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n; Nuclear protein; SH2 domain; Polymorphism.
1     58     FCH.
0     550     SH2.
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l; PROTEIN_KINASE_DOM;
protein_KINASE_TYR;
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ATP (BY SIMILARITY).

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BY SIMILARITY.
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0491CD69392DB415 CRC64;
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Search completed: April 8, 2003, 10:23:43 Job time: 37 secs

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521	1015 GTGGTCACCTGCTTGCTCTTGGCCGTGCCTGTTATTAAAAAGAATTCCTACCTGCTCTTAGCG:	B 64
511	94 nValProGlnAsnLeuSerProHisSerGlnArgProAspIleLeuLysAl	용
1014	ACACCCTCAAGGGCATGTGCCCCTTAAACACACCCCCAACAGGCCTTGGATACTCCAGCT	Qy
494		B
954	NGAGATCCCTGTGGACAGCCACCGAGGACCAGAAAATCTACATC	Qy
474	uGlnAlaLeuGluArgA	밁
894	AGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAC	Qy
454	nLeuTyrMetGluLeuAsnAlaLeuMetLeuGlnLeuGlv	Дb
4	TGGTGAACACA	Qy
434		В
822	805AAAGAGGGTCCAGGAAC	Ϋ́
414	luGlyThrCysLeuHisArgLeuGluGluGluLeuValMetArg 4	ф
804	TTTTGGGATGGA 8	Qγ
394	SerGlnAlaGluTrpArgGluGluValLysLeu	뮹
783	AGACAGCCTTCTTCTCATCCCAGGGCCAGGAGT	Qy
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744	TGGTGAGCCAGATGAAGGACCCGACTTTTGCCACCTTCATGTATG	Qy
365	::::::	용
584	GCTGGGACACTAAGCCAGAGAGCGACCG	γ
345	GlyPheLy:	망
542	CGGTTCTGGGGCAGCCGGAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGA	Qy
329	leTrpGlyValGlySerAsnSerLeuH1sLeu	ర్థ
82	-GCACTGGGCCACCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGC 5	γO
818	lAspSerSerAlaIle 3	B
28	GGACAGCGCCT 5	VΩ
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78	ThrLysMetSerPheAlaGlyThrValAlaTrpMetAla 2	В
35	GGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACTCCTGGCTACCAGGCC 4	Qy
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78	TGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTC	Qy
43	ArgAspLeuLysSerProAsnMetLeu 2	문
18	GGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTG 3	Q.
23	07ProValThrProSerLeuLeuValAspTrpSerMetGlyIleAlaGlyGly 2	당 .
58	99 TCCTTTATACCCCTGGGACACATGCTCACCCAAAAAATAGCCTACCAGATCGCCTCGGGC 2	Ω <sub>γ</sub>
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ο<sub>γ</sub>

55 CAGGAGGCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATC 114

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12	: 1ty:	-711A-16 e 16, Application US/ No. 6358720 INFORMATION: INFORMATION: ANT: Muramatsu, Masa ANT: Shirasawa, Taku ANT: Shirasawa, Taku ANT: Tokumitsu, Hiro OF INVENTION: SERINE ETEIRENCE: 06501-0450 T APPLICATION NUMBER: T FILING DATE: 1999- APPLICATION NUMBER: FILING DATE: 1999-03 APPLICATION NUMBER: FILING DATE: 1997-04 OF SEQ ID NOS: 21 TRE: FastSEQ for Wind NO 16 NO 16 PRT PRT 1050 PRT 1100 PRT	TTCTGCGGGGTCCCCAGCC-       SerProAspSerProGlyG	OPTO	CAGCT	TTACGT        euArgGlyLeuHisHis	GGCTGGAGCCCT        ProGlySerPro	TGGTACAGCAATGGGCCGGGC    ::: sGlySerCysGlyAspLeuPr	AACC   	CTGT     yCys	GCCTCGCCGATGGG     :::   LeuSerGlyValGl
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×	онхохг	8711A ruhisa EONINE 09/428, 8 JP98/01 /124798	CCCTCAGGG	CTCCAC        hrProP	GGAGG        yarg	euLeu	lyGly	TGTCA    euArg	GGCCA	CAACA   ::: roSer	GTTTC
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QY 331 GACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCG	OY 271 CACAAGAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTT	Qy 211 CTGGGACACATGCTCACCCAAAAAATAGCCTACCAGATCGCCTCGGGCCTGGCCTACCTG :::	Qy 151 CCGCTCAGCAGCCTCAACACCGTGCTGTCCGAGAAACGCCAGAGATTCTTCCTTTATACCC                   : : Db 102 AspTyrLeuHisThrMetArgThrLeuSerGluAspThr	Qy 115 AGCATCCACCGGTTGGTTCGCCCTGGAGCTCGCG :::	55 CAGGAGGCCAGCATGCTGCACGCGCGCGCAGCACCCCTGCATCGTGGCGCC:::	Alignment Scores: 1.18e-10 Length: 1051 Pred. No.: 245.00 Matches: 178 Score: 245.00 Matches: 178 Percent Similarity: 32.92% Conservative: 87 Best Local Similarity: 22.11% Minatches: 259 Best Local Similarity: 6.04% Indels: 281 Ouery Match: 6.04% Gaps: 35 DB: 4 Gaps: 35	Db 705 laAlaPheGlyThrGlnAlaProAspProGlySerThrGluSerLeuGlnGluLySProM Oy 1989 CCGAAGGCTGACTCCGCATGGGGTGCTGGTGGATGCTGCCGTGGTGGAAGGACAC Oy 2046 TGTTGTGTGCACCTTTGAAAATGAAAACACAGAGTGGTGCTGGCGTGTGGAAGGACAC Oy 2046 TGTTGTGTGCACCTTTGAAAATGAAAACACAGAGTGGTGCCGTCTGGAGGGGCTG Oy 2106 GGGGCCAGGGAGTTCGACATTTTCTACCAGTCCTACGAGGGCTG Oy 2106 GGGGCCAGGAGTTCGACATTTTCTACCAGTCCTACGAGGGCTG Oy 2106 GGGGCCAGGAGTTCGACATTTTCTACCAGTCCTACGAGGGCTG Oy 2106 GGGGCCAGGAGTTCGACATTTTCTACCAGTCCTACGAGGGCTG OY 2106 GGGGCCAGGAGTTCGACATTTTCTACCAGTCCTACGAGGGC 2149  Ob 765 roProGlnGlyProArgThrArgMetPheSerAlaGlyProThrGlySerThrP OS -09-428-711A-14 Sequence 14, Application US/09428711A Sequence 14, Application US/09428711A Sequence 14, Application US/09428711A Sepence 14, Application US/09428711A Sequence 14, Application US/09428711A Sepence 14, Application US/09428711A
GGATTTCG 378	GGTCCCTT 330 ::: erAsnPro 149	CCTACCTG 270     rgLeuLeu 129		AGCTCGCG 150 ::      spLeuAla 101		051)	AGGACAC 2045 AAAAGIYG 745 AGGGGCTG 2105 /SerThrP 765 [49

Db 150 GlyGlyArgAlaAsnproseris:	GAG	1192 GACGCACGGCAGAACCCCTACCCAGTGAAGGCCATGGAGGTGGTGATCAACAGCGGCTCTGAG	Qy
150 GlyGlyArgArgAlaAsnProSerAsnTleArgValLySlCAAAAAAPPeleGlyPh 379 AGGCAGTCATTCCATGAGGGGGCCTTAGGGGTGGAGGGCATCCTGCTATTCCATGAGGGGGCCTTAGGGGTGGAGGGCATCCTGCTATTCCATGAGGGGGCCTTAGGGCATGGAGGGCCTTGCCTTATTCATGATGAGAAAGTTAGATGAGAAAAGTTCTCCTTATTCTCCTTATTATAGATGAAGAAAGTTAGATGAGAAAAGTTCCTGCTATTCATGATGAAGAAGTAGATATTTTCTCCTTATTATAGATGAAGAAGTAGATATTTTCTCCTTATTATAGATGAAGAGGAAAAGTTTCCAGGCCAGCTTCAAGGACAGGGCCCCTGCACTGGGCCACCACAGTTCTAGGACAAGGGCATCCGGCCCGTTTCTGGGGCCAGCCA	leG	25 gTyrGlyAlaSerValProIleProVal	당
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150 GlyGlyArgAlaAsnProSerAsnIleArgY::     170 ArgGract-CASTCATGAGGGGGCCCTAGGCGTGGAGGGCACTCCTGGCTAFAGGGACACTCCTAGGCATGAGGGCACTCCTAGGCATGAGGGCACTCCTAGGCATTGAGAGAGTAGAGGCACTCCTAGGCTTAGAGAGAG	i O	8 TCCTACCTGTGCTCACACACAG	Qy
150 GlyGlyAHagArgAlaAsnProSerAsnTleAcrySill(11:1:11)  379 AGGCACTCATTCATGAGGGGCGCCTAGGGGGTGGAGGGCACTGGGGGAGGCACTGGAGGGCACTGCTGGAGGGCACTGGAGGGCACTGGAGGGCACTGGAGGGCACTGGAGGGCACTGGAGGGCACTGGAGAGGTTGAGAAGATTCATGAGAAGGTTAGATATCTCCTAGGCCACAGGGCACTCCTAGACATTGATATATAT		/ GGCACCCCAAAGGACAGGT	Дb
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379 AGGCACTCATTCCATGAGGGCGCCTTAGGAGGACTCCAGGACACTCAGGCCTAGGGCGCCTTAGGGCACTCCTGGCCTAGGGCCACTCCTGGCCTAGGGCCACTCCTGGCCTAGGGCCACTCCTGGCCTAGGGCCACTCCTGGCCTAGGGCCACTCCTGGCCTAGGGCCACTCCTGGCCTAGGGCCACTCCTGGCCTAGGGCCACTCCTGGCCTAGGGCCACTCCTGGCCTAGGGCCACTCCTGGCCACTCCTAGGACATCGCAGGACTCGCAGGACTCGCAGGACTCGCAGGACTCGCAGGACATCGCCCTGCAGGACATGGACAGGCCTGCTAGGACAGGCCCTGCACTGGGCCACCACACAGGCCTTCTAAGACACAGGCCTTCTCGAGACACGCCCCTATGASAGCACTGCACACACACACGCCCTAGGACACTCCACACACA		52 saspThraspaspPheValMetValProAlaGInPheProGlyAspLeuVa	ф
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                                                                             rPheSerThrSer 695
                                                                                                                   ATTTTCTACCAGT 2137
                                                                                                                                                                                                                                                                   CATGGGGTGCTGGATGCTGCCGTGGTGGCAAAGGACACTGTTGTGTGCACCTTTGAA 2064
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 Application US/08469537A
                                                                                                                                                     ---GlySerGlyLeuArgProAlaGluAspThrArgGlyProPheGlyArgSe 691
                                                                                                                                                                                                                                                                                                                                                                                                                           -TCCCCAGGCGCGGTGGAGATGTTATCGTCATTGGCCTGGAGAAGG--
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Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: US-08-469-537A-72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                            139
                                                                                                                                                                                                                           64 AGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGC-----ATCAGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Kempler, Ph.D., Gail | REGISTRATION NUMBER: 32,143 REFERENCE/DOCKET NUMBER: RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 777 Old CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: USSN 08/406,247 FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                     4 CTGAGGCACCTGCGGGCCACCGATGCCATGAAGAACTTCTCCGAGTTCCGGCAGGAGGCC
TCCTTTATACCCCTGGGACACATGCTCACCCAAAAAATAGCCTACCAGATCGCCTCGGGC
                                   IleMetArgSerProHisSerAspValGlyCysSerSerAspGluAspGlyThrValLys
                                                                                                           GluGlnProValCysMetLeuPheGluTyrTleAsnGlnGlyAspLeuHisGluPheLeu
                                                                          CTGGAGCTCGCGCCCCAGCAGCCTCAACACCGTGCTGCTCCGAGAACGCCAGAGATTCT
                                                                                                                                                    ATCCACCCGCTCTGC----
                                                                                                                                                                                      SerLeuMetAlaGluLeuHisHisProAsnIleValCysLeuLeuGlyAlaValThrGln 407
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1060 TACCTGGTCTTAGCGGGCCTCGCCGATGGGCTTGTGGCTGTGTTTCCCGTGGTGCGGGGC 1119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AsnGlnGluValIleGluMetValArgLys----ArgGlnLeuLeuProCysSerGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGCGACCGCTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACCTTC 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AspCysPro---ProArgMetTyrSerLeuMetThrGluCysTrpAsnGluIleProSer 597
                                                                                                                                                                                                                                                                                                                                                                                                               TyrProAsnTyrMetPheProSerGlnGlyIle-----
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                                                                                                                                                                                              ACCCCAAAGGACAGCTGCTCCTACCTGTGCTCACACAGCCCAACAGGT-----
                                                                                                                                                                                                                                         PheIleProIleAsnGlyTyr-ProIle-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACTACACGGTGGTGAACACAGAGAAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCT 879
                                                             lileGlnHisCysProProProLysSerArgSerProSerSerAlaSerGlySerThrSe
                                                                                                                                                 ProProGlyTyrAlaAlaPheProAlaAlaHisTyrGlnProThrGlyProProArgVa
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                                                                                                        -CCAAGTTCAGCATCGCGGATGAAGACGCACGGCAGAACCCC 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -AAAGAGGAGTCCAGG 819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: RETELECOMMUNICATION INFORMATION: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: USSN (FILING DATE: 17-MAR-1995)
APPLICATION NUMBER: USSN (FILING DATE: 28-OCT-1993)
APPLICATION NUMBER: USSN (FILING DATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                           408 GluGlnProValCysMetLeuPheGluTyrIleAsnGlnGlyAspLeuHisGluPheLeu
                                                                                                                                                                                                                       368 IleLysThrLeuLysAspTyrAsnAsnProGlnGlnTrpMetGluPheGlnGlnGluAla
  139 CTGGAGCTCGCGCCGCTCAGCAGCCTCAACACCGTGCTGTCCGAGAACGCCAGAGATTCT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 06-JUI
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OPERATING SYSTEM:
                                                                                                                                                                          64 AGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGC-----ATCAGC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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777 Old Saw Mill River Road
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                                                                                                                                              OTHER INFORMATION: US-08-469-537A-105
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APPLICANT: Maison
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                                                                                                                                                                                                    MOLECULE TYPE:
FRAGMENT TYPE:
FEATURE:
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TITLE OF INVENTION: KI
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 914-345-7400
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                                                                                                                                                                         NAME/KEY: Human ROR1
LOCATION: 1...937
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                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 28-OCT APPLICATION NUMBER:
                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: USSN 08/406,247 FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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MENTION: EHK AND
MENTION: KINASES
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28-OCT-1993
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Matches:
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RESULT 9
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Percent Similarity:
Best Local Similarity:
Query Match:
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Patent No.
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                                                                                                                                                                                                        TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1060 TACCTGGTCTTAGCGGGCCTCGCCGATGGGCTTGTGGCTGTTTTCCCGTGGTGCGGGGC 1119
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REFERENCE/DOCKET NUMBER: 82
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US93/00586 FILING DATE: 22-JAN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/
FILING DATE: 4-APR-1994
CLASSIFICATION: 530
                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                      TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
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CITY: South San Francisco
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Wood, William I
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Goeddel, David
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                                                                                                                                                                                                              Sequence 20, applicat Patent No. 6331302 GENERAL INFORMATION:
                                  TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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                     ADDRESSEE:
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Wood, William I
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Best Local Similarity:
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INFORMATION FOR SEQ ID NO:
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LENGTH: 505 amino acids
TYPE: Amino Acid
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NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                    ValAspAsnGluAspIleTyrGluSerArgHisGluIleLysLeuProValLysTrpThr
                                                                                                                                                       ---ValGlyGluH1sAsnIleTyrLysValAlaAspPheGlyLeuAlaArgValPheLys
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                                                 CCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTAGATATG
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                                                                                                                                                                                                                                                                                                  ---HisLeuThrGlnGlnValAspMetAlaAlaGlnValAlaSerGlyMetAlaTyrLeu
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PCT-US95-04228-20
  Query Match:
                                                      Pred. No.:
                                                                 Alignment Scores:
                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application PC/TUS9504228 GENERAL INFORMATION:
                                                                                                                                               SEQUENCE CHARACTERISTICS:
            Local Similarity:
                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 82
TELECOMMUNICATION INFORMATION: 415/225-1994
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/2 FILING DATE: 04-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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CITY: South San Francisco
STATE: California
                                                                                                                                                                          TELEFAX: 415/952-9881
TELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                          TOPOLOGY:
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                                                                                                                                                                                                                                                         NAME: Wendy M. Lee
                                                                                                                                                                                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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Wood, William I.
VENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
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Goeddel, David
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APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACTILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/221, 235
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE:
NUMBER OF SEO ID NOS: 15
NUMBER OF SEO ID NOS: 15
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US-09-221-235-5
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Patent No. 6043040
                                           SOFTWARE: PatentIn
EQ ID NO 5
TYPE: PRT
                        ENGTH: 455
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RESULT 13
US-09-221-928-5
; Sequence 5, Application US/09221928
; Patent NO. 6121030
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan
; TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC
; FILE REFERENCE: MNI-050
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CURRENT FILING DATE: 1998-12-28
FARLIER APPLICATION NUMBER: 09/163,115
LARLIER FILING DATE:
NUMBER OF SEO ID NOS: 15
SOFTWARE: PALENTIN Ver. 2.0
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CURRENT FILING DATE: 1998-12-28
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CURRENT APPLICATION NUMBER: US/09/221,236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 09/163,115 EARLIER FILING DATE: 1998-09-29
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ORGANISM: Homo sapiens
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ATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCTGCACTGGGCCACCACCAGCTCCAG
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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-THR_MIN-0 -ALIGN-15 -MODE-LOCAL -OUTFMT-pct - MORM-ext -HEAPSIZE-500 -MINLEN-0
-MAXLEN-200000000 - USER-US0983592_@CGN_1_1_24_@crunat_08042003_090330_22925
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG
-NCPU-6 -ICPU-3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6
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LOOPCL-0 -LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62
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   Sequence 21,
Sequence 6, A
Sequence 2, A
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## ALIGNMENTS

Application US/09836392

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US-09-836-392-21 ; Sequence 21, Application U ; Patent No. US20020173458A1
Alignment Scores:
                                                            ; ORGANISM: Homo sapiens US-09-836-392-21
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CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: PCT/US00/28066
PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: 60/159,542
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-17
PRIOR APPLICATION NUMBER: 60/165,914
PRIOR APPLICATION NUMBER: 60/165,914
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PRIOR APPLICATION NUMBER: 60/165,914
PRIOR APPLICATION NUMBER: 60/165,914
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                                                                                                                                                                                      SEQ ID NO 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Ruben et al.
TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides
TITLE OF INVENTION: Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: PT020P1
                                                                                                                                                                                                                   SOFTWARE:
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	600	581 SerValProPheSerThrAspCysGluAspSerAspMetLeuHlsThrProGlyAlaAla	рь
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1081 GCCGATGGGCTTGTGGCTGTG	Qy DB	US-09-836-392-8_COPY_22_2205 (1-2184) x US-10-132-382-6 (1-1987)	_
1021 ACCTGCTTCTTGGCCGTGCCTG	Qy	reficilit Similarity: 94.50% Conservative: 0  Best Local Similarity: 94.50% Mismatches: 1  Query Match: 88.09% Indels: 39  DB: 9 Gaps: 1	
961 CTCAAGGGCATGTGCCCC	D Q	nt Scores: 2.43e-200 o.: 3574.50	. (o m h
901 CTCCAGGTCCAGAGATCCCTGT	Qy Db	RGANI	C
841 GAGAAGGGCCTCATGGAGGTGG 	Qy Db	; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 6 ; SEQTH: 1987 ; TYPE: PRT	
1560 TyrThrValValPheTrpAspo	90	; FILE REFERENCE: SCH-1811 ; CURRENT APPLICATION NUMBER: US/10/132,382 ; CURRENT FILING DATE: 2002-04-26 ; NUMBER OF SEO ID NOS: 26	
1540 PheMetTyrGluLeuCysCysC	מ ט	; GENERAL INFORMATION: ; APPLICANT: MEMISS, BERTRAM ; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROIS	
1520 GluLysargProLeuAlaLeuS  721 TTCATGTATGAACTGTGCTGTG	Орь	RESULT 2 US-10-132-382-6 ; Sequence 6, Application US/10132382 ; Publication No. US20030045699A1	
_	Db Qy	Qy 2161 GAGGCTTGCACTCGCAAGAGAAGG 2184	
	QQ da	Qy 2101 GGCTGGGGCGCCAGGGAGTTCGACATTTTCTACCAGTCCTACGAGGAGCTGGGCCGGCTG 2160	
1460 PheSerTyrGlyMetValLeuT 541 CACCAGCTCCAGATTGCCAAGA	Qy Qy	Db 681 AspThrValValCysThrPheGluAsnGluAsnThrGluTrpCysLeuAlaValTrpArg 700	-

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TTTTGGGATGGAAAAGAGGAGTCCAGGAACTACACGGTGGTGAAC 	TACACCGTGGTG	781 1560	Db Qq
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CTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCGACTTTTGCC 	GAGAAGCGACCG             GluLysArgPro	661 1520	Db Qq
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GGCATCCGCCCGGTTCTGGGGC                  	CACCAGCTCCAG	541 1480	g 82
TyrGluLeuLeuSerGlyGlnArgProAl	PheSerTyrGly	1460	용

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Sequence 2, Application US/10132382
Publication No. US20030045699A1
GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS FOR ST
FILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
UNMBER OF SEQ ID NOS: 26
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                                                          ACCTGCTTCTTGGCCGTGCCTGTTATTAAAAAGAATTCCTACCTGGTCTTAGCGGGCCTC
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Sequence 8, Application US/10132382

Publication No. US20030045699A1

GENERAL INFORMATION:
APPLICANY: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS FOR SETILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LENGTH: 2014
; TYPE: PRT
; ORGANISM: Homo :
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Percent Similarity:
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Query Match:
DB:
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Publication No. US20030045699A1
GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS FC
FILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2003-04-26
NUMBER OF SEQ ID NOS: 26
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      APPLICANT: Yoganathan, Thillainathan
APPLICANT: Voganathan, Thillainathan
APPLICANT: Delaney, Allen
TITLE OF INVENTION: Cancer Associated Protein Kir
FILE REFERENCE: KINE-023
CURRENT APPLICATION NUMBER: US/10/143,133
CURRENT FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: 60/290,555
PRIOR FILING DATE: 2001-05-10
NUMBER OF SEQ ID NOS: 4
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                                                                                              Sequence 2, Application US/10143133 Publication No. US20020197658A1 GENERAL INFORMATION:
SOFTWARE: FastSEQ for Windows Version 4.0
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818	818	Q
415	396 GlnGluGlyTrpLysArgGluIleGlnGlyLeuPheAspGluLeuArgAlaLysGluLys	밁
818	GATGGAAAAGAGGAGTCCA	Qy
395	uGluAlaLeuGluAlaGlnVal	₽
791	G-CTGTGGGAAGCAGACAGCCTTCTTCTCATCCCAGGGCCAGG	Qy
375	367ProAspPheAlaSerIleLeuGlnGln	망
732	SACTTTTGCCACCTTCATGTATGA	Qy
366	351PheAlaGlnLeuMethlaAspCysTrpAlaGlnAspProHisArgArg	망
672	3 TTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGGACACTAAGCCAGAGAAGCG	Qy
350	335 AlavalAsnLysLeuThrLeuProIleProSerThrCysProGluPro	₽ D
612	GCATCCGCCCGGTTCTGGGGCAGCCGGAC	Qy
558 334	508 TTGCTGTCAGGACAGCGCCCTGCACTGGGCCACCACCAGCTCCAGATTGCC	Qy Db
314	rPheSerLysGlySerAspValTrpSerPheGlyValLeuLeuT	B
507	ATGAGAAGGTAGATATGTTCTCCTATGGAATGGTGCTCTACGA	Qy
294	 AlaGlyThrTyr	밁
447	SCGTGGAGGGCACTCCTGGCTACCAGGCCCCAGAGATCAG	Ş
274	  AspMetGluHisLysThrLeuLysIleThrAspPheGlyLeuAlaArgGluT	밁
387	ATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCAGT	Qγ
	GlnProIleG	g
327	CTGTGACCTGAAGTCGGACAACATTCTGGTGTGG	δ
ω´ ·	16 ValAsnTrpAlaValGinileAlaArgGlyMetHisTyrLeuHisCysGluAlaLe	₽ :
279	:CTACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAA~	Q
	02 SerargalaLeualaGlyargargValproProHisVa	B :
S	66 AACACCGTGCTGTCCGAGAACGCCAGAGATTCTTCTTCTTTATACCCCTGCGACACATACAT	Ŷ
165 · 201	112 ATCASCATCCACCCGCTCTGCTTCGCCCTGGAGCTCGCGCCGCTCAGCAGCCTC	B 5
181	62 ArgGlnGluAlaArgLeuPheAlaMetLeuAlaHisProAsnIl	₽
111	2 CGGCAGGAGGCCAGCATGC	γQ
	)9-836-392-8_COPY_22_2205 (1-2184) x US-10-143-133-2 (1-847)	us-o
	ignment Scores:  ed. No: 3.68e-12  Fed. No: 37.50  Matches: 195  ore: 34.094  Conservative: 75  st Local Similarity: 24.624  Mismatches: 241  ery Match: 9.328  Gaps: 38.	Alig Pred Scor Perc Best Quer DB:
	DOID NO 2 LENGTH: 847 TYPE: PRI ORMANISM: Homo sapien (0-143-133-2	; SE ; ; ;

1537	1478 CCAGCCCCTCAGGGACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCA	Qy
749	oArgGlyGlyThrValSe	뫄
1477	CTTGGTGATGTACCACTCCACCACCTACCAGCTGTGTGCCCGGGTACTTCTGCGGGGGTCC	Qy
733	714 LeuAspLeuGlyIleProValGlyGlnArgSerAlaLysSerProArgArgGluGluGlu	D
1417	CGTCTGGTGCCTGGATGACAAGGCCAACT	Qy
713	694 ProLeuIleCysPheSerLeuLysThrProAspSerProProThrProAlaProLeuLeu	Db
1378	CTCTGAG	Qy
693	676 ThrThrProPhrProThrProAlaProCysProThrGluProProProSer	DЪ
1348	TGCCTCCCTGGAGATCTGCAGGCGGCTGGAGCCCTACATGGCCCCCCCC	Qy
675	656 GlyLeuGlyArgAspLeuGlnProProGlyGlyProGlyArgGluArgGlyGluSerPro	ġ
1288	;	οy
655	a –	В
1282	GCTCTGAGGTCTGGTACAGCAATGGGCCGGGC	Qy
638	624 LysargProValProAlaGluArgGlySerSerSerGlyThrPro	рь
1222	AGTTCAGCATCGCGGATGAAGACGCACGGCAGI	Qy
623	607 ProAlaLeuAsnGlyAsnProProArgProSerLeuGluProGluGluPro	рь
1162	ACACACAGCCA	Qy
606	ThrPro	ф
1105		Qy
586	567 GlyProSerSerProLysProGlyGluAlaGlnAsnGlyArgArgArgSerArgMetAsp	망
1054	Α	δō
566	556 SerAsnGlyGluArgArgAlaCysTrpAlaTrp	뫄
1009	CATCTACACCCTCAAGGGCATGTGCCCCCTTAAACACACCCCCAACAGGCCTTGGATACTC	Qy
555	536 GluProAlaGluProGlyGlnAlaTrpGlyArgGlnSerProArgArgLeuGluAspSer	DЪ
949		<b>Q</b> .
535	516 ValPheGluValGlyProGlyAspSerProThrPheProArgPheArgAlaIleGlnLeu	Db
922	GCTCCAGGTCCAGAGATCCCTGT	Qy
515	496 LeuAspPheLysHisArgIleThrValGlnAlaSerProGlyLeuAspArgArgArgAsn	뫄
968	879 TGGGATGAAGGTGAGCTG	Qy
495	476 GlyThrPheLysArgSerLysLeuArgAlaArgAspGlyGluArgIleSerMetPro	рь
878	TGCTG	οy
475	456 GluLeuThrLeuLeuGlnGlnValAspArgGluArgProHisValArgArgArgArg	В
854	840AGAGAAGGGCCTCAT	Ωy
455		Дb
688	819 GAACTACACGGTGGTGAACAC	0y
435	416 GluLenLenSerArgGluGluGluLenThrArgAlaAlaArgGluGlnArgSerGlnAla	B

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US-09-836-392-8_COPY_22_2205 (1-2184) x US-09-771-161A-255 (1-1036)  Oy 13 CTGCGGGCCACGATGCATGAAGAACTTCTCCGAGTTCCGGCAGGAGGCCAGCATGCTG 72		PRIOR APPLICATION NUMBER: 09/724,676 PRIOR APPLICATION NUMBER: 136776 PRIOR FILING DATE: 2000-11-28 PRIOR REPLICATION NUMBER: 135776 PRIOR APPLICATION NUMBER: 135679 PRIOR FILING DATE: 2000-06-15 PRIOR FILING DATE: 2000-04-12 NUMBER OF SEQ ID NOS: 273 SOFTWARE: PAtentin version 3.0 SEQ ID NO 255 LENGTH: 1036	11A-255 155, Application US/09771161A US20020110811A1 PROUMATION: VARIANTS OF PROTEIN K: RENCE: 802620-2005.1 PPLICATION NUMBER: US/09/771,1614	Qy       1766       AGGACTCAGACATGCTACATACGCCCGGTGCTGCGACAGGTCTGAGCATGACCTGA       1825         Db       810	750 ProGlyThrProGlyThr
994 480 1054 500 1072	Qy 844 AAGGGCCTCATGGAGGTGCAGAGGATGTGCCCCTGGGATGAAG 888  Db 431	Db 376ProThrPheValAlaLeuArgAspPheLeuLeuGluAlaGlnProThrAspMet 393  Qy 760.TTCTCATCCCAGGGCCAGGAGTAC 783  Qy 760.ArgAlaLeuGlnAspPheGluGluProAspLysLeuHisIleGlnMetAsnAspValIle 413  394 ArgAlaLeuGlnAspPheGluGluProAspLysLeuHisIleGlnMetAsnAspValIle 413  Qy 784 ACCGTGGTGTTTTGGGATGGAAAAGAGGAGTCCAGGAACTACACGGTGGTGAACACAGAG 843       :::   :::   ::   :::   :::   :::   :::   :::   :::   :::   :::   :::   :::   ::	3 5 5 8 0 3 4 9 3 6 6 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	409 GTGGAGGCACTCCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGAT 289 HisargLysValProPheAlaTrpCysAlaProGluSerLeuLysThrArgThrPheSer 466 GAGAAGGTAGATATGTTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTAAGGACAG 1	Db 202 LysMetValThrGluLeuAlaProLeuGlySerLeuLeuAspArgLeuArgLysHisGln 221  Qy 190 AGAGATTCTTCCTTTATACCCCTGGGACACATGCTCACCCAAAAAATAGCC 240  Qy 190 AGAGATTCTTCCTTTATACCCCTGGGACACATGCTCCCCAAAAAAATAGCC 240  Qy 241 TACCAGATCGCCTGGGCCTGGCCTACCTGCACAAAAAACATCATCTTCTGTGACCTG 300  Qy 241 TACCAGATCGCCTGGGCCTGGCCTACCTGCACAAGAAAACATCATCTTCTGTGACCTG 300     :::       :::   :::   :::   :::   :::    :::

1905 823	1846 TTCAGCCAGCACCTGCAGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCC 1	p dq
806	93ProLeuValProProGlySerSerProLeuProProArgLe	Д
1845	ACCTGACCCCCATGGACGGGGAGACC	Q
792	Ser	B 3
775	755 uSerProAlaProProGlyGluGluGluThrSerGlnTrpProGlyProAlaSerProPr	B B
1728	14 CTCCCCAGCTCCCCA	8
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	AGGCTGCCAGGTCCCCTCAAGC	δ
735	717GlnLeuGlnAlaProGlySerProAlaProSerProSerProGlyGlyAspAspLy	D
716 1690	ATCCCCACCCGCC	රි දි
1641	82 GACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCAGATCCTGATCCACCAGGAATCA	Qy
716	eGlnAlaLeuGlnGlnGluCysMetArg	밁
1581	46 GCCAACCCAAAGGTGCCTGAGGGGGACTCCATCGCG	Qy
701	lyGlyLysProProSerSerAl	. g
1545		Q
681		밁
1528	ACATGTTTCCCGTGCGGCCTTGGACACGGAACCCC	γQ
661	<pre>;:: flulleCysSerIleAsnSerThrLeuValGlyAlaGlyValProAl</pre>	日
1488		Qy
641	pAspValAlaGlnAs	g
1447	ACTCCTTGGTGATGTACCACTCCACCACCTACC	Ωy
626	322 1AspTrpAspAl	뮍
1407	CGTCAGTCGTGTGCAGCTCTGAGGGCAGAGGGGGGAGGAGGTCGTCTGGTGCCTGGATGAC	Qy
622	laLeuProArgProLeuHisProThrProValVa	문
1347	TGGCCCCTCCATGGTT	δ
605	592 uAlaMetAspAlaCysGerLeuLeuAspGluThrProPro (	밁
1308	GTCTGGTACAGCAATGGGCCGGGCCTCCTTGTCCATCGACTGTGCCTCCCTGGAGATC 1	Q
592	alProAlaLeuArgProCysProProSerLeuAlaGlnLe	₽
1248	CTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCT	Qy
572	560 aSer	밁
1194	CCTACCTGTGCTCACACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATGAAGAC	Q
560	540 oGlyLeuProArgGlyLeuTrpLeuAlaLysProSerAlaArgValProGlyThrLysAl	밁
1134		Qy
540	520 oValSerGluAspGlnAspProLeuSerSerAspPheLysArgLeuGlyLeuArgLysPr	Вþ

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	AGCC 240      Ala 233  CCTG 300	CGCC 189 : .sGln 221	CCGCTC 129    :::  Promet 201	GCTG 72 ::: aMet 181	•	PEGGC 1985 826 ATGCT 2025

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80	IleLeuProIleValArgA:	841	ф	
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41	AlaThrProGlnValIleGlnAlaProGlyAlaGlyGlyProC	827	рb	
2025	CGAGTCATTGCCCTTAAAAGCCCGAGAGCTGACTCCGCATGGGGTGCTGGATGCT	1966	Ωу	
826	spProLysTyr	823	망	
1965	AGGCGCGGTGGAGATGTTATCGTCATTGGCCTGGAGAAGGATTCTGAAGCCCCAGCGGGGC	1906	Qy	
823	uSerSerProGlyLysThrMetProThrThrGlnSerPheAlaSer-A	806	탕	
1905	TTCAGCCAGCACCTGCAGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCC	1846	Qy	
908	ProLeuValProProGlySerSerProLeuProProArgLe	793	ДD	
1845	GTCTGAGCATGACCTG	1786	Qy	
792	oArgValProProArgGluProLeuSerProGlnGlySerArgThrProSer	775	Ф	
1785	GCAAGTTCTTCCAGTGTGCCTTTCTCCACCGACTGCGAGGACTCAGACATGCTACAT	1729	γQ	
775	${\tt ProGlyGluGluGluThr} {\tt SerGlnTrpProGlyProAla}$	755	Db	
1728	CTCCCCAGCTCCCCA	1714	Qy	
755	:::	735	밁	
1713		1691	Qγ	
735	erProGlyGlyAsp <i>l</i>	717	ф	
1690	ATCCCCACCCCCCC	1642	γQ	
716		716	DЬ	
1641	GACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCAGATCCTGATCCACCAGGAATCA	1582	Qy	
716		701	ДЪ	
1581	GGGACTCCATCGCG	1546	Qy	
701	oProLeuGluAspAsnLeuPheLeuProProGlnGlyGlyGlyLysProProSerSerAl	681	ф	
1545	CAGCCAGCCACACG	1529	οy	
681	ProPr	661	В	
1528	ACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCC	1489	γQ	
661	uAspAspPheGluIleCysSerIleAsnSerThrLeuValGlyAlaGlyValProAl	641	문	
1488	. ი	1448	ρ	
641	aArgProLeuProProProProAlaTyrAspAspValAlaGlnAs	626	ф	
1447	TGATGTACCACTCCACCCACC	1408	Qy	
626	1AspTrpAspAl	622	Дb	
1407	ACGTCAGTCGTGTGCAGCTCTGAGGGCAGAGGGGAGGAGGTCGTCTGGTGCCTGGATGAC	1348	Qy	
622		606	Db	
1347	GTT	1309	Qy	
605	uAlaMetAspAlaCysSerLeuLeuAspGluThrProPro (	592	망	
1308	ATC	1249	Qy	

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Best Local Similarity:
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COCATION: (1)...(1036)
; OTHER INFORMATION: Xaa -
US-10-014-882-2
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US-10-014-882-2
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APPLICANT: Kieke, James
TITLE OF INVENTION: No. US20020107384A1e1 Hu
FILE REFERENCE: LEX-0279-USA
CURRENT APPLICATION NUMBER: US/10/014,882
CURRENT FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/254,744
PRIOR FILING DATE: 2000-12-11
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 1036
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AGGCCTCGCATTGTATATGATGAGAAGGTAGATATGTTCTCCTATGGAATGGTGCTCTAC
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GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
APPLICANT: Hodge, Wartin R.
TITLE OF INVENTION: No. US20020142428A1el Kinases
FILE REFERENCE: 35800/234862
CURRENT APPLICATION NUMBER: US/09/862,027
CURRENT FILING DATE: 2001-05-21
                                                                                                                                  Sequence 19, Application US/09862027 Patent No. US20020142428A1
PRIOR APPLICATION NUMBER: US 09/345,473
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QY 493 ATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCTGCACTG 534	433 225	Qy 385 TCATTCCATGAGGGCGCCTAGGCGTGGAGGGCACTCCTGGCTACCAG 432 :::                           ::    ::  Db 205 ValTyrArgGluGlyAlaArgLysGluProLeuAlaValValGlySerProTyrTrpMet 224	Qy 331 GACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCAG 384	Qy 271 CACAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTT 330	Qy 211 CTGGGACACATGCTCACCCAAAAAATAGCCTACCAGATCGCCTCGGGCCTGGCCTACCTG 270	Qy 160 AGCCTCAACACCGTGCTGTCCGAGAAACGCCAGAGATTCTTCCTTTATACCC 210 :::	Qy 100 GCGCTCATCGGCATCAGCATCCACCCGCTCTGCTTCGCCCTGGAGCTCGGCCCGCTCAGC 159 Db 114 ArgPheMetGlyValCysValHisGln	Qy 40 TTCTCCGAGTTCCGGCAGGGCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTG 99 :::    :::::::::::::::::::::::::::::	Qy 4 CTGAGGCACCTGCGGGCCACCGATGCCATGAAGAAC 39 :::	10 Gaps: 22_2205 (1-2184) x US-09-862-027-	Pred. No.:  2.07e-07 Length: 626 Score: 255.50 Matches: 150 Percent Similarity: 33.69% Conservative: 71 Best Local Similarity: 22.87% Mismatches: 242 Query Match: 6.30% Indels: 193	; ORGANISM: Homo sapiens US-09-862-027-43	o for	; CURRENT FILING DATE: 2001-05-21 ; PRIOR APPLICATION NUMBER: US 09/345/473 ; PRIOR FILING DATE: 1999-06-30 ; NUMBER OF SEQ ID NOS: 82	; APPLICANT: Hodge, Martin R. ; TITLE OF INVENTION: NO. US20020142428Alel Kinases and Uses Thereof ; FILE REFERENCE: 35800/234862 ; CURRENT APPLICATION NUMBER: US/09/862,027	US-09-862-027-43  ; Sequence 43, Application US/09862027 ; Patent No. US20020142428A1 ; GENERAL INFORMATION:	Db 282 GlnAspAsnTrpLysHisGluIleGlnGluMet 292 RESULT 11	Db 262 LeuThrThrIleGluGluSerGlyPhePheGluMetProLysAspSerPheHisCysLeu 281  Qy 792 GTTTTGGGAAAAGAGGAGTCCAGGAACTA 824
		1304 -AGATCTGCAGGCGCTGGAAGCCCTACAATGCCCCATGGATGCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATG	OY 1234 GICANCAGGGGCUTGTGGACTGT 1293  Db 483 aProGlnLeuProLeuAlaValAlaThrAspAsnPheIleSerThrCysSerSerAlaSe 503  OV 1294 GCCTCCCTGG	1174 TTCAGCATCGCGGATGAAGACGCCACGCAGAACCCCATGCAAGGCAATGGAGGTG	1144 CTGTGCTCACACACACACACACACACACACACACACACAC	1099 GTGTTTCCCGTGGTGCGCGCCCCAAAGGACAGCTGCTCCTAC  429	1039 CCTGTTATTAAAAGAATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTTGTGGCT	9/9 THAMACACUCCAACAGGCTTUGGTACTCCAGCTGCTTCGTTGGTGGTCGCCTGCTTCGTTGGTGGCCGTGCTTGGTGG	374 snLeuThrArgValAsnProPheSerLeuArgGluAspLeuArgGlyGlyLysIleLysL	354 rgSerArgSerAspLeuPheLeuProProSerProGluSerProProAsnTrpGlyAspA	Oy 874 TGCCCTGGGATGAAGGTGAGCTGCCAGGTCCAGAGATCCCTGTGGACAGCCACC 933	Qy 814 TCCAGGAACTACACGGTGGTGAACACAGAGAAGGGCCTCATGGAGGTGCAGAGGATGTGC 873 Db 340 341	Qy 754 GCCTTCTTCTCATCCCAGGGCCAGGAGTACACCGTGGTGTTTTGGGATGGAAAAGAGGAG 813	Qy 694 CAGATGAAGGACCCGACTTTTGCCACCTTCATGTATGAACTGTGCTGTGGGAAGCAGACA 753    :::	Qy 655 AAGCCAGAGAAGCGACCGCTGGCCCTGTCG	Qy 595 CAGCCGGAGGAAGTGCAGTTCCGGCGACTCATGATGGAGTGCTGGGACACT 654 :::	Qy 535 GGCCACCACCACCACATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGG 594     :::     Db 265 GluAspPheGlyLeuAspValProAlaPheArgThrLeuValGly 279	:::            ::::: 245 IleValLeuCysGluLeuIleAlaArgValProAlaAspProAspTyrLeuProArgThr

QY 295 GACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATC 354	Db 151 GlyArg	Qy 127 CTCTGCTTCGCCCTGGAGCTCGGGCCGCTCAGCAGCACCCGTGCTGTCCGAGAAC 186	73 CACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCCG	US-09-836-392-8_COPY_22_2205 (1-2184) x US-09-835-081-2 (1-752)  QY 13 CTGCGGGCCACGATGCCATGAAGAACTTCTCCGAGTTCCGGCAGGAGGCCAGCATGCTG 72	cal Similarity: 24.70% Mismatches: 23 indels: 24 indels: 24 indels: 36 indels	Length: Matches: Conservative:	: TYPE: PRY ; ORGANISM: Human US-09-835-081-2	; NOMBER OF SEQ ID NOS: 4 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 2 ; LENGTH: 752	RENCE: (PPLICAT:	; GENERAL INFORMATION: ; APPLICANT: YAR, Xianghe et al. ; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES	US-09-835-081-2 ; Sequence 2, Application US/09835081 ; Patent No. US20020151020A1		Qy 1603 GAGGACCTGGGCAGATCCTGATCCACCAGGAATCACTCAC	160	Qy 1483 CCCTCAGGGACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCAGC	Qy 1423 GTGATGTACCACCTCCACCTACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCAGC 1482	rLeuProArgAlaAlaAlaLeuGluArgThrGluPro
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                                                                                                                                                                                                                                                                                                                                                                      260 GluAspPheGlyLeuAspVal--
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RESULT 14
US-09-974-298-129
; Sequence 129, Application US/09974298
; Patent NO. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hue1-Me1
; TITLE OF INVENTION: GENES EXPRESSED
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FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte
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SOFTWARE: PERL Program
SEQ ID NO 129
LENGTH: 937
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CURRENT APPLICATION NUMBER: US/09/97-
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR EILING DATE: 2000-05-10
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US-09-836-392-8_COPY_22_2205 (1-2184) x US-09-974-298-129 (1-937)
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                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/977,260 CURRENT FILING DATE: 2001-10-16 PRIOR APPLICATION NUMBER: 08/232,545 PRIOR FILING DATE: 1994-04-22 NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 6 LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09977260 Publication No. US20020192790A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     APPLICANT: ULLRICH, AXEL
APPLICANT: GISHIZKY, MIKHAIL
APPLICANT: SURES, IRMINGARD
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
FILE REFERENCE: 038602/1260
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OTHER INFORMATION:
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ORGANISM: Unknown Organism
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                                                                                                                                                                          ProSerAsnCysPro---GlnGlnPheTyrAsnIleMetLeuGluCysTrpAsnAlaGlu
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-Q-/cgn2_l/USPF0_spool/US99836392/runat_08042003_090540_23400/app_query.fasta_1.903
-D3-genEmbl -OFMT-fastap -SUFFIX-P2n.rge -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-b1ts -START=1 -END--1 -MATRIX-b1osum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-PCt -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US9836392 _GCGN_1_1_2189_@runat_08042003_090540_23400 -NCPU-6 -ICPU-3
-NORMLTINEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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Ygapop 10.0 , Y
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36: em_htg_roi:*
37: em_htg_vrt:*
38: em_sy:*
40: em_htgo_num:*
41: em_htgo_other:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

444	CCC CCC L4333333333333333333333333333333	o 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Result No. 1 1 2 3 3 5 6
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Submitted (27-MAR-2001) Osamu Ohara, Kazusa DNA KSeulch, L...
Submitted (17-MAR-2001) Osamu Ohara, Kazusa DNA KSeulch, L...
Department of Human Gene Research; 1532-3, Yana, Kisarazu,
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nagase, T., Nakayama, M., Nakajima, D., Kikuno, R. and prediction of the coding sequences of unidentified The complete sequences of 100 new cDNA clones from for large proteins in vitro DNA Res. 8 (2), 85-95 (2001)
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GYLGVESSDVNWKKKKSGGKKIVCQSEVRDESAMAFTDHVNSLIDQWFPALTATESD
GTPLMEQYVPCPVCETAWAQHTDPSEKSEDQYYFDMEDCVLTAIERDFISCPRHPDLP
GTPLMEQYVPCPVCETAWAQHTDPSEKSEDQYFDMEDCVLTAIERDFISCPRHPDLD
GTPLMEQYVPCPVCETAWAQHTDPSEKSEDQYFDMEDCVLTAIERDFISCPRHPDLD
VPLQELVPELFMTDEPARLFLENSKLEHSEDEGSVLGQGGSGYYYRARXQQQPVAVK
RFHIKKFKNEANVPADTMLRHLRATDAMKNESEFQEASMLHALQHPCIVALIGISIH
PLCFALELAPLSSLNRVLSESHARDSSFIPGALGYEGTPGVAPEIRPRIVTDEK
VDMFSYGMVLYELLSGQRPALGHQLQIAKKLSKGIRPVLGQPESVGPERLQALMMEC
WDTKPEKFLALSVYSQMKDDTFATEMYELCGKQTAFFSGGGETYVVFWDGKEESR
NYTVVNTEKGLMEVQPKKNSLLVAGLANGLVYPFVRGPENDSCSYLCSHTANR
NTVVNTEKGLMEVQFKCCPGMKVSCQLQVGRSLWTATEDQKIYITLKGMCPLNTPQ
QALDTPAVVTCFLAVPVIKKSLYLLAGLANGLVXPFVVRGPENDSCSYLCSHTANR
SKFSIADEDARQNFYPVKAMEVVNSGSEVWYSNGPGLLVIDCASLEICRRLEPYMAPS
MYTSVVCSSEGREEVVWCLDDKANSLVMYHSTTYQLLARFECCVPSPLEDMFPVRAPL
MYTSVVCSSEGREEVTWCLDDKANSLVMYHSTTYQLLARFECCVPSPLEDMFPVRAPL
MYTSVVCSSEGREEVTWCLDDKANSLVMYHSTTYQLLARFECCVPSPLEDMFPVRAPL
MYTSVVCSSEGREEVTWCLDKANSLVMYHSTTYQLLARFECCVPSPLEDMFPVRAPL
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AVKILAVRDLIWVPRRGGDVIYGLEKDSSEAQRGRVIAVIKARELTPHGYLVDAAVVA
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/protein_1d="BaB47419:1"
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/translation="PRQGKSTLLEILQTGRAPQVVHGEATIRTTKWELQRPAGSRAKV
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                                                                                                                                                                                                                                                                                                                                                     NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Huma Genome Center; 3'-end one pass sequencing: RAB; clone selection full insert sequencing; RAB and Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (24-OCT-2001) Sumio Sugano, Institute of Medica University of Tokyo, Laboratory of Genome Structure, Huma Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens stomach mucosa clone: STM07710.
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Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takigue
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AK058028
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Fax:81-3-5449-5416)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human cDNA sequencing project
                                                                                                                                                                                            /tissue_type="stomach mucosa"
/clone_lib="STM"
/note="cloning vector: pME18SFL3"
1198 c 1157 g -- 879 t
                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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ture, Human Genome
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	400	1 TyrLeuCysSerHisThrAlaAsnArqSerLysPheSerIleAlaAspGluAspAlaArq	)y 38	~
	1908	9 GCCGATGGGCTTGTGGCTGTGTTTCCCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTC	b 184	~
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÷	220 1428	1 GluGluValGlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysPro 	λy 20 )b 136	~~
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	1 PheSerTyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeuGlyHis 180 	Qy 16
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9d 9	21 SerAspTyrGlyIleSerArgGlnSerPheHisGluGlyAlaLeuGlyValGluGlyThr 140 	Qy 121 Db 4336
Q D .	01 LysSerAspAsnIleLeuValTrpSerLeuAspValLysGluH1sIleAsnIleLysLeu 120 	Qy 101 Db 4276
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Ov Db	41 HisProLeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSer 60 	Qy 4
O D 1	21 AlaSerMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIle 40 	Qy 21 Db `4036
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Qy	1 (bases 1 to 6045) Plowman, G.D., Whyte, D., Manning, G., Suda	REFERENCE
Db	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.	1
Qy	human SM Homo sapiens	SOURCE ORGANISM
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                                                                                                                  through
Series:
                                                                                                                                                                          cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                            USA
NIH-MGC Project URL: ht
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                              Submitted (27-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                        This clone was select passed the following
                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens, Similar to MGC:5630 IMAGE:3463078, m BC005408 BC005408.1 GI:13529310
                                                                               analysis
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                                                                                        distribution: MGC clone distribution yh the I.M.A.G.E. Consortium/LLNL at: s: IRAK Plate: 4 Row: n Column: 18 clone was selected for full length sec d the following selection criteria: He
   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="McC:5630 TMAGE:3463078"
/tissue_type="Cervix, carcinoma
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                                                                              Submitted (24 OCT-2001) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax.81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan, cDNA full insert sequencing: Research Association for Blotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB and
                                                                                                                                                                                                                                                                                                                                          Nishi,T., Nakagawa,S., Senoh,A., Mizuguchi,H., Inagaki,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishia,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanakomi,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Naga
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                                     AsnSerTyrLeuValLeuAlaGlyLeuAlaAspGlyLeuValAlaValPheProValVal
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                             AATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTTGTGGCTGTTTTCCCGTGGTG
                                                           CAGGCCTTGGATACTCCAGCTGTCGTCACCTGCTTCTTGGCCGTGCCTGTTATTAAAAAG
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/cell_type="neuroglioma"
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/note="cloning vector: pME
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٠		GGAGCTGGGCCGGCTGGAGGCTTGCACTCGC	1801	뮍
		lnSerTyrGluGluLeuGlyArgLeuGluAlaCysThrArgLysArgAr	712	VΩ
	1800	AGTGGTGCCTGGCCGTCTGGAGGGGCTGGGGGCGCCAGGGAGTTCGACATTTTCT	1741	В
	711	rGluTrpCysLeuAlaValTrpArgGlyTrpGlyAlaArgGluPheAspIlePh	692	Q
	1740	GTGGATGCTGCCGTGGCAAAGGACACTGTTGTGTGCACCTTTGAAAATGAAAA	1681	망
	169	euValAspAlaAlaValValAlaLysAspThrValValCysThrPheGluAsnC	672	Qy
	1680	GCCCAGCGGGCCGAGTCATTGCCGTCTTAAAAGCCCGAGAGCTGACTCCGCATGGGGTG	1621	뫄
	671	laGlnArgGlyArgValIleAlaValLeuLysAlaArgGluLeuThrProHisGl	652	Qγ
•	1620	ATTTGGGTCCCCAGGCGCGT-GGAGATGTTATCGTCATTGGCCTGGAGAAGGATTCTGAA	1562	망
	651	leTrpValProArgArgGlyGlyAspValIleValIleGlyLeuGluLysAspSerG	632	Qγ
•	156Ì	CCAGCACCTGCAGGCCGTGAAGATCCTCGCCGTCAGAGAC	1502	g
	631	spGlyGluThrPheSerGlnHisLeuGlnAlaValLysIleLeuAlaValArgAs	612	20.
	1501	GACATGCTACATACGCCCGGTGCTGCCTCCGACAGGTCTGAGCATGACCTGACCCCCATG	1442	В
	611	spMetLeuHisThrProGlyAlaAlaSerAspArgSerGluHisAspLeuThrProMe	592	Qγ
	1441	CTCCCCAGCTCCCCAGCAAGTTCTTCCAGTGTGCCTTTCTCCACCGACTGCGAGGACTCA	1382	<sub>당</sub> 1
(	591	euProSerSerProAlaSerSerSerSerValProPheSerThrAspCysGluAspSe	572	Q V
	1381	GCTCCATGTCCTCCTACTCCTCATCCCCACCCCCAGGCTGCCAGGTCCCCCTCAAG	1322	뮍
	571	sSerMetSerSerTyrSerSerSerProProArgGlnAlaAlaArgSerProSerS	552	Qy
	1321	ATGTACAGTGAGGAGCTGGGCACGCAGATCCTGATCCACCAGGAATCACTCAC	1262	뮍
	551	etTyrSerGluGluLeuGlyThrGlnIleLeuIleH1sGlnGluSerLeuThrAspTy	532	Qy
	1261	GCCAGCCACACGGCCAAACCCCAAAGGTGCCTGAGGGGGACTCCATCGCGGACGTGAGCATC	1202	В
	531	laSerHisThrAlaAsnProLysValProGluGlyAspSerIleAlaAspVals	512	Qy
	1201	GTCCCCAGCCCCTCAGGGACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCGGCA	1142	. <b>D</b>
	511	alProSerProLeuArgAspMetPheProValArgProLeuAspThrGluProProAl	492	Qy
	1141	ACTCCTTGGTGATGTACCACTCCACCACCTACCAGCTGTGTGCCCGGTACTTCTGCGGG	1082	뫄
	491	snSerLeuValMetTyrHisSerThrThrTyrGlnLeuCysAlaArgTyrPheCysG	472	Qy
	1081	GTCGTGTGCAGCTCTGAGGGCAGAGGGGAGGACGTCGTCTGGTGCCTGGATGACAAGGCC	1022	밁
	471	alValCysSerSerGluGlyArgGlyGluGluValValTrpCysLeuAspAspLysA	452	Qy
	1021	GCCTCCCTGGAGATCTGCAGGCGGCTGGAGCCCCTACATGGCCCCCTCCATGGTTACGTCA	962	В
	451	laSerLeuGluIleCysArgArgLeuGluProTyrMetAlaProSerMetValThrS	432	Qγ
	961	GTCAACAGCGGCTCTGAGGTCTGGTACAGCAATGGGCCGGGCCTCCTTGTCATCGACTGT	902	рь
	431	$\verb alasnSerGlySerGluValTrpTyrSerAsnGlyProGlyLeuLeuValIleAspC  $	.412	Qy
•	901		4	뫄
	411	eSerIleAlaAspGluAspAlaArgGlnAsnProTyrProValLysAlaMetGluVa	392	ρ <sub>γ</sub>

AK094556 LOCUS DEFINITION

AK094556 Homo sap

2790 bp sapiens cDNA FLJ37237 fis,

mRNA clone B

NA linear BRAMY2002638.

PRI 15-JUL-2002

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                              LeuValIleAspCysAlaSerLeuGluIleCysArgArgLeuGluProTyrMetAlaPro
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Oligo cappi
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Fukuzumi, Y., Fujimori, Y., Komiyama, M., Sugiyama, T., Irie, R.
Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Is
Kawai-Hio, Y., Salto, K., Nishikawa, T., Kimura, K., Yamashita,
Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Wagatsuma, M., Murakawa, K., Kamehori, K., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
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Isogai, T. and Yamamoto, J.
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/clone_lib="BRAMY2"
/note="cloning vector: processed to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of t
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Eutheria; Primates;
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ng; fis (full insert sequence).
nNA to mRNA, clone_11b:BRAMY2
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a, K., Yamashita, H.,
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                                                   BC027199
Mus musculus,
MGC:28646 IMAG
BC027199.1 GI
Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                 house mouse.
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                                                                         Similar to hypothetical 
3E:4224922, mRNA, complet
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complete cd°
  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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FLJ23119, clone
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                                                                          CACACAGCCAACAGGTCCAAGTTCTGCATCCCCGACGAAGATGCACGGCAGAACCCTTAC
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Baylor College of Medicine Human
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.g. Series: IRAK Plate: 37 Row: k Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, '
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin,
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Submitted (04-APR-2002)
Gene Collection (MGC), C
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PVEECIADVSIMYSEELGTQIITHQDSITDYCSMSSYSSSPHQDPRSBSSLPSSITS
YSSVFFSANYEDSDRLQEFSVTSDRTEHDLSFBWDGETFSGHLQAVKVLAKVBLHVFF
HGGDIIVIGLEKDSGAQRGRVIAVLKARELNRHGYLVDAAVVAKDTVVCGFANENTEW
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/product="Similar to hypothetical protein FLJ23119"
/protein_1d="AAH27199.1"
/db_xref="GI:20073185"
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/db_xref="taxon:10090"
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/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B"
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Cancer Genomics Office, National Cancer
rive, Room 11A03, Bethesda, MD 20892-2590,
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                                                    ArgGluPheAspIlePheTyrGlnSerTyrGluGluLeuGlyArgLeuGluAlaCysThr
                                                                                               CysThrPheGluAsnGluAsnThrGluTrpCysLeuAlaValTrpArgGlyTrpGlyAla
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             SerThrAspCysGluAspSerAspMetLeuH1sThrProGlyAlaAlaSerAspArgSer 604
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346 ValProVal---IleLysLysAsnSerTyrLeuValLeuAlaGlyLeuAlaAspGlyLeu 364

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	T 1635	TGGGAATGGAAGCGACCGCTTTAGCAAATCTAAGAGTGGCCGCACAAAAGCTTATTGCC	1694	밁
	- 635		635	Q
	T 1695	TCCTTACAGGTCATGTGGGGAGGCAGGTGCTGTTCTTCCAAGAGGGTTGGTT	1754	ઠ
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	T 1755	CATCCAGGGCACGCCCACTGCTCCTGCTCTGGGGACAGAGCAAGGGGGAAGCCCCCTGGC	1814	밁
	- 635		635	Qy
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	635	leLeuAlaValArqAspLeuIleTrpValPro	625	Q
	3 1874	GAGCATGACCTCCATGGACGGGGAGACCTTCAGCCAGCACCTGCAGGCCGTGAAG	1933	밁
•	s 624	luHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLeuGlnAlaValLy	605	Q.
		CAGGTC		밁
	r 604	rThrAspCysGluAspSerAspMetLeuHisThrProGlyAlaAlaSerAspArqSe	585	Q
	ш	GCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTCCCCAGCAGCTCTTCCCAGTGTGCCTTT	2053	쁗.
	e 584	$\mathtt{aAlaArgSerProSerSerLeuProSerSerProAlaSerSerSerValProPh}$	565	VΩ
	G 2054	ATCACTCACTGACTACTCCTCCATGTCCTCCTACTCCTCATCCCCACCCCGCCA	2113	日
	n 564	nGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSerProProArgGl	545	Q
	S 544     C 2114	TCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCAGATCCTGATCCA	7	B 8
		TT  0A  0A  0A  0A  1	υ	2
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	G	uAspThrGluProProAlaAlaSerHisThrAlaAsnProLysValProGluGly&	505	Ş
	Ñ	CCCGGTACTTCTGCGGGGTCCCCAGCCCCCTCAGGGACATGTTTCCCGTGCGGCC	2293	망
	504	${ t salaargTyrPheCysGlyValProSerProLeuArgAspMetPheProValArgPr}$	485	Ş
	22	TCCACCACCTACCAGCT	2353	밁
	u 484	rpCysLeuAspAspLysAlaAsnSerLeuValMetTyrH1sSerThrThrTyrGlnLe	465	Q
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	1 464	laProSerMetValThrSerValValCysSerSerGluGlyArqGlyGluGluValVa	445	Qy
	 G 2414	GGCCTCCTTGTCATCGACTGTGCCTCCCTGGAGATCTGCAGGCGGCTGGAGGCCTACAT	2473	8
	t 444	yLeuLeuVallleAspCysAlaSerLeuGluIleCysArgArgLeuGluProTyrMe	425	Q
	G 2474	ATGGGCC	2533	뫄
	0 424	oValLysAlaMetGluValValAsnSerGlySerGluValTrpTyrSerAsnGlyPr	405	Qy
•	2534	CACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATGAAGACCGCACGGCAGAACCCCCTAC	2593	ğ
	r 404	lsThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaArgGlnAsnProT	385	Q
	T 384     2594	ValalaValPheProValValArgGlyThrProLysAspSerCysSerTyrLeuCysSe 	365 2653	B 8
	T 2654	:::        atcctgtcttccttcagaattcctacctggtcttagcggccctcgccgatgggct	2713	В

TOURNAL REFERENCE BAUTHORS ACCORDANCE GOOD GOOD GOOD GOOD GOOD GOOD GOOD GOO		REFERENCE 1 AUTHORS E TITLE JOURNAL C REFERENCE 2 AUTHORS E	ACCESSION A VERSION A KEYWORDS F SOURCE F ORGANISM F	RESULT 10 AC090907/c LOCUS DEFINITION E	Qy 660 Val     Db 1334 GTC	Qy 640 Asp       Db 1394 GA3	Qy 636 Db 1454 GAGC	Db 1514 AA	Qу 635	1574	ρν 1634 GCC
ubmitted (17-MAR-2001) usesearch, 320 Charles ( (bases 1 to 178529) diren,B., Linton,L., linton,L., loukingalter,B., Barna,N., oukingalter,B., Brown,L., hazaro,B., Chopell,Y., ook,A., Cooke,P., DeAlaro,S., Ferreira,P., rand-Pierre,N., Hagos, ohnson,R., Jones,C., F	Bastlen, V., Boguslavkiy, L., Boukhgalter, Campopiano, A., Chang, J., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dodge, S., Farro, S., Ferreira, P., FitzHug, Gardyna, S., Ginde, S., Goyette, M., Graire, M., Hagos, B., Heaford, A., Horton, L., Johnson, R., Jones, C., Karatas, A., LaRocc, M., Larders, T., Lehoczky, J., Levine, R., Larders, T., Lehoczky, J., Levine, R., Matchews, C., McKernan, K., McPheeters, R., Meldrim, J., Macdonald, P., Marquis, N., Matthews, C., McKernan, K., McPheeters, R., Meldrim, J., Macdonald, P., Marphy, T., Naylor, J., Nguyen, M., Mathara, V., Mathara, P., O'Connort, T., O'Donnell, P., O'Connort, T., O'Donnell, P., O'Connort, T., O'Donnell, P., O'Reil, D., Phunkhang, P., Pierre, N., Pollara, V., Fieback, M., Riley, R., Rise, C., Rogov, P., Royy, A., Santos, R., Schauer, S., Strauss, N., Subranian, A., Talamas, T., Travers, M., Subranian, A., Talamas, T., Travers, M., W., M., W., W., Zembek, L., Zimmer, A. and Zody, M.	<pre>1 to 178529) Linton,L., Nusbaum,C. and Lander,E. ns, clone Rp11-505E24 3, clone Rp11-505E24 1 to 178529) Linton,L., Nusbaum,C., Lander,E., Allen,N., Ander</pre>	AC090907. 4 GI:21306825 AC090907. 4 GI:21306825 HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN. human. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.	iens cl	alLeuLysAlaArgGluLeuThrProHisGly 670 	ASPVAII1eVAII1eG1yLeuG1uLySASPSerG1uA1aG1nArgG1yArgVaI11eA1a 659 	GACGGCTACCGACAAATCGCTTCCCCTTCTGGGTTTTGGTTGCTTAGGCGCGGTGGA 1395	AAACTGCATGTCTGTTGCCTCCCTCCCGCACCTTTCTGCACACCGGCTTCACTCCCCGGA 1455	635	TGCTTTGAAGTCTGTCCCCTCCCCATAACTTAATCCCTTAGCAG 1	GCCAGAGAGCTTAAGGTGCCACACAAGGAAAGCCACAGTCAACTGTGACTCAGTTTCCAC 1575

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Percent Similarity:
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                                                      US-09-836-392-21 (1-728) x AC090907 (1-178529)
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346 ValProVal---IleLysAsnSerTyrLeuValLeuAlaGlyLeuAlaAspGlyLeu 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 1, 2002 this sequence version replaced gi:16259005.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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133082 133181: gap of 28087 bp
133182 161268: contig of 28087 bp
161269 161368: gap of 100 bp
161369 165097: contig of 3729 bp
165098 165197: gap of 100 bp
165098 165197: gap of 12427 bp
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/db_xref="taxon:966"
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                       TGGGAATGGAAGCGATCGCTTTAGCAAATCTAAGAGTGGCCGCACAAAAGCTTATTGCCT 7441
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                         Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkly, L., Boukhgalter, B., Camarata, J., Charg, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-plearre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Menus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Pomman, T., Roy, A., Schwinsky B., Samman, G., Gusery, P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkly, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (31-DEC-1999) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
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Birren, B., Nusbaum, C.
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            Schauer, S.,
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            Schupback, R.,
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                                                                                                                              , Norman, C.H.,
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* SEQUENCING
                                              Rogov, P.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                           14759 ATCCCTGTCCTTCCTTCAGAATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
Match:
                                                                                                                                                                                                                                                                                                                                                            365 ValAlaValPheProValValArgGlyThrProLysAspSerCysSerTyrLeuCysSer 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     346 ValProVal---IleLysLysAsnSerTyrLeuValLeuAlaGlyLeuAlaAspGlyLeu 364 ::::||||||
                                                                                                                                                                                                                           CACACAGGCCAACAGGTCCAAGTTCAGCATCGCGGATGAAGACGCACGGCAGAACCCCCTAC
                                                                                                                                                                                                                                                                        HisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaArgGlnAsnProTyr
                                                                                                                                                                      ProValLysAlaMetGluValValAsnSerGlySerGluValTrpTyrSerAsnGlyPro 424
                                                                                                                                                                                                                                                                                                                                   GTGGCTGTGTTTCCCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTCCTACCTGTGCTCA
                                                                                                                   CCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTACAGCAATGGGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smit, A.F.A. & Green, P. (1990-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tesfaye, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       All repeats were identified using RepeatMasker Smit, A.F.A. & Green, P. (1996-1997)
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58974 59173: gap of 100 bp

59074 91153: contig of 32080 bp in length

91154 91253: gap of 100 bp

91254 178876: contig of 87623 bp in length
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/clone_llb="RPCI-11 Human Male BAC"
/4853 c 42570 g 42356 t 246 others
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., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Homo sapiens"
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source 1183401
ES Loca
* 16758 28859: * 28860 28959:
preserve
* runs of N, but the This record will the things as soon as it is
is not know
* NOTE: This is a 'working drait' sequence. It * consists of 4 contigs. The true order of the
ality
Insert size: 174146; Insert size: 183101;
Consensus quality: 178788 bases Consensus quality: 180438 bases Consensus quality: 181007 bases
Chemistry: Dye-terminator Big Dye; Chemistry: Dye-terminator Big Dye; Assembly program: Phrap; version 0
Sequencing
Center clone name: Ct
Web site: http://sequence-www.stanford. Contact: hum-info@sequence.stanford.edu 
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AL
Glukhov,S., Hansen,N., Hymu Mozehouse,A.J., Oefner,P., Yu,S. and Davis,R.W. Tirect Submission
Yu,S. and Davis,R.W. JOURNAL Unpublished REFERENCE 2 (bases 1 to 18340 AUTHORS Bruno.D., Conn.L., D
AUTHORS Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D., Federspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R., Mao, J., Lam, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M., Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.M., Wilhelmy, J.,
f Homo Eukar Mamma
ACCESSION AC020578.8 GI:12831370 VERSION AC020578.8 GI:12831370 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; SOURCE Homo sapiens.
ACO20578/c ACO20578 LOCUS 183401 bp DEFINITION Homo sapiens chromosome 15 clone SEQUENCE, 4 unordered pieces.
660 ValleuLysAlaArgGluLeuThrProH1sGly

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BASE COUNT	49346 a 42604 c 44323 g 46782 t	
Alignment Pred. No. Score: Sercent S Percent S Best Loca Query Mat		
US-09-836	-392-21 (1-728) x ACO20578 (1-183401)	
Qy 346 Db 60726	ValProValIleLysLysAsnSerTyrLeuValLeuAlaGlyLeuAlaAspGlyLeu 364 :::       arccorgrocotrocotroAgaatrocotagototraGogggcotcGccGargggctr 60667	
Qy 365 рь 60666	ValAlaValPheProValValArgGlyThrProLysAspSerCysSerTyrLeuCysSer 384 	
Qy 385 Db 60606	HisThralaAsnArgSerLysPheSerIleAlaAspGluAspAlaArgGlnAsnProTyr 404	
Qy 405 Db 60546	ProValLysAlaMetGluValValAsnSerGlySerGluValTrpTyrSerAsnGlyPro 424 	
Qy 425 Db 60486	GIYLeuLeuValIleAspCysAlaSerLeuGluIleCysArgArgLeuGluProTyrMet 444 	
Qy 445 Db 60426	AlaProSerMetValThrSerValValCysSerSerGluGlyArgGlyGluGluValVal 464	
Qy 465 Db 60366	TrpCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThrThrTyrGlnLeu 484 	
Qу 485 Db 60306	CysAlaArgTyrPheCysGlyValProSerProLeuArgAspMetPheProValArgPro 504	
Qу 505 Db 60246	LeuAspThrGluProProAlaAlaSerHisT 	-
Qy 525 Db 60186	SerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGlnIleLeuIleHis 544 	
Qy 545 Db 60126	GINGLUSerLeuThTASPTYTCYSSETMetSerSerTyTSerSerSerProProArgGln 564 	
ду 565 рь 60066	AlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSerSerValProPhe 584	

University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,

Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Fax:81-3-5449-5416)

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CCCATGGACGGGGAGACCTTCAGCCAGCACCTGCAGGCCGTGAAGATCCTCGCCGTCAGA
                                                           GACTCAGACATGCTACATACGCCCGGTGCTGCCTCCGACAGGTCTGAGCATGACCTGACC
                                                                       AspSerAspMetLeuH1sThrProGlyAlaAlaSerAspArgSerGluH1sAspLeuThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agency).
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RRGGDVIVIGLEKDSGAQRGRVIAVLKARELTPHGVLVDAAVVAKDTVVCTFENENTE
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574 c 536 g 456 t
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99.61%
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Matches:
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sequencing vector: M13; 08
Sequencing vector: plasmid; 1008
Chemistry: Dye-primer ET; 08 of reads
Chemistry: Dye-terminator Big Dye; 1008 of re
Chemistry: Pre-terminator Big Dye; 1008 of re
Assembly program: Phrap; version 0.990319
Consensus quality: 283337 bases at least 040
Consensus quality: 284790 bases at least 030
Consensus quality: 284790 bases at least 020

NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this squence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence

Center project name: M\_BA0049I18 Contact: submissions@watson.wustl.edu

Summary Statistics

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Information -----

Web site:http://genome.wustl\_edu/gsc/index.shtml

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REFERENCE
AUTHORS
TITLE
JOURNAL
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                                                                                                                          Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 288428) McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                           2 (bases 1 to 288428)
McPherson, J.D. and Wat
Direct Submission
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McPherson, J.D. and Waterston, R.H.
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Mus musculus chromosome UNK clone
SEQUENCE, 12 unordered pieces.
Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                            Submitted (17-JUL-2002) Genome Sequencing Center, 4444 Forest Park
                                                                                                                                                                                                                                        The sequence of Mus musculus Unpublished
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                          Parkway, St.
On Aug 11, 2
                                                                                           Submitted (11-AUG-2002) Genome Sequencing Center,
                                                                                                           Direct Submission
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                                                           t. Louis, MO 63108, USA
2002 this sequence version replaced g1:21887033
                               ---- Genome Center ---
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                                                                                                                                                                                                                                                            clone
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             Sequencing Center
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'db_xref="taxon:10090"
'chromosome="UNK"
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68244 c 66493 g 73022 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ote="assembly_name:Contigl1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e="assembly_name:Contig12"
                                                                                                                                                                                                                                                                                                                            e-"assembly_name:Contig20"
                                                                                                                                                                                                                                                                                                                                                                             e="assembly_name:Cont1g18"
41. . . 220583
                                                                                                                                                                                                                                                                                                                                                                                                                      e-"assembly_name:Contig17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e-"assembly_name:Contig14"
1. .63521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e="assembly_name:Contig13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e="assembly_name:Cont1g15"
2. .88523
                                                                                                                                                                                                                                                                                                                                                                                                                                       ="assembly_name:Contig16"
. .124000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1542: contig of 1542 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of unknown tengen. contig of 1098 bp in length.
                                                                                                                                                                                                                                                                                                                                                            _name:Contig19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of unknown length
g of 44943 bp in length
of unknown length
lg of 65376 bp in length
of unknown length
of unknown length
g of 1071 bp in length
                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 30321 bp in length
unknown length
of 24902 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 35377 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown length of 24471 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 3430 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51440 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          own length
                                                                                                                                                                                                                                                       1140 others
                                                                                                               288428
335
30
79
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9
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-----LeuGln 302
                                                          300
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rProMetAs; :        CCCCATGGAr 3AspLeuIl		191	o ob o
erPro	53 SerMetSerSerTyrSerSerSerProProArgGlnAlaAlaArgSerProSerSerLeu	1 5 5	Qy Db 19 Qy Db 19
SPVA       ATGTO  ATGTO  -     TCACO	13 SerHisThrAlaAsnProLysValProGluGlyAspSerIleAlaAspValSerIleMet	513 190950 533 191010	24 45 45
TyrPh        ACTT         	3 SerLeuValMetTyrHisSerThrThrTyrGlnLeuCysAlaArgTyrPheCysGlyVal	.473 190833 - 493 190893	24 50 50 50
Metva. Hetva. Hetva. HIIII	3 AACAGTGGGTCTGAGGTCTGGTACAGCAACGGGCCTGGCCTCCTCGTCATTGACTGCACC 3 AACAGTGGGTCTGAGGTCTGGTACAGCAACGGGCCTGGCCTCCTCGTCATTGACTGCACC 3 SETLeuGluIleCysArgArgLeuGluProTyrMetAlaProSerMetValThrSerVal	190	04 04 04 04 04 04 04 04 04 04 04 04 04 0
ASDAR		373 190533 393 190593	5 B 8 8
ProvalileLysLysAsn	CyspheLeuAlaValCyspheLeuAlaVal	342 190413 353 190473	B 5 B 5
TCTGA( ProAl: :: GTGTC	≽−r ດ	1902 3 1903	P 60 P
ralaTh:  ::::: \TCATC' \TYTTh:	03 ValGlnArgSerLeuTrp	1902 3	δ <b>δ</b> δ
TGGCTT		Db 190176	<b>≍</b>

	DD 192329 GICACICATCCTIGGACAAAGGICTTGATTCATCTTTAATATCATCGCACAGTCCCATTC 192388
Db 193409 GAGCTGGGCCGGCTGGAGGCTTGT	670
716	Db 192269 CCCTAAAGCCAAACGTGTGAAGTATTTCCCATCGTAGTAGATTCACTGGCAGCATGCGCT 192328
\text{Y} \ \text{OFF} \ O	Qy 670 670
y 0 0	Db 192209 GGCATTAAGCCAGAGTTCTTGGCAGTGTTTATCCCCTTACCCTGAAGCTCCCCCATGAAAGT 192268
#ESCOVERED FOR THE FIRST OF THE FOREST AND THE FIRST OF T	Оу 670 670
943 678	Db 192149 TCGCTGCTGTGAGGACAACAGTCCAGGGCACAGCCTTTGTGGCCAGGGAGATGGGAGCCT 192208
103336	Qy 670 670
T.	Db 192089 TGAGCCTGAGAGTGTGACTTGATGCTAATCTGCAGTGAGTAGCGCTAGGAGACATGCCAG 192148
103160	Оу 670 670
193	Db 192029 GCCCCCATGAAGCACCAGATAGGGCCCAGGTGACATGGCCCCCACTCTGCAGCTCCTCTCTC 192088
	670
Db 193049 AACGGGTACCCTTGGCCTTTCAGG	191969 TCACTGTCCTTCCCAAACAGGAGAGGTCCCCCCACCCCA
Оу 670	670
Db 192989 CTGTCTCCTGAGTCTGTCATCTTC	191909 AAAGGTGTATCACCAGGGCCAGATTCAGCTGGGATTGAAACGAAGGTCTCTCCAATTGGT
Qy 670	Qy 670 670
192	Db 191849 CACTGGCCAAGGATATCTATTTCTGGGCTGTCTGTGTACCTGTGGATCAAGTACACTGCC 191908
55555	Qy 670 670
192	Db 191789 AAGGTAGGGTCCTCCAGGCAGCTCCTGAGGTTCAGCATGGTGGCTGAATAGAGCATCAAC 191848
100000	Qy 670 670
767	Db 191729 CTGGGCTCCCACAGATAAGCCTCTGGATCCACCAGTGTGGCCACAGAGTCAAACAGAAGC 191788
10000	Qy 670 670
767	Db 191669 GTGGGGAACCTTAGGACTCACTAACATGCCCACTAGACAGCAGCAGCCCTGCTACCCC 191728
102740	Qy 670 670
192	CGAGAGCTCAATCGGCACGGGTAAGACTGAGAACCCTTCTATATGGCTGGGGGGGG
Qy 670	664 Arad Information Blad Iv
192	Qy 644 IleGlyLeuGluLysAspSerGluAlaGlnArgGlyArgVallLeAlaValLeuLysAla 663
Db 192569 CTCAGAACCAGGTTGGTTGACCTT	Db 191489 TGAGCCAGCTCTTCCCTGTCTTGATTTTGGTCCTTTAGACATGGAGGAGATATCATTGTC 191548
6/0	Qy 638GlyGlyAspValileVal 643
192	Db 191429 GCCGAGCAGGCCTTGCCATTCGGTTTTAGAATTGAGAGTGATCTGGATAGCACAGCATCC 191488
670	Qy 637 637
192	191369 GCTGGGGTGAGTGGAACCCGTGGCTTCCTTAAAGATTCCCAGGTCCATCTGGGCCGTTCT
Оу 670	Qy 637 637
Db 192389 TGCCCAGAGCAGGACAGTCAGTGA	
Оу 670	Db 191250 GGGGAGACGTTCAGCCAGCCACCAGCCTGCAGGCTGCAAAGGTGCTTGCT

	GluLeuGlyArgLeuGluAlaCysThrArgLysArgArg 728	716 193409	dd Qy
715 193408	LeuAlaValTrpArgGlyTrpGlyAlaArgGluPheAspIlePheTyrGlnSerTyrGlu 	696 193349	Qy dd
695 193348	AlaValValAlaLysAspThrValValCysThrPheGluAsnGluAsnThrGluTrpCys 	676 193289	da Vo
ဖ	TGAGGACTCCTGTGGGTGATCGTAGATCCCCCATCTCTGCAGGGTTCTGGTGGATGCC	N	Db ;
75	ValleuValAspAla	67	γQ
193228	CTTAGTAACTCCGCCCCCTTCAAGGATATCCATGAAGAGGGGAGGCCCCACCCTGACCTAG	193169	da
670 .		670	Оу
193168	AGGTAGAATCAGGACTTCCAAGTTCATTCTAGAGCCAGACTGAGCTGTTTATGACACCCT	193109	40
670		670	νο
193108	AACGGGTACCCTTGGCCTTTCAGGTACATTATAAGGTCCCATCCCATAGGCCGGATTACC	193049	фd
670		670	γQ
193048	CTGTCTCCTGAGTCTGTCATCTTCCAGAGCGTTAGTCTACAGCCAATGCTTGCAAAAGTA	192989	ДD
670		670	Qy
192988	GAAACAACGTAAAGAGCCGTGGCCTGAAGATAGTAGATCTTCTGCCTAACATATTCCCCCC	192929	Db
670		670	Qγ
192928	ATGCCTGAGCAGAAACTTGCTATGCATGCACAGGCCATGCACAAACAGCTCACAGCCTCA	192869	da
670		670	Qy
192868	ATACAACCAGACCCAGAGATGGGCCAGCCGCCCTGCAGAGACACCATCAGGACAGAGAGA	192809	뮻
670		670	γо
192808	CTTGGTGAGAGAGAGCCTTCATGTGCAGTGGGGCCTCAGTCACTGGGCCTAGGAGGAGGAG	192749	da
670		670	Qy
192748	AGCAGAAAGACCCGAGTTGGCCAGCTAAAAAAGCAAGGAAGG	192689	ДD
670		670	Qy
192688	AGTCACCCCCCACCCCACCCTGAGACAGGTTTTATCAAGAGTCGGCCACGTTTGCTAGA	192629	đđ
670		670	Оу
192628	CTCAGAACCAGGTTGGTTGACCTTGGCATACCTACTCTGACTATACTGGTATCCTTTTCT	192569	Db
670		670	Qy
192568	TGGCTGACCTGGCCAAAGGAAGCTTTGTGTCCAAGCTGGGCTTTGGGAAACAAATGGGTC	192509	ДD
670		670	Qy
192508	GCCTGCTAGTGAGTCTGGGATCTTCTCTGTGAAATAAGATCAGGCTTTGCTCCTGAGCCC	192449	dd d
670		670	Qy
192448	TGCCCAGAGCAGGACAGTCAGTGACAAACAGCCAGTCACTCATGCCACATCCAGTCGCTT :	192389	Db.
670		670	Qy

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JOURNAL
FEATURES
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ORIGIN
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
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ACCESSION
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AR175612
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CE 1 (bases 1 to 526)

RS Robison, K.E.

Nucleic acid molecules encoding human kinase and phosphatase homologues and uses therefor therefor acid patent; US 6309849-A 10 30-0CT-2001;

Location/Qualifiers

1. 526

1. 526

1. 526

1. 526

1. 1526

1. 526

1. 526

1. 526

1. 526
                                                                                              372
                                                                                                                                             312
                                                                                                                                                                                                                                     119 LysLeuSerAspTyrGlyIleSerArgGlnSerPheHisGluGlyAlaLeuGlyValGlu 138
   492
                         258
                                               432
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                                                                                                                                                                                          252
                                                                                                                                                                                                                179
                                                                                                                                                                                                                                                                                       132
                                                                                                                                                                                                                                                                                               139 GlyThrProGlyTyrGlnAlaProGluIleArgProArgIleValTyrAspCluLysVal 158
                                                                                                                                                                                                                                                                                                                                                                             72
                                                                                                                                                                                        lyGlnGluTyrThrVal-ValPheTrpAspGly 268
GCCAGGAGTACACTGTGGGTGTTTTGGGATGGA
                                             TGCCACCTTCATGTATGAACTGTGCTGTGGGAAGCAGACAGCCTTCTTCATCCAGG
                                                         eAlaThrPheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhePhe-SerSerGlnG 258
                                                                                                                                                                                                                                                                                    GGCACTCCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTA
                                                                                                                                                                                                                                                                                                                                  AAGCTATCTGACTACGGGATTTCGAGGCAGTCATTCCATGAGGGGCGCCCTAGGCGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          526 bp
Sequence 10 from patent US 6309849.
AR175612
AR175612.1 GI:17916911
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856.00
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22.408
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Matches:
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Search completed: April 15, 2003, 08:37:18 Job time : 3982 secs

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Command line parameters:

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-MODEL=frame+_p2n.model -DEV=xlh
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-Q=_(cgn2_l/USPTO_spool/US09836392/runat_08042003_090539_23389/app_query.fasta_1.903
-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRAMS=human40.cd1
-LIST=45 -DOCALIGN=200 -THE_SCORE-pct -THE_MAX=100 -THE_MIN=0 -ALIGN=15
-MODE-LOCAL -OUTFMT=ptc -NORM=ext -NEAPSIZE-500 -MINLEN-0 -MALEL-S00000000
-USER=US09836392_26GN 1_1_200_@runat_08042003_090539_23389 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -FGAPOP=6 -FGAPEXT=7
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Maximum Match 100%
Listing first 45 summaries
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3822
1 MLRHLRATDAMKNFSEFRQE.....IFYQSYEELGRLEACTRKRR 728
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2185239 seqs, 1125999159 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/ggdata/geneseq/geneseqn-embl/NA1980.DAT:*
                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA1991.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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	24	24	24	2 243	243.	243.	243	24	246	N	24	251.	253.	256	257.	257.	260.	260		N)	269	269	270	K)	276	28	288.	30		31	330.	LL I			,	156	156	156	156	357	ω.	3728	3815	3822	3822	score
	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.5	6.5	6.6	6.6	6.7	6.7	6.7	•	6.8	6.9	7.0	7.1	7.1	7.1	7.1	7.2	7.5	7.5	8.0	8.2	•	•	8.6	9	0 !			40.8	•	•	93.7	w	97.5	99.8	100.0	100.0	Query Match
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•	Human protein enco	9	encoding a	cDNA encoding huma	tein t	pTK gene LpTK-2.		Drosophila melanog	Arabidopsis thalia	Drosophila melanog	Arabidopsis thalia	cDNA encoding huma.	മ		leucine			<ul> <li>Human cDNA differe</li> </ul>	cDNA encoding huma	human	human		PKIN-12	Human kinase (PKIN	Ħ	Arabidopsis thalia	Drosophila melanog	Pancreas cancer re		Arabidopsis thalia	Polynucleotide seq	Human kinase PKIN-	Drosophila melanog	phila me	protein		1mmune,	1mmune/	immune,	Human kinase (PKIN	Nucleotide sequenc	ncoding no	secreted	secreted	n pr	Description

## ALIGNMENTS

B	×	X	a	×	Ü	RESU
Human protein tyrosine kinase receptor (PTK) cDNA from clone HDPSB68.	02-JUL-2001 (IIIST entry)		AAD03995;		AAD03995 standard; cDNA; 3496 BP	RESULT 1 AAD03995
tyrosine	rirst er				ard; cDt	
e kinase	icry)				NA; 3496	•
receptor					BP.	
(PTK)						
CDNA						•
from						
clone						
HDPSB68.						

Human; protein tyrosine kinase receptor; PTK; antibacterial; antiviral; antifungal; antiparasitic; sarcoidosis; infiammation; asthma; arthritis; cardiovascular disorder; severe combined immunodeficiency; SCID; vaccine; hyperproliferative disorder; atherosclerosis; brain disorder; leukaemia; hyperproliferative disorder; atherosclerosis; brain disorder; thrombosis; neurodegenerative disorder; disease; vascular dementia; thrombosis; blood coagulation disorder; trauma; cerebrovascular disorder; tendonitis; gene therapy; nephrotic syndrome; glomerulonephritis; allergy; neoplasm;

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                                                                                                                                                                                                                                                                                                   CC providing immunological probes for differential identification of the Ctissues or cell types present in a biological sample. PTK is used in CC methods for the diagnosis, prevention and treatment of various disorders CC related to pTK such as immune system disorders (severe combined CC immunodeficiency (SCID), inflammation); hyperproliferative disorders (neoplasm, sarcoidosis); cardiovascular disorders (arhythmia, CC atherosclerosis); central nervous system disorders (arhythmia, CC neurodegenerative disorders (Alzheiner's disease, Parkinson's disease); CC incorderosclerosis); crohn's disease; respiratory disorders (asthma, CC allery); gastrointestinal disorders (inflammatory bowel disease); CC erebrovascular disorders (thrombosis, vascular dementia); brain CC disorders (phenylketonuria); behavioural disorders (Tourette's cyndrome); musculo-skeletal disorders (arthritis, trauma, tendonitis); CC erenal disorders (nephrotic syndrome, glomerulonephritis); metastases of CC malignancies and related disorders (leukaemia, multiple myeloma); and consections caused by bacteria, viruses, fungi and parasites. PTK is also useful for screening therapeutic compounds. PTK is used as an antigen in CC a vaccine to raise an immune response against infectious disease. PTK cnucleic acids are useful in gene therapeutic.
                                                                           US-09-836-392-21 (1-728) x AAD03995
                                                                                                                                                                                                           Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human protein tyrosine kinase (PTK) and their corresponding cDNA molecules, PTK receptors are use providing immunological probes for differential identification tissues or cell types present in a biological sample. PTK is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 265-266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid molecule for producing human protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-290976/30.
P-PSDB; AAE00669.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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17-NOV-1999; 99US-0165914.
14-MAR-2000; 2000US-0189027.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present cDNA sequence encodes human protein tyrosine kinase receptor
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Location/Qualifiers 22..2208
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/product= "Human PTK protein from clone HDPSB68"
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                                                                                                ASPThrValValCysThrPheGluAsnGluAsnThrGluTrpCysLeuAlaValTrpArg
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             GluAlaCysThrArgLysArgArg
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immunomodulatory; immunosuppressive; antibacterial; antipsoriatic; gene therapy; autoimmune disease; Huntington's disease; meningitis; demyelinating disease; peripheral neuropathy; congenital malformation; spinal cord injury; peripheral neuropathy; ischaemia; perception; multiple sclerosis; infarction; haemorrhage; schizophrenia; dementia; depression; panic disorder; learning disability; ALS; feeding disorder; hyperproliferative disorder; sleep pattern; cardiovascular disorder; hyperproliferative disorder; sleep pattern; cardiovascular disorder; perproductive disorder; digestive system disorder; behavioural disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; secreted protein; immune disorder; antiallergic; antirheumatic; rheumatoid arthritis; breast neoplasia; breast cancer; antiarthritic; neurological disease; Alzheimer's disease; Parkinson's disease; trauma Tourette syndrome; encephalitis; cytostatic; haemostatic; anaemia; man antiinflammatory; ophthalmalogical; dermatological; immunostimulatory;
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WO200216390-AI

17-JAN-2001; 2001WO-US01435

18-AUG-2000; 2000US-226282P

(HUMA-) HUMAN GENOME SCI INC

Rosen Moore Ni J; Komatsoulis GA, Wei P, Ebner R, Baker Duan DR KP Shi Y, CE, Soppet, Choi GH, : DR, Olse Olsen ella M; SH

2002-304113/34. )B; AAE21217.

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RESULT

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An isolated nucleic acid molecule (lencodes a polypeptide useful in the disorders e.g. immune disorders -(I) comprising a polynucleotide ne diagnosis and treatment of which

Claim 1; Page 457-458; 534pp; English

AAD33692-AAD33736 represent cDNAs corresponding to 21 human secreted protein genes, and AAE21191-AAE21235 represent the proteins they encode. AAE21236-AAE21280 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 21 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of immune or autoimmune diseases e.g. AIDS (acquired immune disease) and breast cancer, neurological diseases e.g. Alzheimer's disease, can breast cancer, neurological diseases e.g. Alzheimer's disease, and braskt cancer, neurological diseases e.g. Alzheimer's disease,

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PheMetTyrGluLeuCysCysGlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGlu
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Db 788 TICANGTANGANCTGTGCTGTGGGAAGCAGCAGCAGCAGGAG 847  Q2 261 TypThyralValbaFrpaspdlyygsdluGluserAcysarTyrThrValValamThr 280  261 TypThyralValbaFrpaspdlyygsdluGluserAcysarTyrThrValValamThr 280  261 TypThyralValbaFrpaspdlyygsdluGluserAcysarTyrThrValValamThr 280  261 TypThyralValbaFrpaspdlyygsdluGluserAcysarTyrThrValValamThr 280  261 ThrCacGTGGTGTTTTGGATTGCAMAGAGGTGCCAGGAACTACACGTGTGTACCCAG  272 ThrCacGTGCAGAAAACCCCTGGAAAACCACCAAAAATTACACGTTGGTACAACCACAA  273 TLAUGLIPAGLUGAAACCACCACAAAACCACCAAAAATTACACCACAACAACA										:				:					
261 TyrThrValvalheFTrpAspGlyLysGluGluSerArgAsrTyrThrValvalAsnThr 28 261 TyrThrValvalheFTrpAspGlyLysGluGluSerArgAsrTyrThrValvalAsnThr 28 261 GluLysGlyEumetellvalidlillillillillillillillillillillillill																			
788 TTCATGTATGAACTGTGCTGTGGGGAAGCAGACCAGCCTTCTTCTCATCCCAGGGCCAGGAC 261 TyrThrValValPheTrpAspGjyLysGluGluSerArgAsnTyrThrValValAsnThr 28 848 TACACGGGGGTTTTGGGATGGAAAAGGACGACCAAAGGACCAAAGGACCAAAGGACCTCAAGGACCAAAGACCAAAGACCAAAAGACCAAAAGACCAAAAAA	D Q	B 6	g Qy	В 6 6	B 64	B 64	B 6	8 성	B 8	D 8	D Q	DP QA	Оy	D Oy	Дb	P Cy	Оy	g Qy	В
TRAIGIANGAACTGTGCCTGTGGGAAGCAGACAGCCTTCTTCTCATCCCAGGGCCAGGAC 97 ThrvalvalvalpheTrphspGlyLysGluGluSerArgAsnTyThrvalvalAsnThr 28	.86	0 8	6 4	4 8	.62	50	.50	46	38	NN	.26	0 . 0	0 4	-4 co·	N N	6 6	0 8	0 4	œ.
	eraspargSerGluHisaspLeuThrProMetaspGlyGluThrPheSerGlnHisLeu 6 	erValProPheSerThrAspCysGluAspSerAspMetLeuHisThrProGlyAlaAla 6 	roProArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSer 5 	leLeuIleHisGlnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSer 5 	TOGLUGIYASPSETILEALAASPVALSETILEMETTYTSETGLUGIULEUGIYThTGID 5 	roValArgProLeuAspThrGluProProAlaAlaSerHisThrAlaAsnProLysVal 5 	hrTyrGlnLeuCysAlaArgTyrPheCysGlyValProSerProLeuArgAspMetPhe.5 	luGluValValTrpCysLeuAspAspLysAlaAsnSerLeuValMetTyrHisSerThr 4 	luProTyrMetAlaProSerMetValThrSerValValCysSerSerGluGlyArgGly 4 	erAsnGlyProGlyLeuLeuVallleAspCysAlaSerLeuGluIleCysArgArgLeu 4 	lnAsnProTyrProValLysAlaMetGluValValAsnSerGlySerGluValTrpTyr 4 	yrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaArg 4 	laAspGlyLeuValAlaValPheProValValArgGlyThrProLysAspSerCysSer 3 	hrCysPheLeuAlavalProValIleLysLysAsnSerTyrLeuValLeuAlaGlyLeu 3 	euLysGlyMetCysProLeuAsnThrProGlnGlnAlaLeuAspThrProAlaValVal 3 	euGlnValGlnArgSerLeuTrpThrAlaThrGluAspGlnLysIleTyrIleTyrThr 3 	luLysGlyLeumetGluValGlnArgMetCysCysProGlyMetLysValSerCysGln 3 	yrThrValValPheTrpAspGlyLysGluGluSerArgAsnTyrThrValValAsnThr 2 	TCATGTATGAACTGTGCTGTGGGAAGCAGACAGCCTTCTTCTCATCCCAGGGCCAGGAG 8
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                                                                                                                                                                                                                                                                                                                                                                                                     immunomodulatory; immunosuppressive; antibacterial; antipacriatic; gene therapy; autoimmune disease; Huntington's disease; meningitis; demyelinating disease; peripheral neuropathy; congenital malformation; spinal cord injury; peripheral neuropathy; ischaemia; perception; multiple sclerosis; infarction; haemorrhage; schizophrenia; dementia; depression; panic disorder; learning disability; ALS; feeding disorder; hyperproliferative disorder; sleep pattern; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; immune disorder; antiallergic; antirheumatic; rheumatoid arthritis; breast neoplasia; breast cancer; antiarthritic; neurological disease; Alzheimer's disease; Parkinson's disease; trauma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted
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                                                                                                                                                                                                                                                   sig_peptide
       Rosen CA,
                                                                    18-AUG-2000; 2000US-226282P.
                                                                                                                                                                                                                                                                                                                                                                             gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tourette syndrome; encephalitis; cytostatic; haemostatic; anaemia; man antiinflammatory; ophthalmalogical; dermatological; immunostimulatory;
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                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                  17-JAN-2001; 2001WO-US01435
                                                                                                                                28-FEB-2002
                                                                                                                                                              WO200216390-A1
                                                                                                                                                                                                                                                                                                                                                                                            ceproductive disorder; digestive system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluAlaCysThrArgLysArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASPThrValValCysThrPheGluAsnGluAsnThrGluTrpCysLeuAlaValTrpArg
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                                                                                                                                                                                                                                                                                                                                               sapiens.
         Komatsoulis GA,
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212..2257
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/product=
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                                                                                                                                                                                                                                                       140..211
                                                                                                                                                                                                                                                                   product-
                                                                                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                   "Human secreted protein"
                                                                                                                                                                                            "Human mature
           Baker KP,
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         Soppet DR,
           Olsen
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Moore PA, Wei P,
                                                                     P-PSDB; AAE21194.
                                                                        WPI; 2002-304113/34
                                                                              Ebner R,
                                                                              Duan DR,
                                                                              Shi Y,
                                                                              Choi GH,
                                                                              Fiscella M;
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An isolated nucleic acid molecule (I) comprising a polynucleotide which encodes a polypeptide useful in the diagnosis and treatment of disorders e.g. immune disorders -

Claim 1; Page 442-443; 534pp; English.

cc amount of the new protein in a sample or by determining the presence of commutations in the new genes. Specific uses are described for each of the c21 genes, based on the tissues in which they are most highly expressed, cc 21 genes, based on the tissues in which they are most highly expressed, cc and include developing products for the diagnosis or treatment of immune of include developing products for the diagnosis or treatment of commune of include developing products for the diagnosis or treatment of immune of include cancer. An anaemia and rheumatoid arthritis, breast neoplasia cc and breast cancer, neurological diseases e.g. Alzheimer's disease, cc parkinson's disease, Huntington's disease, Tourette syndrome, cc meningitis, demyelinating disease, peripheral neuropathies, neoplasia, cc trauma, congenital malformations, spinal cord injuries, toxic neuropathies induced by neurotoxins, peripheral neuropathies, multiple cc sclerosis, ischaemia and infarction, haemorrhages, schizophrenia, mania, congenital main disorders in feeding, sleep patterns, balance and perception, encephalitis, disorders in cardiovascular, neural/ AAD33692-AAD33736 represent cDNAs corresponding to 21 human secreted protein genes, and AAE21191-AAE21235 represent the proteins they encode. AAE21236-AAE21280 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the sensory, reproductive and digestive systems, behavioural disorders and hyperproliferative disorder. The present sequence represents a human secreted protein-encoding cDNA of the invention.

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Sequence 3564 844 A; 1014 C; 958 G; 748 Ŧ other;

Alignment Scores:	1.46e-294	Length:	3564
	3815.00	Matches:	727
Percent Similarity:	99.86%	Conservative:	0
2	99.86%	Mismatches:	<b>1</b> —
y Matc	99.82%	Indels:	0
	24	Gaps:	0

US-09-836-392-21 (1-728) x AAD33695 (1-3564)

433	>	374	рь
120	LysSerAspAsnIleLeuValTrpSerLeuAspValLysGluHisIleAsnIleLysLeu	101	Qy
373		314	밁
100	TyrGlnIleAlaSerGlyLeuAlaTyrLeuHlsLysLysAsnIleIlePheCysAspLeu	81	Qy
313		254	망
0.8	GluasnalaargaspSerSerPheIleProLeuGlyHisMetLeuThrGlnLysIleAla	. 61	QУ
253		194	D
60	H1SProLeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSer	41	Qy
193	GCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATC 193	134	B
40	AlaSerMetLeuHisAlaLeuGlnHisProCysIleValAlaLeuİléGlyIleSerIle	21	Qy
133	ATGCTGAGGCACCTGCGGGCCACCGATGCCATGAAGAACTTCTCCGAGTTCCGGCAGGAG 133	74	皮
. 20	MetLeuArgH1sLeuArgAlaThrAspAlaMetLysAsnPheSerGluPheArgGlnGlu	1	Qγ

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                                                GlnAsnProTyrProValLysAlaMetGluValValAsnSerGlySerGluValTrpTyr
                                                                                                                                                              TyrLeuCysSerHisThrAlaAsnArgSerLysPheSerIleAlaAspGluAspAlaArg
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                                                                                           SerAsnGlyProGlyLeuLeuValIleAspCysAlaSerLeuGluIleCysArgArgLeu
                                                                                                                                                                                     GCCGATGGGCTTGTGGCTGTTTTCCCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTCC
                                                                                                                                                                                              AlaAspGlyLeuValAlaValPheProValValArgGlyThrProLysAspSerCysSer
                                                                                                                                                                                                                                                                                                                         GAGAAGGGCCTCATGGAGGTGCAGAGGATGTGCCTGCCCTGGGATGAAGGTGAGCTGCCAG
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                                                                                                                    CAGAACCCCTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTAC
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RESULT AAS7223 ID 7223 ID 7223 AAC AAC AA AC AAC AAC AC AAC AAC AC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC AAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical CC imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed constitution but was obtained in electronic format directly from WIPO CC and to produce other stated on the patent did not appear in the printed constitution but was obtained in electronic format directly from WIPO can be appeared to the products of the construction of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
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P-PSDB; ABG08051.
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                                                                       LysSerAspAsnIleLeuValTrpSerLeuAspValLysGluH1sIleAsnIleLysLeu
AAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTA
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SpAspLysAlaAsnSerLeuValMetTyrH1sSerThr 480	GluGluValValTrpCysLeuAspAspLysAl	461	Ϋ́
	GAGCCCTACATGGCCCCCCCCATGGTTACGTC		Db
etValThrSerValValCysSerSerGluGlyArgGl	GluProTyrMetAlaProSerMetValThrSe	441	Qy
/allleAspCysAlaSerLeuGluIleCysArgArgLeu 440	SerAsnGlyProGlyLeuLeuVallleAspCy	421	Qy
		1705	Db
NlaMetGluValValAsnSerGlySerGluValTrpTyr 420	GlnAsnProTyrProValLysAlaMetGluVa	401	Qy
		1645	Db
\snArgSerLysPheSerIleAlaAspGluAspAlaArg 400	TyrLeuCysSerH1sThrAlaAsnArgSerLy	381	Qy
		1585	Db
PheProValValargGlyThrProLysAspSerCysSer 380	AlaAspGlyLeuValAlaValPheProValVa	361 1525	Qy
/alileLysLysAsnSerTyrLeuValLeuAlaGlyLeu 360	ThrCysPheLeualaValProValTleLysLy	341	Qy
		1465	Db
\snThrProGlnGlnAlaLeuAspThrProAlaValVal 340	LeuLysGlyMetCysProLeuAsnThrProG	321	Qy
		1405	Db
PrpThrAlaThrGluAspGlnLysIleTyrIleTyrThr 320	LeuGlnValGlnArgSerLeuTrpThrAlaTh	301	Qy
		1345	Db
	GluLysGlyLeuMetGluValGlnArgMetCy	281	Qy
		1285	Db
3lyLysGluGluSerArgAsnTyrThrValValAsnThr 280	TyrThrValValPheTrpAspGlyLysGluGl	261	. Qy
		1225	
SlyLysGlnThrAlaPhePheSerSerGlnGlyGlnGlu 260	PheMetTyrGluLeuCysCysGlyLysGlnTh	241	Db Qy
		1165	
SerValValSerGlnMetLysAspProThrPheAlaThr 240	GluLysArgProLeuAlaLeuSerValValSe	221	Qy
		1105	Db
.euGlnAlaLeumetMetGluCysTrpAspThrLysPro 220	GluGluValGlnPheArgArgLeuGlnAlaLe	201	Db Db
		1045	
ysleuserLysGlyIleArgProValLeuGlyGlnPro 200 	H1SG1nLeuG1nIleAlaLySLySLeuSer	181 985	Qy.
yrGluLeuLeuSerGlyGlnArgProAlaLeuGlyHis 180	PheSerTyrGlyMetValLeuTyrGluLeuLe	161	Qy
		925	Db
:leArgProArgIleValTyrAspGluLysValAspMet 160                    CAGGCCTCGCATTGTATATGATGAGAAGGTAGATATG 924	ProglyTyrglnAlaProgluIleArgProAr 	141 865	Db dg
lnSerPheHisGluGlyAlaLeuGlyValGluGlyThr 140 	SerAspTyrGlyIleSerArgGlnSerPheH1                     CTGACTACGGGATTTCGAGGCAGTCATTCCA	121 805	Qy Db

1825 GAGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACTCCACC

1884

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
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US-08-446-648-20
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Sequence 7, Appli	Sequence 2, Appli	Sequence 108, App	Sequence 40, Appl	Sequence 12, Appl	Sequence 76, Appl	Sequence 57, Appl		Sequence 2, Appli	Sequence 27, Appl	•	Sequence 2, Appli	Sequence 2, Appl1	Sequence 2, Appli	Sequence 29, Appl	Sequence 15, Appl	Sequence 4, Appli	Sequence 23, Appl
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Ap 218.5 5.6 306 4 US-09-457-040B-40 Sequence 108, Ap 215.5 5.6 382 2 US-08-737-715-2 Sequence 7, Ap 216.5 5.6 1382 4 US-09-457-040B-7 217.5 5.6 382 4 US-09-457-040B-7 218.5 5.6 382 4 US-09-457-040B-7 219.5 5.6 382 4 US-09-457-040B-7 219.5 5.6 382 4 US-09-457-040B-7 219.5 5.6 382 4 US-09-457-040B-7 219.5 5.6 382 4 US-09-457-040B-7 219.5 5.6 382 4 US-09-457-040B-7 219.5 5.6 382 4 US-09-457-040B-7 219.5 5.6 382 4 US-09-457-040B-7 219.5 5.6 382 4 US-09-457-040B-7 219.5 5.6 382 4 US-09-457-040B-7 219.5 5.6 382 4 US-09-457-040B-7 219.5 5.6 382 4 US-09-457-040B-7 219.5 5.6 382 4 US-09-457-040B-7	228.5 6.0 590 4 US-09-529-279-15 Sequence 15, A 228 6.0 296 2 US-08-701-191A-29 Sequence 29, A 228 6.0 668 1 US-08-205-018-2 Sequence 2, Ap 228 6.0 859 1 US-08-395-580-2 Sequence 2, Ap 228 6.0 859 1 US-08-395-580-2 Sequence 2, Ap 224.5 5.9 94.3 US-08-469-537A-107 Sequence 27, Ap 224.5 5.8 1584 4 US-09-457-040B-27 Sequence 27, Ap 223.5 5.8 1584 4 US-09-457-040B-27 Sequence 27, Ap 219.5 5.7 283 2 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US-09-529-279-15 228 6.0 296 2 US-08-701-191A-29 228 6.0 668 1 US-08-205-018-2 228 6.0 668 1 US-08-205-018-2 228 6.0 859 1 US-08-205-018-2 228 6.0 859 1 US-08-395-302-2 228 6.0 859 5 PCT-US95-0-792-2 228 6.0 859 5 PCT-US95-0-792-2 228 5.9 943 2 US-08-469-537A-107 221.5 5.8 1584 4 US-09-457-040B-70 221.5 5.7 263 2 US-08-596-319-2 21.5 5.7 263 2 US-08-596-319-2 21.6 5.7 263 2 US-08-596-319-2 21.6 5.7 263 2 US-08-596-319-2 21.6 5.7 263 2 US-08-596-319-2 21.6 5.6 306 4 US-09-228-986-76 21.6 5.6 306 4 US-09-228-986-76 21.5 5.6 306 4 US-09-457-040B-40 21.5 5.6 306 4 US-09-457-040B-40 21.5 5.6 382 2 US-08-737-715-2 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7 21.5 5.6 382 4 US-09-457-040B-7

## ALIGNMENTS

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GENERAL INFORMATION
                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                          REGISTRATION NUMBER: 82
REFERENCE/DOCKET NUMBER: 82
TELECOMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        APPLICATION NUMBER: 07/826935
FILING DATE: 22-CAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST TITLE OF INVENTION: ANTIBODIES NUMBER OF SEQUENCES: 42
                                   SEQUENCE CHARACTERISTICS LENGTH: 505 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Generation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
ZIP: 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/
FILING DATE: 4-APR-1994
                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
TOPOLOGY:
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Wood, William I
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Goeddel, David
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Matches
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                                               NFORMATION FOR SEQ ID NO:
                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          SOFTWARE: WinPatin (Ge
                                                                                                                                                                                                                                                                                                                                        OMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 HHQLQIAKKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQMKDPTFA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 ------OSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLS-GORPALG
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                                                                                                             ELECOMMUNICATION
                                                                                                                                                                        RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2
FILING DATE: 04-APR-1994
FORNEY/AGENT INFORMATION:
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                                                                          TELEFAX:
                                                                                            TELEPHONE:
                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          T: 460 Point San Bruno Blvd
South San Francisco
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Amino Acid
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                                                                              415/952-9881
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TENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
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                                                                                                             INFORMATION
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                                                                                                                                                                                                                                                                                                                                                        1.44 Mb floppy disk
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Pred. No. 1.3e-14;
9; Mismatches 77;
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Best Local Similarity
Matches 75; Conserv
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CT-US95-04228-20
                                         INFORMATION FOR SEQ ID
                    SEQUENCE CHARACTERISTICS
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                           TELEFAX: 910/371
                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                NTTORNEY/AGENT INFORMATION:
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                                                                                                                                                           NAME: Wendy M. Lee
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 HMLTQKI--AYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKLSDYGISR--- 127
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                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                   TELEPHONE:
ENGTH:
                                                                                                                                                                                                                     PPLICATION NUMBER: 08/
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South San Francisco
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-221-235-5
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/221,235
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-221-235-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver.
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                                                                                                                                                                       125 ISRQSFHEGALGVEGTPGYQAPEIRPRIVYDEKYDMFSYGMVLYELLSGQRPALGHHQLQ 184
                                   240 TEMYELC 246
                                                                           214 VAWL------VVEKNERLTIPSSCPRSFAELLHQCWEADAKKRPSFKQIISILESMSND
                                                                                                               185 IAKKLSKGIRPVLGQPEEVQF-----RRLQALMMECWDTKPEKRPLALSVVSQMKDPTFA
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                                                                                                                                                                                                                                                                 68 FIPLGHMLTQKIAYQIASGLAYLHKK---NIIFCDLKSDNILVWSLDVKEHINIKLSDYG 124
                                                                                                                                                                                                                                                                                                         43 AVKKLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNR--SE 100
                                                                                                                                                                                                                                                                                                                                            10 AMKNESEFRQEASMLHALQHPCIVALIGISIHPLCFAL--ELAPLSSLNTVLSENARDSS 67
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TSLPDKC 273
                                                                                                                                                   ASRFHNHTTHMSLVGTFPWMAPEVIQSLPVSETCDTYSYGVVLWEMLTREVPFKGLEGLQ
                                                                                                                                                                                                                                 EMDMDHIMTW--ATDVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGV-----LKICDFG
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27.9%;
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                                                                                                                                                                                                                                                                                                                                                                                  52; Mismatches 100;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 243; DB 3;
Pred. No. 1.2e-14;
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RESULT 5 US-09-221-928-5 ; Sequence 5, Application US/09221928

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APPLICANT: Acton, Susan
TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC
FILE REFERENCE: MNI-050
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Best Local Similarity
Matches 69; Conserv
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Patent No. 614683
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CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
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SOFTWARE: PatentIn Ver. 2.0
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CURRENT FILING DATE: 1998-12-28
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TYPE: PRT
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Pred. No. 1.2e-14;
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Pred. No. 1.2e-14;
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RESULT 8
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SOFTWARE: PatentIn Ver
SEQ ID NO 5
                                                                                                                                         Sequence 5, Application US/09221416
Patent No. 6153417
GENERAL INFORMATION:
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TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND USES THEREFOR FILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/221,416
CURRENT FILING DATE: 1998-12-28
EARLIER APPLICATION NUMBER: 09/163,115
EARLIER FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                        PPLICANT: Acton, Susan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FIPLGHMLTQKIAYQIASGLAYLHKK---NIIFCDLKSDNILVWSLDVKEHINIKLSDYG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMKNESEFRQEASMLHALQHPCIVALIGISIHPLCFAL--ELAPLSSLNTVLSENARDSS
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Pred. No. 1.2e-14;
52; Mismatches 100
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LENGTH: 455;
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; ORGANISM: Homo sapiens
US-09-221-416-5
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US-09-221-245-5
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Best Local
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Best Local Similarity
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CURRENT FILING DATE: 1998-12-28
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TYPE: PRT
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214 VAWL-----VVEKNERLTIPSSCPRSFAELLHQCWEADAKKRPSFKQIISILESMSND 266
                                   185 IAKKLSKGIRPVLGQPEEVQF-----RRLQALMMECWDTKPEKRPLALSVVSQMKDPTFA 239
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                                                                                                         ISRQSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLSGQRPALGHHQLQ 184
                                                                                                                                             EMDMDHIMTW--ATDVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGV-----LKICDFG 153
                                                                                                                                                                                                                   AVKKLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNR--SE 100
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Pred. No. 1.2e-14;
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US-09-163-115-5
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US-09-221-528-5
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SEQ ID NO 5
LENGTH: 455
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LENGTH: 455
TYPE: PRT
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Best Local Similarity
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CURRENT FILING DATE: 1998-12-28
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CURRENT FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
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 43 AVKKLLKIEKEAEILSVLSHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNR--SE 100
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                               AMKNFSEFRQEASMLHALQHPCIVALIGISIHPLCFAL--ELAPLSSLNTVLSENARDSS 67
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US-09-593-553-5
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US-09-221-237-5
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                                                                         APPLICANT: Acton, S
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PRIOR FILING DATE: 1998-09-28
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Vor
                                                                                                              Sequence 5, Application US/09221237 Patent No. 6214597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/593,553
CURRENT FILING DATE: 2000-06-14
FILE REFERENCE: MNI-050
CURRENT APPLICATION NUMBER: US/09/221,237
CURRENT FILING DATE: 1998-12-28
                                                      TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC ACID MOLECULES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 27.9
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                                                                                                                                                                                                                                                                TEMYELC
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                                                                                                                                                                                                                           TSLPDKC
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Best Local Similarity
Thes 69; Conserve
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/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-221-237-5
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tent No. 6326469
                                                                                                                                                                                              CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                 PRIOR APPLICATION DATA:
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               NAME: COTUZZÍ, LAUTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 76
ELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                    ZIP: 10036-2711
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TLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
TELEPHONE:
                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                  CITY: New York,
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N: 435
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27.9%;
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Pred. No. 1.2e-14;
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                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                              ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                 FILING DATE:
                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                             STATE:
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                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
     REFERENCE/DOCKET NUMBER:
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Hofgarten Str. 2
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                                                                                                                                                                                            PatentIn Release #1.0, Version #1.25
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3: No. 6326469e
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                     NUMBER:
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                                                                                                                                             24-APR-1995
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30.2%;
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30,742
ER: 7683-074
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEFAX: (212)869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENCTH: 511 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
PCT-US95-05008-6
Search completed: April 8, 2003, 10:26:57 Job time: 37 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.3%; Score 241.5; DB 5; Best Local Similarity 30.2%; Pred. No. 2.1e-14; Matches 74; Conservative 49; Mismatches 79;
                                                                                                                                                                                                                                                                                                                 489 LRWKL 493
                                                                                                                                                        128 -----QSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLS-GQRPALGH 180
                                                                                                                                                                                                                                                                                                                                                                                              278 NDFLREAQIMKNLRHPKLIQLYAVCTLEDPIYIITELMRHGSLQEYL-QNDTGSKI---- 332
                                                                                                                   241 FMYEL 245
                                                                                                                                                                                                                                     388 DNEDIYESRHEIKLPVKWT----APEAIRSNKFSIKSDVWSFGILLYEIITYGKMPYSGM 443
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 43; Gaps
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Minimum DB :
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Maximum Match 100%
Listing first 45 summaries
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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1428.283 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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3822
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                                                      probable mitogen
probable serine,
probable protein
protein-tyrosine
serine/threonine
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serine/threonine
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protein-tyrosine
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T48115 S24550	S04328 F96701	T00574	S43532	I49663	S27396	A45082	T04688	T02725	T51791	T50811	T01451	G71410
protein kinase ATM protein-tyrosine k	protein-tyrosine k hypothetical prote	probable protein k serine/threonine-p	protein-tyrosine k	tyrosine kinase (f	phytochrome / prot	neurotrophic recep	hypothetical prote	probable serine/th	.ser/thr specific p	ser/thr specific p	protein kinase hom	probable protein k

## ALIGNMENTS

RESULT 1 T33475

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Qy 290 MCCPGMKVSCQLQVQRSLWTATEDQKIYIYTLKGMCPLNTPQQALDTPAVVTCFLAVP 347	QY 182 QLQIAKKLSKGIRPYLGQPEEVQFRRLQALMMECMDTKPEKRPLALSVVSQMKDPTFATF 241	Qy 70 PLGHMLTQKIAYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKLSDYGI 125    : :	Ouery Match  10.5%; Score 402; DB 2; Length 1090;  Best Local Similarity 27.7%; Pred. No. 6.8e-16;  Matches 123; Conservative 86; Mismatches 175; Indels 60; Gaps 19;  Qy 10 AMKNFSEFROEASMLHALQHPCIVALIGISIHPLCFALELAPLSSLNTVLSENARDSSFI 69    :	A;Reference number: Z21354 A;Accession: T33475 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1090 <zhu> A;Cross-references: EMBL:AF098504; PIDN:AAC67413.1; GSPDB:GN00019; CESP:T27C10.5 A;Experimental source: strain Bristol N2; clone T27C10 C;Genetics: A;Experimental source: strain Bristol N2; clone T27C10 A;Experimental source: strain Bristol N2; clone T27C10 A;Experimental source: strain Bristol N2; clone T27C10 A;Experimental source: strain Bristol N2; clone T27C10 A;Experimental source: strain Bristol N2; clone T27C10 A;Experimental source: strain Bristol N2; clone T27C10 A;Experimental source: strain Bristol N2; clone T27C10 A;Experimental source: strain Bristol N2; clone T27C10 A;Experimental source: strain Bristol N2; clone T27C10</zhu>	T33475 hypothetical protein T27C10.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T33475 C;Accession: T33475 R;Zhu, H.J.; Graves, T.; Hawkins, M. submitted to the EMBL Data Library, October 1998 submitted to the EMBL Data Library, October 1998 A;Description: The sequence of C. elegans cosmid T27C10.

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protein kinase
C;Species: Arah
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                                                                                                                                                                                                                                                                                                               R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujli, M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tall euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ver Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                    probable protein kinase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002 C;Accession: G84635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: kinase-rela
F;135-392/Domain: protein
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A; Accession: T10671
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                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-407 <STO>
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;Species: Arabidopsis thaliana (mouse-ear cress)
;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 19-May-2000
                                                                                                                                                                                                                                                      Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis Reference number: A84420; MUID:20083487; PMID:10617197 A84635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match.
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: kinase-related transforming protein; protein kinase homology;135-392/Domain: protein kinase homology <KIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA
Residues: 1-412 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; ibmitted to the Protein Sequence Database, June
                                                                                                                                                                 Cross-references: GB:AE002093; NID:g4337195; PIDN:AAD18109.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: EMBL:ALI049914; GSPDB:GN00062; ATSP:F6E21.
Experimental source: cultivar Columbia; BAC clone F6E21
                                                                             Superfamily: kinase-related transforming protein;
                                                                                                                                                                                                                                Status: preliminary
  Best Local
Matches
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                                                                                                      position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 GVRPTVPADCLPVLGE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 AVMQ--ALDVARGMAYVHERNFIHRDLKSDNLLI-SAD----RSIKIADFGVARIEVQTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 MLTQKIAYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKLSDYGISRQSFH-E 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 EFRQEASMLHALQHPCIVALIGISIHPL--CFALELAPLSSLNTVLSENARDSSFIPLGH 73
                                                                                                                            At2g24360
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  . Similarity
82; Conser
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                   8.2%;
36.8%;
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Score 314; DE Pred. No. 3e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 315; DB 2; 1
Pred. No. 2.7e-11;
4; Mismatches 73;
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                                       DB 2;
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1999
                                     Length 407
                                                                                  protein kinase
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  16;
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LEAIENHNLADTVLKITDFGLARE

254

QKIAYQIASGLAYLHKK---NIIFCDLKSDNILVWSLDVKEHIN----IKLSDYGISRQ 128

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P: Dorow, D.S.; Devereux, L.; Tu, G.
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C:Date: 28-Oct-1996 #sequence revision 13-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: ATP; leucine zipper; phosphotransferas; F; 23-76/Domain: SH3 homology <SH3>
F; 96-364/Domain: protein kinase homology <KIN>
F; 104-112/Region: protein kinase ATP-binding motif; 384-405/Region: leucine zipper motif F; 419-440/Region: leucine zipper motif F; 419-463/Region: leucine zipper motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mixed-lineage protein kinase 2 (EC 2.7.1.-) -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:362654; GDB:624810; OMIM:600137
A;Map position: 19q13.1-19q13.2
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A;Title: Identification of a new family of
A;Reference number: $32467; MUID:93238756;
A;Recession: $32468
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A; Residues: 1-461, 'A', 'V', 465-470, 'S', 472-806, 'R', 808-817, 'A', 819-954 <RES>
A; Residues: 1-461, 'A', 'V', 465-470, 'S', 472-806, 'R', 808-817, 'A', 819-954 <RES>
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A; Cross-references: EMBL: Z48615; NID: g758592; PIDN: CAA88531.1; PID: g758593
A; Cross-references: EMBL: Z48615; NID: g758592; PIDN: CAA88531.1; PID: g758593
A; Cross-references: EMBL: Z48615; NID: g758592; PIDN: CAA88531.1; PID: g758593
A; Cross-references: EMBL: Z48615; NID: g758592; PIDN: CAA88531.1; PID: g758593
A; Cross-references: EMBL: Z48615; NID: g758592; PIDN: CAA88531.1; PID: g758593
A; Cross-references: EMBL: Z48615; NID: g758592; PIDN: CAA88531.1; PID: g758593
A; Cross-references: EMBL: Z48615; NID: g758592; PIDN: CAA88531.1; PID: g758593
A; Cross-references: EMBL: Z48615; NID: g758592; PIDN: CAA88531.1; PID: g758593
A; Cross-references: EMBL: Z48615; NID: g758592; PIDN: CAA88531.1; PID: g758593
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A; Cross-references: EMBL: Z48615; NID: g758592; PIDN: CAA88531.1; PID: g758593
A; Cross-references: EMBL: Z48615; NID: g758592; PIDN: CAA88531.1; PID: g758593
A; Cross-references: EMBL: Z48615; NID: g758592; PIDN: CAA88531.1; PID: g758593
A; Cross-references: EMBL: Z48615; NID: g758592; PID: g758593
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A;Residues: 1-954 <DO
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QEARLFGALQHPNIIALRGACLNPPHLCLVMEYARGGALSRVLAGRR-----VP-PHVLV 197
                                                                                 QEASMLHALQHPCIVALIGISIHP---LCFALELAPLSSLNTVLSENARDSSFIPLGHMLT
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                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                       7.5%;
                                                                                                                                                                            Score 285; DB 1;
Pred. No. 4.1e-09;
93; Mismatches 275
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A; Residues: 1-546 <STO>
                                                                                                                                                                                                                                                   A; Reference number: A84420; A; Accession: D84555
                                                                                                                                                                                                                                                                                                     R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beníto, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                             probable protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: D84555
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                                                                                                                                                                               A; Cross-references:
                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                      A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana, A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                        A; Map position:
                                                                                                                         Genetics.
;Gene: At2g17700
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                                              Local 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAMNKLTLPIPSTCPEP----FAR---LLEECWDPDPHGRPDFGSILKRLEVIEQSALFQ 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WHKTTKMSAAGTYAWMAPEVIRLSLFSKSSDVWSFGVLLWELLTGEVPYREIDALAVAYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAASDRSE-----HDLTPMDG 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPAEPSPGARAPWEPTPSAPPARWGHGARRRCDLALLGCATLLGAVGLGADVAEARAADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VCSSEGRGEEVVWCLDDKANSLVMYHSTTYQL-----CA-;--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSGSEVWYSNGPGL----LVIDCASLEICRRL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- CGGSSSGSSSGGSGTWSRGGP-PKKEELVGGKKKGRTWGPSSTLQKERVGGEERLKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLCSHTANRSKFSIADEDARQNPYPVK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLREGGSHISLPSGFEHKITVQASPTLDKRKGSDGASPPASPSIIPRLRAIRLTPVD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLNTPQQALDTPAVVTCFLAV---PVI--KKNSYLVLAGLADGLVAVFPVVRGTPKDSCS 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRNYTVVNTEKGLMEVQRMCCPGMKVSCQLQVQRSLWTATEDQKIYIYTLKG-----MC 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPLESFHSLQEDWKLEIQHMFDDLRTKEKELRSREEELLRAAQEQRFQEEQLRRREQELA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---KKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLSGQRPALGHHQLQIA---
EFRQEASMLHALQHPCIVALIGISIH--PLCFALELAPLSSLNTVLSENARDSSFIPLGH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GOSLIPTHVTAVCAVSRGHRRTPSDG 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VSLSSVSDCNSTRSLLRSDSDEAAPAAPSPPPSPPAPTPTPSPSTNPLVDLELESFKKDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EEQRRWLDGLFFPRAGRFP-RGL--SPPARPHGRREDVGPGLGLAP-----SATL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IHQESLTDYCSMSSYSSSPPRQAA-RSPSSLPSSPASSSSVPFST----DCEDSDMLHTP 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----RYFCGVPSPLRDMFPVRPLDTEPPAASHTANPKVPEGDSIADVSIMYSEELGTQIL 542
                                                                    Similarity
                                                       Conservative
                                                                                                                                                                               GB:AE002093;
                                                                  7.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --- ATTEMYELCCGKQTAFFSSQGQEYTVVFWDGKEE---
                                                     45;
                                                                                                                                                                             NID:g6598802;
                                                Score 278.5; DB 2;
Pred. No. 5.1e-09;
                                                                                                                                                                               PIDN:AAB80785.2;
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                                                       Indels
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                                                                                      546;
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                                                   Gaps
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Eur. J. Biochem. 213, /U1-/10, 1233
A;Title: Identification of a new family of human epithelial
A;Reference number: S32467; MUID:93238756; PMID:8477742
A;Accession: S32467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mixed-lineage protein kinase 1 - human C; Species: Homo sapiens (man) C; Date: 31-Dec-1993 #sequence_revision C; Accession: S32467; JU0229
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F;1-269/Domain: catalytic <CAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:141921; OMIM:600136
A;Map position: 14q24.3-14q31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Dorow, D.S.; Devereux, L.; Dietzsch, Eur. J. Biochem. 213, 701-710, 1993
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A; Residues: 1-394 <DO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  9-17/Region: protein kinase ATP-binding motif
289-310/Region: leucine zipper motif
324-345/Region: leucine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                       354-368/Region:
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                                                                                                                                                                                                                                                                                                                           RHLRATDAMKNFSEFRQEASMLHALQHPCIVALIGISIHP--LCFALELAPLSSLNTVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLRPKI--PKKTH-PKVKGLLERCWHQDPEQRPLFEEIIEMLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQMK
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                                                                                                                                                                                                                                                      ENARDSSFIPLGHMLTQKI----AYQIASGLAYLHKK---NIIFCDLKSDNILVWSL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VMTAETGTYRWMAPEVIEHKPYNHKADVFSYAIVLWELLTGDIPYAFLTPLQAAVGVVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLTQKIAYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKLSDYGISRQSFHEG
                                                                                                                                             GDLSNKI-LKITDFGLAREWHRTTKMSAAGTYAWMAPEVIRASMFSKGSDVWSYGVLLWE
                                                                                                                                                                               -DVKEHINIKLSDYGISRQSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LL -- KVALDVAKGMSYLHQNNIIHRDLKTANLL ---- MDEHGLVKVADFGVARVQIESG
                                   LALSVVSQM 233
                                                                        LLTGEVPFRGIDGLRVAYGVAMNKLALPIPSTCPEP----FAKLMEDCWNPDPHSRP
                                                                                                      LLSGQRPALGHHQLQIA-----KKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRP
                                                                                                                                                                                                                  -----GKRIPPDILVNWAVQIARGMNYLHDEAIVPIIHRDLKSSNILILQKVEN 141
                                                                                                                                                                                                                                                                                                                                                              Similarity 78; Conserv
                                                                                                                                                                                                                                                                                                                                                              7.2%;
llarity 31.3%;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                       basic
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                                                                                                                                                                                                                                                                                                                                                                Score 275.5; DB 2
Pred. No. 5.2e-09;
2; Mismatches 92
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hypothetical protein F8D20.290 - Arabidopsi C;Speckes: Arabidopsis thaliana (mouse-ear C;Date: 23-Apr-1999 #sequence\_revision 23-A C;Accession: T04683

Arabidopsis thaliana

cress

T04683 RESULT 7

R; Bevan,

Rose,

M.; Hempel,

: :

Entian, K.D.; Jesse,

T.; Heijnen, L.; Vos,

23-Apr-1999 #text\_change 21-May-1999

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RESULT 8
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A;Accession: T04683
A;Molecule type: DNA
A;Residues: 1-553 <BEV>
A;Cross-references: EMBL:AL031135
A;Experimental source: cultivar Columbia; BAC clone F8D20
                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1171 <CHO>
A;Residues: 1-1171 <CHO>
A;Cross-references: EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.50
A;Experimental source: cultivar Columbia; BAC clone T6H20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Choisne, N.; Robert, C. submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T6H20.50 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #:C;Accession: T12956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S
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A; Introns: 69/2; 107/3; 176/2; 194/3; 231/3; 289/2; 325/2; 350/1; 408/3; 440/3; 467/3;
                                                                                                                                                                                                                                                                                                                                                                               A;Gene: ATSP:T6H20.50
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                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reference number: Z17586
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                                         1039
                                                                                                                                                                                    925 KPSEQERMIDDFWNEAQNLAGLHHPNVVAFYGVVLDSPGGSVATVTEYMVNGSLRNALQK 984
                                                                                                                                                                                                                                                                                                                                                         position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                        6 RATDAMKNFSEFRQEASMLHALQHPCIVALIGISIH----PLCFALELAPLSSLNTVLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYFS 546
-ALGHHOLQIAKKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQMKD
                                                                        DYGISR---QSFHEGALGVEGTPGYQAPEI--RPRIVYDEKVDMFSYGMVLYELLSGQRP 176
                                                                                                             NVRN-----FDRCKRQLIAMDIAFGMEYLHGKKIVHFDLKSDNLLVNLRDPHRPI-CKVG
                                                                                                                                                 NARDSSFIPLGHMLTQKIAYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VMTAETGTYRWMAPEVIEHKPYDHRADVFSYAIVLWELLTGELPYSYLTPLQAAVGVVQK 485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFROEASMLHALQHPCIVALIGISIHP - LCFALELAPLSSLNTVLSENARDSSFIPLGH 73
                                                                                                                                                                                                                                                                                                                                    :ion: 3
780/1; 857/3; 881/3; 932/3; 987/2; 1036/3; 1077/3; 1107/1
                                                                                                                                                                                                                                                                     80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robert, C.; Brottier, P.; Wincker, P.; he Protein Sequence Database, July 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255
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                                                                                                                                                                                                                                                                                7.18; 32.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                     GVRGTLPWMAPELLNGTSSLVSEKVDVFSFGIVLWELFTGEEP
                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                                                                                                                               Score 270.5; DB 2
Pred. No. 3.7e-08;
2; Mismatches 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 270.5;
Pred. No. 1.
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                                                                                                                                                                                                                                                                                                DB 2;
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                                                                                                                                                                                                                                                                 100;
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                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                  Length 1171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cattolico, L.; Artiguenave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                               Gaps
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235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Al. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
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A; Residues: 1-438 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A86141; A; Accession: C86273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE005172; NID:g5080776; PIDN:AAD39286.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Species: Arabidopsis thallana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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  375
                                                                                                                                         128 QSFHE--GALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLSGQRPALGHHQLQI 185
                                                                                                                                                                                                                                                                                       204 DFRHEVDLLVKLRHPNIVQFLGAVTERKPLMLITEYLRGGDLHQYLKEKG------GLTP 257
                                                                                                                                                                                                                                     74 MLTOKIAYQIASGLAYLHKKN--IIFCDLKSDNILVWSLDVKEHINIKLSDYGISR---- 127
                                                                                                                                                                                                                                                                                                                                       16
                                               AKKLSKGIRPVLGQPEEVQFRR-----LQALMMECWDTKPEKRPLALSVVSQMK 234
                                                                                                                                                                                        TTAVNFALDIARGMTYLHNEPNVIIHRDLKPRNVLLVNSSAD----HLKVGDFGLSKLIKV 314
                                                                                            ONSHDVYKMTGETGSYRYMAPEVFKHRRYDKKVDVFSFAMILYEMLEGEPPFANHEPYEA
                                                                                                                                                                                                                                                                                                                                  EFRQEASMLHALQHPCIVALIGISIH--PLCFALELAPLSSLNTVLSENARDSSFIPLGH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -TMAT 1156
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                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          7.0%;
31.5%;
FRSKGCTPDLRELIVKCWDADMNQRPSFLDILKRLE
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Pred. No. 1.
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probable protein kinase (EC 2.7.1.-) T6H20.40 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Dete: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 21-Jan-2000 C; Accession: T12955 R; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, submitted to the Protein Sequence Database, July 1999 A; Reference number: Z17586 A; Accession: T12955 A; Molecule type: DNA A; Residues: 1-475 <CHO> A; Experimental source: cultivar Columbia; BAC clone T6H20 C; Genetics: A; Gene: ATSP:T6H20.40 A; Experimental source: cultivar Columbia; BAC clone T6H20 C; Genetics: A; Gene: ATSP:T6H20.40 A; Map position: 3 A; Introns: 39/1; 226/3; 376/3 A; Introns: 39/1; 226/3; 376/3 C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinase; protein kinase

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RiTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-620, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome l of the plant Arabidopsis.
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A;Molecule type: DNA
A;Residues: 1-1147 <STO>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
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A;Accession: F86297
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Best Local Similarity
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Best Local
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1122 IAGRLR 1127
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                                         229 VVSQMK 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 EFRQEASMLHALQHPCIVALIGISIHPLCFALELAPLSSLNTVLSENARDSSFIPLGHML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOKIAYOIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKLSDYGISROSFHEGAL 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFIVEATLLSRLSHPNVVKFVGVNTGN-CIITEYVPRGSLRSYLHKLEQKS--LPLEQLI
                                                                                                                                                                   PI-CKVGDFGLSKIKRNTLVSG--GVRGTLPWMAPELLNGSSSKVSEKVDVFSFGIVLWE 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -KGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQMK 234
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                                                                                                                                                                                         HINIKLSDYGIS---RQSFHEGALGVEGTPGYQAPEI--RPRIVYDEKVDMFSYGMVLYE
                                                                                                                                                                                                                                                    GS---LRHVLVRKDRHLDRRKRLIIAMDAAFGMEYLHAKNIVHFDLKCDNLLVNLKDPSR 1007
                                                                                                                                                                                                                                                                            SSFIPLGHMLTQK------IAYQIASGLAYLHKKNIIFCDLKSDNILYWSLDVKE
                                                                                                                                                                                                                                                                                                                                       RSSEQERLTGEFWGEAEILSKLHHPNVVAFYGV-----VKDGPGATLATV-TEYMVD 950
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                                                                                   ILTGEEPYANMHYGAIIGGIVNNTLRPTIPSYCDSDWR---ILMEECWAPNPTARPSFTE 1121
                                                                                                                      LLSGQRP-ALGHHQLQIAKKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALS
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33.3%;
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Fitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712

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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein-tyrosine kinase (EC 2.7.1.112) - slime mold (Dictyostellum discoldeum)
C;Specles: Dictyostellum discoldeum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Feb-2000
C;Accession: T18287
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A;Molecule type: DNA
A;Residues: 1-1338 <ADL>
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A; Residues: 1-1029 <STO>
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C; Keywords: ATP; 1
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                                                                                                                                                                                                   A; Cross-references:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSEQARQTKDFWREARILANLHHPNVVAFYGV-----VPDGPGGTMATVTEYMVNGS
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6.9%; Score 263; DB 2;
28.6%; Pred. No. 1.2e-07;
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Matches

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Indels

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Gaps

Qy	gb Qy	da dy	dg Qy	Que Bes Mat		A; Cros A; Map C; Supe C; Keyv		** ** **	A;T1t A;Ref A;Acc	A; Cro R; Ing Oncog	A; Mol	A; Ref	R;Gal	C; Dat	N; Alte C; Spec	+ (A M	D		Дb	Qγ	D	Ş	
187KKLSKGIRPVLGOPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQMKDPTFATFMYE 244	130 FHEGALGVEGTPGYQAPEIRPRIYYDEKYDMFSYGMVLYELLSGQRPALGHHQLQIA 186 		18 RQEASMLHALQHPCIVALIGISIHPLCEALELAPLSSLNTVLSENARDSSFIPLGHML 75	atch 6.8%; Score 260.5; DB 1; Length 847; cal Similarity 22.6%; Pred. No. 9.8e-08; 162; Conservative 84; Mismatches 223; Indels 249; Gaps 3	123-131/Region: protein kinase momology <kin> 123-131/Region: protein kinase Afp-binding motif 403-424/Region: leucine zipper motif 438-459/Region: leucine zipper motif 468-482/Region: basic</kin>	<pre>ys*reterences: GDB:134/35; OMIM:600050 position: 11q13.1-11q13.3 pritamily: mixed-lineage protein kinase 3; protein kinase homology; SH3 vords: ATP; leucine zipper; phosphotransferase; serine/threonine-specifi0//Domain: SH3 homology <sh32></sh32></pre>	GB:L32976; NID:g488295	eliminary; translated from GB/EM/pe: mRNA   Pe: mRNA   1847 < RES>	A;Pitle: MIK-3; identification of a widely-expressed protein kinase bearing & A;Reference number: 158395; MUID:94239754; PMID:8183572 A;Accession: 158395	Cross-references: GB:U07747; NID:g464027; PIDN:AAA19647.1; PID:g464028 Ing, Y.L.; Leung, I.W.; Heng, H.H.; TSuil, L.C.; Lassam, N.J. ROGENE 9, 1745-1750, 1994	A; Modecule type: mRNA A; Residues: 1-847 <gal></gal>	A;Reference number: A53800; MUID:94253068; PMID:8195146	Q.; Godowski, P.J.	.0-Sep-1999 #sequence_revision 10-Sep-1.on: A53800; I58395		. 14	1259 AAFENYRPAIPPDCPYSLRKLITKCWASDPSQRPSFTEILTELE 1302		1199 LSDDMTLSGITNPRWRSPELTKGLVYNEKVDVYSFGLVVYEIYTGKIPFEGLDGTASAAK 1258	129 SFHEGALGVEGTPGYQAPEIRPRIYIDEKVDMFSYGMVLYELLSGQRPALG-HHQLQIAK 187	1144 IKLNPLMMYKMIHDLSIGMEHLHSIQMLHRDLTSKNILLDEFKNIKIADFGLATT	69 IPLGHMLTOKIAYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKFHTNIKLSDYGISDO	FEEC STATES AND A STATE OF THE PROPERTY OF THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    387 M---PRDSFHSMQ------EGWKREI------QGLFDELR-----AKEKELLSR 420
691 PPSPLICFSLKTPDSPPTPAPLLLDLGIPVGQRSAKSPRREEEPRGGTVSPPPGTSRS 748
                                                                                                                                                                                               525 SIADVSIMYSEELGTQILIHQESLTDYCSMSSYSSSPPRQAARSPSS------LPSSP 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 CASLEICRRLEPYMAPSMVTSVVCSSEG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 AVNKLTLPIPSTCPEP-----FAQLMADCWAQDPHRRPDFASILQQL-EALEAQVLRE 386
                                                                     ASSSSVPFSTDCEDSDMLHTP---
                                                                                                                                                                                                                                                                                                                                                                                                 -----RRLED-----SSNGERRACWAWGPSSPKPGEAQNGRRRSRMDEATW
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                                                                                                                                ---QPPGGPGRERGESPTTPPTPTPAPCPTEP
                                                              ----GAASDRSEHD-----LTPMDGETFS 617
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ologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Al C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar N.F.; Hughes, B.; Huizar, L. 408, 816-820, 2000

ors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Ki Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marz M.; Rooney, T.; Rowley, D.; Sakano, H. tors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tal L.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. e: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

sesion: B96827 etical protein T8K14.1 [imported] - Arabidopsis thaliana ies: Arabidopsis thaliana (mouse-ear cress) : 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001 Match Local Similarity osition: 1 ule type: DNA ues: 1-1248 <STO> s: preliminary sion: B96827 T8K14.1 references: GB:AE005173; NID:g4835752; PIDN:AAD30219.1; GSPDB:GN00141 6.8%; Score 260.5; DB: Pred. No. 1.6e-07 1; Mismatches 89 DB 2; Length 1248;

)52 GS----LRHVLVRKDRHLDRRKRLIIAMDAAFGMEYLHSKNTVHFDLKCDNLLVNLKDPSR 1108 66 SSFIPLGHMLTQK------IAYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKE 114 001 RSSEQERLTGEFWGEAEILSKLHHPNVVAFYGV-----VKDGPGGTLATV-TEYMVD 1051

6 RATDAMKNPSEFRQEASMLHALQHPCIVALIGISIHPLCFALELAPLSSLNTVLSENARD 65

Indels 35; Gaps

10;

Conservative

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Title:
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Maximum Match 100%
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                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             16
98
104
125
125
222
419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                            7.5%;
22.8%;
                                                                                                                                                                                                                                                                                                                                                          103623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STY_pkinase.
Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euk_pkinase
                                                                                                                           ---ATEMYELCCGKQTAFFSSQGQEYTVVFWDGKEE---
                                                                                                                                                                                                                                                                                                                  93;
                                                                                                                                                                                                                                                                                                                                                   REF. 3).
G -> S (IN REF. 2).
G -> R (IN REF. 2).
V -> A (IN REF. 2).
W; 538F4AAA559B0ABA CRC64;
                                                                                                                                                                                                                                                                                                                                                          ¥
                                                                                                                                                                                                                                                                                                               Score 285; DB 1; Length 954;
Pred. No. 1.7e-12;
3; M1smatches 275; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                         LEUCINE-ZIPPER 1 (BY SIMILARITY).
LEUCINE-ZIPPER 2 (BY SIMILARITY).
ARG/LYS-RICH (BASIC).
SRL -> AV (IN REF. 2).
SRL -> AV (IN REF. 2).
LKLREGGSHISLPSGF -> AQAAGRRQPHQPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
                                                              SQEKPRVRKRKGNFKRSRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                         AQAAGRRQPHQPALWL
--- AMEVV
                                                                                                                                                                                                                                                                                                                208;
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RESULT 2
M3K9_HUMAN
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BINDING
ACT_SITE
DOMAIN
DOMAIN
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mitogen-activated protein kinase kinase kinase
lineage kinase 1) (Fragment)
MAP3K9 OR MIKI OR PRKEI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M3K9_HUMAN
P80192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dorow D.S., Devereux L., Dietzsch E., de "Identification of a new family of human containing two leucine/isoleucine-zipper Eur. J. Biochem. 213:701-710(1993).

-1- TISSUE SPECIFICITY: EXPRESSED IN EPIT
                                                                                                                                                                                     PROSITE; PSO0107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein ki
                                                                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                            ProDom; PD00000
SMART; SM00219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                              DOMAIN
                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                                                        Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 600136; -
                                                                                                                                                                                                                                                                                                                                                                                                                            Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Colon epithelium;
MEDLINE-93238756; PubMed-8477742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                   nterPro; IPR000719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEGSKQWSSSAPNIGKSPKHTPIAPGFASLNEMEEFAEAEDGGSSVPPSPYSTPSYLSVP
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                                                                                                                                                                                                                                                                                                                                                                                                                      HGNC:6861; MAP3K9
                                                                                                                                                                                                                                                                                              PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                       IPR002290; Ser_thr_pkin
IPR001245; Tyr_pkinase.
    127
127
324
354
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    17
271
17
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127
310
345
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                                                                                                                                                                                                                                                                                                                                                         Ser_thr_pkinase
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PROTEIN KINAGE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

LEUGINE-ZIPPER 1 (BY SIMILARITY).

LEUGINE-ZIPPER 2 (BY SIMILARITY).

ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Catarrhini; Hominidae;
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in kinase;
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SEQUENCE

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RESULT 3
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P18161;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYKB OR DPYK2.
Dictyostelium discoldeum (Slime mold)
Eukaryota; Mycetozoa; Dictyosteliida;
         Pfam; PF00069; pkinase; 1.

Probom; PD000001; Euk_pkinase; 1.

SMART; SM00221; STYKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR;

PROSITE; PS00109; PROTEIN_KINASE_TYR;

PROSITE; PS50011; PROTEIN_KINASE_DOM;

Transferase; Tyrosine-protein kinase;
                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYK2_DICDI
                                                                                                                                                                                           EMBL; M33784; AAA33203.1;
                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium discoideum.";
Mol. Cell. Biol. 10:3578-3583(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=44689;
                                                                                                                                                 HSSP; P08631; 1AD5
D1ctyDb; DD03011; p
                                                                                                                                                              PIR; B35670; B35670.
HSSP; P08631; 1AD5.
                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                ran J.L., Spudich J.A.;
required protein-tyrosine kinase
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                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: ATP + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFTNILDQL 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDLSNKI-LKITDFGLAREWHRTTKMSAAGTYAWMAPEVIRASMFSKGSDVWSYGVLLWE
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                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                          tyrosine phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLSGQRPALGHHQLQIA-----KKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DVKEHINIKLSDYGISRQSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                       DD03011; pykB.
IPR000719; Euk_pkinase.
IPR004040; STY_pkinase.
IPR001245; Tyr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GKRIPPDILVNWAVQIARGMNYLHDEAIVPIIHRDLKSSNILILQKVEN
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31.3%; Pred. No. 2.4
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                                                                                                                                                                                                                                                                                                                                                       protein tyrosine
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1:
ATP-binding; Phosphorylation
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ches 92;
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Best Local
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NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=92334872; PubMed=1378585;

Ottille S., Raulf F., Barnekow A., Hannig G., Schartl M.;

"Multiple src-related kinase genes, srki-4, in the fresh water sponge spongilla lacustris.";

Spongilla lacustris.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRK4.
                                                                                                                                                                                                                                                                                              Oncogene 7:1625-1630(1992).
-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine •
                                                                                                                                                                                                                                                                                                                                                                                                            Spongilla lacustris (Freshwater sponge).
Eukaryota; Metazoa; Porifera; Demospongiae;
Haplosclerida; Spongillidae; Spongilla.
NCBI_TaxID-6055;
                          EMBL; X61604; CAA43801.1;
HSSP; P00523; 2PTK.
InterPro; IPR000719; Euk_I
                                                                                                                                                                                                                                                                      +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P42690;
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                                                                                   or send an
                                                                                                entities requires a license agreement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 IKKLKIIGDEEQFKERFIREVQNLKKGNHQNIVMFIGACYKPACIITEYMAGGSLYNILH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-NOV-1995
5-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                              SÜBCELLULAR LÓCATION: Cytoplasmic (Probable).
ALTERNATIVE PRODUCTS: 2 isoforms; 1 (AC P42686) and 4 (shere); are produced by alternative splicing.
SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES.
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                   tyrosine phosphate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDYGISRQSFHEGALGVEG----TPGYQAPEIRPRI-VYDEKVDMFSYGMVLYELLSGQR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPNSSTPKVKYSFPLVLKMATDMALGLLHLHSITIVHRDLTSQNILLDELG-----NIKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFSDLDGSQRSAQVA---YAGLRPPIPEYCDPE-----LKLLLTQCWEADPNDRPPFTY 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Conservative
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114
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                                                                                  email to license@isb-sib.
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(Rel.
(Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32, Createq)
32, Last sequence update)
41, Last annotation update)
kinase SRK4 (EC 2.7.1.112).
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122
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46386
; Euk_pkinase.
; SH2.
; SH3.
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27.7%;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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BY SIMILARITY.
GH; E93918B605B9AEC1 CRC64;
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Pred. No. 5.2e-11;
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Best Local Similarity
Matches 73; Conser
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PRINTS; PRO0109; TYRKINASE;
PRODOM; PD000001; ENL_pkinase; 1.
PRODOM; PD000066; SH3; 1.
PRODOM; PD000093; SH2; 1.
SMART; SM00252; SH2; 1.
SMART; SM00252; SH3; 1.
SMART; SM00326; SH3; 1.
SMART; SM00326; SH3; 1.
SMART; SM00329; PROTEIN_KINASE_ATP; 1
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-99248426; PubMed=10231392;

Oishi I., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T.,

Oishi I., Akira S., Matsuda Y., Yamamura H., Otani H., Minami
Hatta T., Akira S., Matsuda Y., Yamamura H., Otani H., Minami
                                                                                                                                                                                                                                                                                                                                                       MOUSE
ROR1_MOUSE
Q9Z139;
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BINDING
ACT_SITE
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                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                 16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
15-CCT-2002 (Rel. 41, Last annotation update)
15-CT-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase transmembrane receptor ROR1 precursor (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related
                                                                                                                               NCBI_TaxID-10090;
                                                                                                                                                                                                               ROR1 OR NTRKR1.
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                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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PROTEIN KINASE.

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AIP (BY SIMILARITY).

BY SIMILARITY.
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Alternative
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                                                                                                                                                  Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                              PRT;
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ive splicing.
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H., Minami
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; Murinae; Mus
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                                   Liu Z.J.,
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the European Bioinformatics Institute. The second proof of the statement is not remove entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mROrl, mROr2, during mouse development: implications in and function of the nervous system."; Genes Cells 4:41-56(1999).
-I- FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR WHOSE ROL
                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS TO
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                                                                                                                                                                                                                                                                                                                                                                          email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIVITY: ATP + a
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SMART; SM00130; F SMART; SM00219; T PROSITE; PS50038; PROSITE; PS00021; PROSITE; PS50070; PROSITE; PS00107; DOMAIN TRANSMEM DOMAIN DOMAIN DOMAIN PRINTS; Pfam; ProDom; PD000001; Euk\_pkinase; ProDom; PD000395; Kringle; 1. SMART; SM00408; IGC2; 1. Immunoglobulin PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.
PROSITE; PS50010; PROTEIN\_KINASE\_TYR; 1.
PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Receptor;
Transferase; Tyrosine-protein; Kringle; Phosphorylation; EMBL; AB010383; HSSP; P00747; 1 InterPro; InterPro; InterPro; InterPro; InterPro; InterPro; PF01392; PR00018; KRINGLE. PR00109; TYRKINASE. PS50070; KRINGLE PS00107; PROTEIN PS50011; PROTEIN PS00021; KRINGLE\_1; IPR000719; Euk\_pkinase.
IPR000024; Fz\_domain.
IPR003006; Ig\_MHC.
IPR003598; Ig\_c2. IPR001 407 428 73 7; 1g; 1. 51; kringle; KR; 1. KR; 1. ;; TYTKC; 1. ?: EZ; 1. ?RING? pkinase; Fz; 1. domain Ror1 PROTEIN\_KINASE\_ATP; FALSE\_NEG Tyr\_pkinase Kringle. FALSE\_NEG CYTOPLASMIC (POTENTIAL)
IG-LIKE C2-TYPE DOMAIN. POTENTIAL.
TYROSINE-PROTEIN KINASE TRANSMEMBRANE
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ATP (BY SIMILARITY).
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PHOSPHORYLATION (AUTO-)

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SEQUENCE FROM N.A.
MEDLINE-95210168; PubMed-7696183;
Cance W.G., Craven R.J., Bergman M., Xu
"Rak, a novel nuclear tyrosine kinase (
"Rak, a novel nuclear tyrosine kinase (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRK_HIMAN STANDARD; PRT; 505 AA. P42685; Q13128; O1-NOV-1995 (Rel. 32, Created) O1-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Tyrosine-protein kinase FRK (EC 2.7.1.112) (N kinase RAK).
                                           MEDLINE-93293373; PubMed-8099900;
Cance W.G., Craven R.J., Weiner T.M.
"Novel protein kinases expressed in
Int. J. Cancer 54:571-577(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                            PARTIAL SEQUENCE FROM N.A. MEDLINE-93293373; Pubmed-8
                                                                                                                                                              Strausberg R.
                                                                                                                                                                                                                                                                                                                           Lee J., Wang Z., Luoh S.-M., Wo
"Cloning of FRK, a novel human
kinase-encoding gene.";
Gene 138:247-251(1994).
                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Lymphoid;
MEDLINE-94171047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-9606;
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                                                                                                                                                                             ISSUE-Urinary bladder;
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                                   CATALYTIC
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
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                                ACTIVITY: ATP
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Luoh S.-M., Wood W.I., Scadden D.T.;
a novel human intracellular SRC-like
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                                                                human
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expressed in epithelial
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cells.
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                                                                                                                                                                                                           ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÷
                                                                                                                                                                                                                                                                            SH3 domain;
                                                                                                                                                                                                                                                                                                                                                                         ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                       SMART;
                                                                                                                                                                                                                                                                                                                                                                 SMART;
                                                                                                                                                                                                                                                                                                                                                                                    ProDom;
                                                                                                                                                                                                                                                                                                                                                                                             ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Piam;
                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nterPro; IPR000719;
 180
                                     128
                                                        327
                                                                                            272
                                                                          73
                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY:
OF LYMPHOID, BRAIN,
SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBFAMILY
HHQLQIAKKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQMKDPTFA
                                                                          HMLTQKI--AYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKLSDYGISR---
                                                                                             NDFLREAQIMKNLRHPKLIQLYAVCTLEDPIYIITELMRHGSLQEYL-QNDTGSKI----
                                                                                                               SEFRQEASMLHALQHPCIVALIGISI--HPLCFALELAPLSSLNTVLSENARDSSFIPLG
                                                       -HLTQQVDMAAQVASGMAYLESRNYIHRDLAARNVL-----VGEHNIYKVADFGLARVFK
                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00017; SH2;
PF00018; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U22322; AAC5011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U00803; AAA18284.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BC012916; AAH12916.1; T.
                                                                                                                                                                                                                                                                                                                                                                          ; PR00109; TYRKINASE;
; PD000001; Euk_pkinas
; PD000066; SH3; 1
; PD000093; SH2; 1
                                                                                                                                                                                                                                                                                                                                              SM00219;
                                                                                                                                  75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000980;
                                                                                                                                                                      115
505
                                -QSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLS-GQRPALG
                                                                                                                                                                                                                                                                           Phosphorylation.
                                                                                                                                  Conservative
                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONTAINS 1
                                                                                                                                                                                                                                                                                                                                              TyrKc;
                                                                                                                                                                                                                                                                                                                                                                                                              SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                         SH3;
SH2;
                                                                                                                                                                                                                                                                                                                  PROTEIN_KINASE_ATP;
PROTEIN_KINASE_TYR;
PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRK.
                                                                                                                                                                                                                                                                                                                                                                                            Euk_pkinase;
                                                                                                                                                                      115
58254 MW;
                                                                                                                                                                                                   208
491
248
262
354
122
                                                                                                                                          6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tyr_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euk_pkinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESTRICTED TO CELLS LINES DERIVED FROBREAST, COLON AND BLADDER ORIGIN.
TO THE TYR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SH2
SH3
                                                                                                                                  49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is not removed
                                                                                                                                 Score 243.5; DB 1;
Pred. No. 6.3e-10;
9; Mismatches 77;
                                                                                                                                                                                                                                              SH3.
SH2.
PROTEIN
                                                                                                                                                                                                                     ATP
ATP
S
                   · APEAIRSNKFSIKSDVWSFGILLYEIITYGKMPYSG
                                                                                                                                                                                ъ
                                                                                                                                                                                                  PHOSPHORYLATION (AUTO-)
G -> R.
                                                                                                                                                                    /FTId-VAR_006283.
P -> A (IN REF. 2).
06EC050DDBCD930B CRC64;
                                                                                                                                                                                                                                                                                      kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bioinformatics
                                                                                                                                                                                                                      SIMILARITY.
                                                                                                                                                                                                                                (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           It is
                                                                                                                                                                                                                             SIMILARITY).
                                                                                                                                                                                                                                                KINASE
                                                                                                                                                                                                                                                                                                                  ---
                                                                                                                                                                                                                                                                                      ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                  Indels
                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                       SH2 domain;
                                                                                                                                                                                                           AB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restrictions
                                                                                                                                                     505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEMBL
                                                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM TISSUES
                                                                                                                                  45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRC
                                                                                                                                  Gaps
 239
                    436
                                                                           127
                                                                                             326
                                                                                                                72
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RESULT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT OF THE COMMENT
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01-NOV-1995 (Rel. 32, Createu,
16-OCT-2001 (Rel. 40, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Protein kinase APKLB (EC 2.7.1.-).
----- OR AT2G28930 OR T914.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APKB_ARATH
P46573; Q9S
                                                                                                                                                                                                                                                                                       InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. The are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., To Fujil C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldbl Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Uma Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T. Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C., Venter J.C.;
                                              PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00108; PROTEIN_KINASE_ST; 1 PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARATH
Transferase;
ATP-binding;
                                                                                                                                        ProDom; PD000001; Euk_pkinase; SMART; SM00221; STYKC; 1.
                                                                                                                                                                                                                                                                                                                                                                         EMBL; D10152;
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AC005315; AAC33221.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb~sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Novel protein kinase of Arabidopsis thaliana phosphorylates tyrosine, serine and threonine. Plant Mol. Biol. 20:653-662(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20083487; PubMed-10617197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hirayama T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-93081726; PubMed-1450380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 143-346 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-3702;
                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence and analysis of chromosome 2 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SERINE/THREONINE ACTIVITY. IN VIVO, CAN PHOSPHORYLATE TYROSIN RESIDUES OF LIMITED SUBSTRATES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: POSSIBLE BI-FUNCTIONAL KINASE. IN VITRO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLRWKL 487
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                                                                                                                                                                                                                          PF00069;
                                                                                                                                                                                                                                                 IPR000719; Euk_pkinase.
IPR004040; STY_pkinase.
IPR002290; Ser_thr_pkinase.
IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Columbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oka A.;
                          Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                         BAA20968.
                                                                                                                                                                                                                          pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
Myristate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shea T.P., Benito M.-I., Town (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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                          Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (APK1) that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Umayam L.,
Y T.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Town C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rosidae;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
DOMAIN
NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  P25848; P93100;
01-MAY 1992 (Rel. 22, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Light-sensor Protein kinase [Includes: Phytochrome;
(EC 2.7.1.-)]
                                                                                                                                                                                                                                                                                                                          Ceratodon purpureus (Moss).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Bryopsida; Dicranidae; Dicranales; Ditrichaceae; Cer
                                                                                                                                                                phytochrome gene in the moss chain reaction.":
                                                                                                                                                                                 SEQUENCE OF 49-538 FROM N.A.
MEDLINE-91085543; Pubmed-2261981;
Thuemmler F. Beetz A., Ruediger W.;
"Phytochrome in lower plants. Detection
                                                                                                                                                                                                                                      Thuemmler F., Dufner M., Kreisl P., Dittrich P.; Molecular cloning of a novel phytochrome gene of t purpureus which encodes a putative light-regulated plant Mol. Biol. 20:1003-1017(1992).
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-93099252; PubMed-1463836;
                                                                                                                                                                                                                                                                                                                                                             PHY1 OR PHY
                                                                                                                   STRAIN-WT3
                                                                                                                              REVISIONS TO
                                                                                                                                                                                                                                                                                                                NCBI_TaxID-3225;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PHY1_CERPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEKRPLALSVVSQMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -AVDKNRPPGEQKLVEWARPLIANKRKL-FRVIDNRLQDQYSMEEACKVATLALRCLTFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PALGHHOLQIAKKLSKGIRPVLGQPEEVQFR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLAK - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSFIPLGHMLTQKIAYQIASGLAYLH -- KKNIIFCDLKSDNILVWSLDVKEHINIKLSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                 275:125-129(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DGPTGDKSHVSTRIMGTYGYAAPEYLATGHLTTKSDVYSYGVVLLEVLSGRR
                                                                                                                              C-TERMINUS
                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYRISTATE (BY SIMILARITY).
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 238.5;
Pred. No. 1.
                                                                                                                                                                        Ceratodon
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EB1CA0B1A626A5DA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    1307
                                                                                                                                                                      n and partial purpureus usi
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                                                                                                                                                                                                                                                                                                                           yta; Bryophyta;
Ceratodon.
                                                                                                                                                                       using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                 Ceratodon kinase.";
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                                                                                                                                                                                                                                                                                                                                                                                 kinase
                                                                                                                                                                                  of.
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Best
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS500245; PHYTOCHROME_1; 1.
PROSITE; PS50046; PHYTOCHROME_2; 1.
PROSITE; PS50046; PAS: 1
                                             Matches
                                                                                        BINDING
NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                               SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U87632; AAB47762.1; EMBL; X17084; CAA34936.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long modified and this statement is not removed.
 1036
                                                                                                                                                                                                                    PROSITE; PS50113; PAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP;
                                                                                                                                                                                                   Transferase;
                                                                                                                                                                                                               Transcription
                                                                                                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PRO1033;
                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00069;
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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InterPro; IPR003018;
                                                                                                                                                                 DOMAIN
                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                      Match
Local (
                       12 KNFSEFRQEASMLHALQHPCIVALIGTSIH--PLCFALELAP---LSSLNTVLSENARDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLASMA MEMBRANE
PTM: CONTAINS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESPONSES. PFR CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBUNIT OF RIBULOSE-BISPHOSPHATE CARBOXYLASE, CHLOROPHYLL A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE(S) IN A NEGATIVE FEEDBACK FASHIOSUBCELLULAR LOCATION: LOCATED IN A FIXED POSITION CLOSE TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY:
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S27396; S2739
RNNEDFKREVEILAELCHPNITSMFCSPLYRRKCSIIMELMDGDLLALMQRRLDRN-EDH
                                                                                                                                                                                                                                                                                                                                                                               PF01590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P08631; 1ADS
                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR00001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR000700;
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                                                                                            609
683
779
1004
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1010
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1031
1127
1307
                                              Conservative
                                                                                                                                                                                                  Serine/threonine-protein
                                                                                                                                                                                                               regulation;
                                                                                                                                                                                                                                                                                                                                                                                         phytochrome; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  pkinase; l
                                                                                                                                                                                                                                                                                                                                  GAF;
                                                                                                                                                                                                                                                                                                                                                                               GAF;
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                                                                                                                                                                                                                                                                                                                                                                   PHYTOCHROME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ONE COVALENTLY LINKED TETRAPYRROLE (
N THE N-TERMINAL SECTION; BELONGS TO
                                                                                                       680
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1003
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Phytochrome.
STY_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAS-assoc_C
PAS_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euk_pkinase
GAF.
                                                                                        O7 PROTEIN KINASE.

CHROMOPHORE (BY SIMILARITY)

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY.

145843 MW; E5E77A9FEF301A5C CRC64;
                                                        286
                                                                                                                                                                                                                                                                                                                                                        pkinase;
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                                                       .28;
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                                                                                                                                                                                                                                                                                                                                                                                                                           thr_pkinase.
                                                                                                                                                                                                 Photoreceptor; Phytochrome; Chromophore; nine-protein kinase; ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALT_SEQ.
                                              49;
                                             Score 238.5;
Pred. No. 5.3e
9; Mismatches
                                                                                                                                                               HINGE
                                                       238.5;
No. 5.
                                             .3e-09;
les 98;
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                                              Indels
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                                                                   1307;
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                                              59;
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16-OCT-2001 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Tyrosine-protein kinase transmembrane
(EC 2.7.1.112) (Neurotrophic tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1155
          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                 kinase, lacking both extracellular and Oncogene 13:1555-1559(1996).
-I- FUNCTION: TYROSINE PROTEIN KINASE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROR1_HUMAN
Q01973; Q9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reddy U.R., Phatak S., Pleasure D.;
"Human neural tissues express a truncated Rorl receptor tyrosine
"human neural tissues express a truncated Rorl receptor tyrosine
"human neural tissues express a truncated Rorl receptor tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97030043; Reddy U.R., Phatal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (LONG ISOFORM)
MEDLINE-93100347; PubMed-1334494;
Masiakowski P., Carroll R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROR1 OR NTRKR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                -1- SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A novel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biol.
                                                                                                                                                                                                                                                                              SÜBCELLULÄR LÓCATION: TYPE I MEMBYANE PROTEÍN.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND
SHORT FORM/T-RORI; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED STRONGLY IN HUMAN HEART, LUNG, AN
KIDNEY, BUT WEAKLY IN THE CNS. THE SHORT ISOFORM IS STRONGLY
EXPRESSED IN FETAL AND ADULT CNS AND IN A VARLETY OF HUMAN
CANCERS, INCLUDING THOSE ORIGINATING FROM CNS OR PNS
                                                                                                                                                                             DEVELOPMENTAL STAGE: EXPRESSED AT HIGH LEVELS DURING EARLY EMBRYONIC DEVELOPMENT. THE EXPRESSION LEVELS DROP STRONGLY DAY 16 AND THERE ARE ONLY VERY LOW LEVELS IN ADULT TISSUES SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. IS SUBFAMILY.
                                                                                                                                                               SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: ATP + a
                                                                                                                                                                                                                                                                                                                                                                                                 tyrosine phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                   CLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: TYROSINE-PROTEIN KINASE RECEPTOR WHOSE ROLE IS NOT
                                                                                                                                                                                                                                                                  NEUROECTODERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CWDTKPEKRPLALSYVSQMKDPTFATFMYELCCGKQTAFFSSQGQEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---DMFSYGMVLYELLSGQRPALGHHQLQIAKKL-SKGIRPVLGQPEEVQFRRLQALMME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267:26181-26190(1992)
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                                                                                                                            CONTAINS 1 FRIZZLED (FZ) DOMAIN CONTAINS 1 IMMUNOGLOBULIN-LIKE (CONTAINS 1 KRINGLE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed-8875995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell surface receptors with tyrosine kinase-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update
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                                                                                                                                                 C2-TYPE DOMAIN
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                                                                                   a collaboration -
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ProDom; PD000395; K1ngle; 1
SMART; SM00408; IGC2; 1.
SMART; SM00130; KR; 1.
SMART; SM00219; TyrKC; 1.
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PROSITE; PS00021;
PROSITE; PS50070;
PROSITE; PS50017;
PROSITE; PS50011;
PROSITE; PS00109;
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Pfam; PF00051; kringle; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF01392; Fz; 1.
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EMBL; U38894; AAC50714.1;
HSSP; P00747; 1CEA.
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                     107
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                                                                                                                    Local Similarity 25.1 tes 79; Conservative
                                                                                                 N
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                                                                                       LELAPLSSINTVLSENARDSSFIPLGHMLTQKIAYQIASGLAYLHKKNIIFCDLKSDNIL 106
                    VWSLDVKEHINIKLSDYGISRQSFHEGALGVEGTP----GYQAPEIRPRIVYDEKVDMFS
                                      IMRSPHSDVGCSSDEDGTVKSSLDHGDFL--HIAIQIAAGMEYLSSHFFVHKDLAARNIL
                                                                            IKTLKDYNNPQQWMEFQQEASLMAELHHPNIVCLLGAVTQEQPVCMLFEYINQGDLHEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGNC: 10256; ROR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD000001; Euk_pkinase; PD000395; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR00109; TYRKINASE.
-IGEQLHVKISDLGLSREIYSADYYRVQSKSLLPIRWMPPEAIMYGKFSSDSDIWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR000719; Euk_pkinase.
IPR000024; Fz_domain.
                                                                                                                                                                             645
79
47
66
184
315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRINGLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRINGLE_1; FALSE_NEG.
KRINGLE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN_KINASE_ATP;
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427
937
139
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66
184
315
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                                                                                                                                                           104312
                                                                                                                             6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                 Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                          tein kinase; ATP-binding; Receptor;
ycoprotein; Kringle; Phosphorylation;
                                                                                                                     53;
                                                                                                                                                           MW;
                                                                                                                                                                  BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . .) (POT

N-LINKED (GLCNAC. . . .) (POT

MISSING (IN SHORT ISOFORM).
                                                                                                                             Score 238;
Pred. No. 3
                                                                                                                                                                                                                                                                    SER/THR-RICH
                                                                                                                                                                                                                                                                                       PROTEIN KINASE.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                              TYROSINE-PROTEIN KINASE TRANSMEMBRANE
                                                                                                                                                                                                                                                                                PRO-RICH
                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR ROR1
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                                                                                                                                                                                                                                                                                                            KRINGLE
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                                                                                                                    Mismatches
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                                                                                                                                                                                                                                               (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                FALSE_NEG
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.6e-09;
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                                                                                                                                    Length 937;
                                                                                                                                                          CRC64;
                                                                                                                                                                                       (POTENTIAL).
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RESULT 10
SPK1_DUGTI
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Pfam; PF00069; rt/
ProDom; Pro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPKI_DUGTI STANDARD: PRT: 497 AA. P42687; O1-NOV-1995 (Rel. 32, Created) O1-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Tyrosine-protein kinase SPK-1 (EC 2.7.1.112).
  Tyrosine-I
SH2 domain
DOMAIN
DOMAIN
DOMAIN
NP_BIND
                                                                              PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                                            SMART; SM00252; SH2; 1.
SMART; SM00326; SH3; 1.
SMART; SM00219; TYTKC;
                                                                                                                                                                                ProDom; PD000001;
ProDom; PD000066;
ProDom; PD000093;
                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Burgaya F., Garcia-Fernandez J., Riutort M., Baguna "Structure and expression of Spk-1, an src-related in the planarian Dugesia (G) tigrina.", Oncogene 9:1267-1272(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dugesia tigrina (Planarian)
Eukaryota; Metazoa; Platyhe
                                                                                                                                                                                                                                                                                                               EMBL; X75310; CAA53058.1; -. HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paludicola; Dugesiidae; NCBI_TaxID=6162;
                                                                                                                                                                                                                                                           InterPro; IPR000719; Euk_pkinase.
InterPro; IPR000980; SH2.
InterPro; IPR001452; SH3.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-94181282;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            791
                                                                                                                                                                                                                                                                                                                                                                                                                                                         tyrosine phosphate.
SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES
SIMILARITY: CONTAINS 1 SH2 DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----FPSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGVVLWEIFSFGLQPYYGFSNQEVIEMVRK--RQLLBCSEDCP-PRMYSLMTECWNEIPS
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                                                                                                                                                                                                           PD000001; Euk_pkinase;
                                                                                                    PS00107; PROTEIN_KINASE_ATP;
PS00109; PROTEIN_KINASE_TYR;
PS50011; PROTEIN_KINASE_DOM;
                                                                  protein kinase;
     33
100
220
226
                                                                                                                                                                                                                          pkinase;
                                                        domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=7510865;
                                                                                 SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258
                                                                                                                                                                                    SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Platyhelminthes; Turbellaria;
lae; Girardia.
                                                                  Phosphorylation;
SH2.
PROTEIN KINASE.
ATP (BY SIMILARITY).
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                                                                     ATP-binding;
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RX MEDLINE-21016721; PubMed-11130714;
RRA Tabata S., Kaneko T., Nakamura T., Hosouchi T., Kawashima K.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Miyajima N., Sasamoto S., Kimura T., Hosouchi T., Kawashima K.,
RA Makazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
RA Makazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
RA Matanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
RA Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
RA Habermann K., Murray. J., Johnson D., Rohlfing T., Nelson J.,
RA Habermann K., Murray. J., Johnson D., Rohlfing T., Nelson J.,
RA Habermann K., Murray. J., Johnson D., Rohlfing T., Nelson J.,
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RA Habermann K., Murray. J., Johnson D., Rohlfing T., Nelson J.,
RA Habermann K., Murray. J., Johnson B., Lamar E., Latreille P.,
RA Leonard S., Meyer R., Mulvaney E., Ozarsky P., Riley A., Strowmatt C.,
RA Magner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,
RA Magner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N.,
RA Martienssen R., McCombbe W.R., Wilson R.K., Muller B., Marra M.,
RA Martienssen R., McCombbe W.R., Wilson R.K., Murphy G., Bancroft I.,
RA Martienssen R., McCombbe W.R., Wilson R.K., Murphy G., Bancroft I.,
RA Martienssen R., McCullagh B., Robben J., Stiekema W., Pohl T.,
RA Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,
RA Ramsperger U., Wedler H., Balke K., Wedler E., Peters S.,
RA Van Staveren M., Dirkse W., Mooilman P., Klein Lankhorst R.,
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ACT_SITE
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine-protein kinase CTR1 (EC 2.7.1.37).
CTR1 OR AT5G03730 OR F17C15_150.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTR1_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kieber J.J., Rothenberg M., Roman G., Feldmann K.A., Ecker J.R.; "CTR1, a negative regulator of the ethylene response pathway in Arabidopsis, encodes a member of the raf family of protein kinas Cell 72:427-441(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-cv. Columbi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-cv. Columbia; TISSUE-Seedling;
MEDLINE-93161417; PubMed-8431946;
                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-cv. Columbia;
MEDLINE-21016721; Pu
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342
212
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D -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 236.5;
Pred. No. 1.9
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647

DERRRLSMAYDVAKGMNYLHNRNPPIVHRDLKSPNLL----

-VDKKYTVKVCDFGLSRLK

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72

591

15

SEFRQEASMLHALQHPCIVALIGISIHP--LCFALELAPLSSLNTVLSEN-ARDSSFIPL

NEFLREVAIMKRLRHPNIVLFMGAVTQPPNLSIVTEYLSRGSLYRLLHKSGAREQ-----L

GHMLTQKIAYQIASGLAYLHKKN--IIFCDLKSDNILVWSLDVKEHINIKLSDYGISR--

Matches Query Match

Local

Similarity

45;

Migmatches

56;

Gaps

10;

Score 236; DB 1; Pred. No. 4.2e-09; 5; Migmatches 75;

Length

SEQUENCE

821 AA;

90306 29.0%;

₹,

2922D3DCD0CC15BC CRC64;

TREATED PHENOTYPE.
D->E: IN CTR1-1; EXHIBITS
TREATED PHENOTYPE.

ETHYLENE. ETHYLENE

EXHIBITS

MUTAGEN

MUTAGEN

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PROTEIN KINASE.

ATP (BY SIMILARITY

ATP (BY SIMILARITY

BY SIMILARITY.

E->K: IN CTR1-4;

(BY SIMILARITY).
(BY SIMILARITY).

DOMAIN

DOMAIN

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796

-PSFATIM

762

AVGFKCKRLEIPRNLNP

ALGH--HQLQIAKKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQMK

-QVAAIIEGCWTNEPWKR-

795

QSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLSGQRP------

**ASTFLSSKSAAGTPEWMAPEVLRDEPSNEKSDVYSFGVILWELATLQQPWGNLNPAQVVA** 

235

DPTFATFM

242 802

702

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InterPro; IPRO00719; Euk_pkinase.
InterPro; IPRO04040; STY_pkinase.
InterPro; IPRO02490; Ser_thr_pkinase.
InterPro; IPRO02290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00221; STYKC; 1.
SMART; SM00221; STYKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weitzenegger T., Bothe G., Rose M., Haur W., Weitzenegger T., Bothe G., Rose M., Lamberth S., Villarroel R., Gielen J., Ardiles W., Bents O., Lemcke K., Kolesov G., Mayer K.F.X., Rudd S., Schoof H., Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.F.; Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is the second the the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the second the secon
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the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 408:823-826(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP + a protein = ADP + a phospho TISSUE SPECIFICITY: EXPRESSED IN BOTH SEEDLINGS AND A MISCELLANBOUS: CTRI MUTANTS DISPLAY ETHYLENE-TREATED RESULTING IN PLANTS WITH SMALL, UNEXPANDED LEAVES AND COTYLEDON GROWTH IS IMPAIRED.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL162506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L08789; AAA32779.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L08790; AAA32780.1;
                                                        135
551
557
578
596
                                                                                                                                                                                                                                                              Serine/threonine-protein
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                                                        141
169
809
565
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596
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                                                                                                                                                                                                                                   POLY-GLY
                                                                                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                              kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP + a phosphoprotein SEEDLINGS AND ADULT PL
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                                                                                                                                                                                                                                                           ATP-binding
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01-MAR-1989
15-JUN-2002
                                                                                                                        NP_BIND
BINDING
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Novel protein-tyrosine kinase cDNAs related to cloned using anti-phosphotyrosine antibody."; oncogene 3:521-527(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLK_RAT P09760;
                                                                                                              SEQUENCE
                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as modified and this statement is not re entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X13412; CAA31778.1; PIR; S04328; S04328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tyrosine-protein kinase FLK (EC 2.7.1.112) (Fragment).
                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILARITY: BELONGS TO
                         105
                                                                                                                                                                                                                                                                                 SMART; SM00219;
                                                                                                                                                                                                                                                                                            roDom; PD000001; Euk_pkinase; roDom; PD000093; SH2; 1.
                                                                                                                                                                                                                                                                                                         ProDom; PD00000
                                                                                                                                                                                                                                                                                                                                                                           ISSP; P11362; 1FGK.
InterPro; IPR000719; Euk_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    etwin K., Yee S.P., Pawson T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94167102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat)
                                                                                                                                                                                                                             ROSITE; PS50001; PSSITE; PS50002;
                                                                                                                                                                                                                                                                                                                                                       nterPro; IPR001452;
                                                                                                                                                                                                                                                                                                                       fam; PF00069;
                                                                                                                                                                                                                                                                                                                                                                   nterPro; IPR000980;
   74
                                          16 EFRQEASMLHALQHPCIVALIGISI--HPLCFALELAPLSSLNTVLSENARDSSFIPLGH
                                                                             Local
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MLTQKIAYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKLSDYGISRQSFHEG
                     KFLQEAKILKQYDHPNIVKLIGVCTQRQPVYIIMELVPGGDFLSFLRKRKDELKLKQL--
                                                                                                                                                                                                                   ferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
la; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                   Similarity
72; Conserv
                                                                                                                                                                                                                                                                                                                                          IPR001245; Tyr_pkinase
                                                                                                            1
64
70
92
185
215
                                                                   Conservative
                                                                                                                                                                                                              Tyrosine-protein kinase; Phosphorylation; ATP-binding;
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                                                                                                                                                                                                                          07; PROTEIN_KINASE_ATP;
09; PROTEIN_KINASE_TYR;
11; PROTEIN_KINASE_DOM;
11; SH2; PARTIAL.
102; SH3; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                      pkinase; 1.
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215
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                                                                                                            37104 MW;
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                                                                                                                                   PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                           Score 235.5;
Pred. No. 1.
                                                                                                            D7BA8BDE50C3EAC1 CRC64;
                                                                                                                                                                              SH2 (PARTIAL)
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                                                                Mismatches
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                                                               1.3e-09;
hes 82;
                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASES. FES/FPS
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                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restrictions
                                                                                       323;
                                                                31;
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RESULT 13
SRK1_SPOLA
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01-NOV-1995
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE-92334872; PubMed-1378585;
MEDLINE-92334872; PubMed-1378585;
Ottille S., Raulf F., Barnekow A., Hannig G.
"Multiple src-related kinase genes, srkl-4,
Spongilla lacustris.";
                                                                                                                                                                                                                                                              EMBL; X61601; CAA43798.1; -. HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                     entities requires a license agreement or send an email to license@isb-sib.cl
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Elbetween the Swiss Institute of Bioinformatics.
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Haplosclerida; Spon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
15-JUN-2002 (Rel. 41, Last ann
Tyrosine-protein kinase SRK1 (
                                                                                                                         ProDom;
                                                                                                                                     ProDom;
                                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oncogene 7:1625-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spongilla lacustris (Freshwater sponge).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P42686;
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                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           SÜBCELLULÄR LÖCATION: Cytoplasmic (Probable)
ALTERNATIVE PRODUCTS: 2 isoforms; SRK1 and S
produced by alternative splicing.
SIMILARITY: BELONGS TO THE TYR FAMILY OF PRO
                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ygene 7:1625-1630(1992).
CATALYTIC ACTIVITY: ATP + a protein tyrosine =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tyrosine phosphate
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                                                                                                                                                                                                                IPR001245;
                                                                                                                                                                                                                            IPR001452;
                                                                                                                                                                                                                                                                                                     email to license@isb-sib.ch)
                                                                                                                                    01; Euk_pkinase;
                                                                                                                                                                        pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         szoa; Porifera; Demospongiae;
Spongillidae; Spongilla.
                                                                                                                                                  ; TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                      CONTAINS 1 SH3 DOMAIN.
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41, Last annotation update)
kinase SRK1 (EC 2.7.1.112).
                                                                                                                                                                                                                                                 Euk_pkinase
                                                                                                                                                                                                            Tyr_pkinase
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                                                                                                                                                                                                                                                                                                                              Usage
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PROSITE; PS00107; PROTEIN\_KINASE\_ATP; PROSITE; PS00109; PROTEIN\_KINASE\_TYR; PROSITE; PS50011; PROTEIN\_KINASE\_DOM;

SH2;

PROSITE; PS50002;

Tyrosine-protein kinase; ATP-binding; SH2 domain;

SMART; SM00326; SMART; SM00219; SMART: SM00252;

ProDom;

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Best Local S
Matches 70
      Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtls K.C., Busam D.A., Butler H., Caddeu E., Center A., Chandra I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
BINDING
ACT_SITE
SEQUENCE
                                                                                                                                                                     STRAIN-Berkeley;
MEDLINE-20196006;
                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                           Thermond P., Busson D., Guillemet E., Terracol R., Tricoire H., Lamour-Isnamolecular organisation and expression
                                                                                                                                                                                                                                                                                                     STRAIN-Oregon-R; TISSUE-Ovary, Er
MEDLINE-94206843; PubMed-8155575;
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Mandibulata;
Insecta; Pterygota; Neoptera; Endopterygota;
Muscomorpha; Ephydroidea; Drosophilidae; Dros
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUSE_DROME STANDARD; PRT; 805 AA P23647; Q9YWR7; Q27412; Q26346; Q26347; Q1-NOV-1991 (Rel. 20, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                               organisation and expression pattern of of Drosophila melanogaster."; 44:65-80(1993).
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122
240
246
268
359
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 Cawley
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                    SPECIFICITY
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(EC 2.7.1.-).
                                                                                                                                                                                                                                                                                      Limbourg-Bouchon
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.5e-09;
                                                                                                                                                                                                                                                                                                                                                                            ata; Pancrustacea; Hexapoda;
ota; Diptera; Brachycera;
Drosophila.
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ter A., Chandra
Davies P.,
                                                                                                                                                                                                                                                           segment polarity
                                                                                                                                                                                                                                                                                        В.,
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EMBL; AE003509; AAF48871.1; -.
EMBL; S69165; AAB29840.1; -.
EMBL; S69166; AAB29841.1; -.
EMBL; X55759; CAA39285.1; -.
PIR; S11380; S11380.
HSSP; Q00534; 1BI8.

FlyBase;

; FBgn0001079; c; IPR000719; E c; IPR002290; S

Euk\_pkinase.
Ser\_thr\_pkinase

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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.
Dorbin K.J., Evangelista C.C., Ferraz C., Ferrara S., Fleischmann W.
RA Posler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., Linn X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.
RA McNunt S.M., Moy M., Murphy B., Murphy L., Murphy D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purl V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Globs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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                                                                                       entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Preat T., Therond P., Lamour Isnard C., Limbourg-Bouchon B.,
Tricoire H., Erk I., Mariol M.-C., Busson D.;
"A putative serine/threonine protein kinase encoded by the segment-
polarity fused gene of Drosophila.";
Nature 347:87-89(1990).

"I successful the serine/Threonine-Protein Kinase, Maternally
"I revoluted for Correct Patterning in the Posterior Part of Each
EMBRYONIC METAMERE. MAY BE INVOLVED IN CONTROL OF CELL DIVISION
DURING METAMORPHOSIS AND OVARIAN DEVELOPMENT. MAY INTERACT WITH
                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      de Pab
Dodson
                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-155 FROM N.A., AND MEDLINE=94140077; PubMed=8307322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90370097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-273 FROM N.A., AND MEDLINE-90370097; PubMed-2168522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics 135:1047-1062(1993).
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                                                                                                                                                                                                                                                                                                         LOW EXPRESSION IS PRESENT IN MALES, LARVAE AND FUFAE. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
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X80468; CAA56640.1; -. L34782; AAA28552.1; -.
                                                                                       s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Segmentation polarity protein; Developmental protein; Serine/threonine-protein kinase; ATP-binding.
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T: IN FU-H63.
> M (IN REF. 2).
> L (IN REF. 1).
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RESULT 15
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Nishisho I., Nakamura Y., Miyoshi Y., Miki Y., Ando H., Horii A.,
Koyama K., Utsunomiya J., Baba S., Hedge P., Markham A., Krush A.J.,
Petersen G., Hamilton S.R., Nilbert M.C., Levy D.B., Bryan T.M.,
Preisinger A.C., Smith K.J., Su L.-K., Kinzler K.W., Vogelstein B.;
"Mutations of chromosome 5q21 genes in FAP and colorectal cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                            the European Bioinformatics Institute. Thuse by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE-91117224; PubMed-1990274;
Hao Q.-L., Ferris D.K., White G., Heisterkamp N.,
"Nuclear and cytoplasmic location of the FER tyro:
Mol. Cell. Biol. 11:1180-1183(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94067791; PubMed=8247543;
Lee S.-T., Strunk K.M., Spritz R.A.;
"A survey of protein tyrosine kinase mRNAs expressed in normal human
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine -
                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT LEU-439
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SUBCELLULAR LOCATION: CYTOPLASMIC
                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation.
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tyrosine kinase.";
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EMBL; J03358; AAA61190.1; PIR; A31943; TVHUFE.

entities requires a

an email to license@isb-sib.ch

license agreement (See http://www.isb-sib.

for

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US-09-757-982-5
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-757-982-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09757982 Patent No. US20020094559A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                             SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL CSAPK-1 NUCLEIC FILE REFERENCE: MNI-050 CURRENT APPLICATION NUMBER: US/09/757,982 CURRENT FILING DATE: 2001-01-10 PRIOR APPLICATION NUMBER: 09/163,115
                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09904389
Patent No. US20020129404A1
                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/218,307 PRIOR FILING DATE: 2000-07-14
                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/904,389
CURRENT FILING DATE: 2001-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1998-(NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                APPLICANT: Schuster, Debra K.
TITLE OF INVENTION: CTR1 HOMOLOGUE FROM MELON
FILE REFERENCE: 4257-0029.30
                                                                                                                                                                                                                                                            APPLICANT: Clendennen, Stephanie K. APPLICANT: Schuster, Debra K.
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                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                    NUMBER OF SEQ ID NOS:
                                   LENGTH: 850
TYPE: PRT
              ORGANISM: Cucumis melo
EATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 EMDMDHIMTW--ATDVAKGMHYLHMEAPVKVIHRDLKSRNVVIAADGV-----LKICDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                           267 TSLPDKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 AMKNESEFROEASMLHALQHPCIVALIGISIHPLCFAL--ELAPLSSLNTVLSENARDSS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 27.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISROSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLSGQRPALGHHQLQ 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IAKKLSKGIRPVLGQPEEVQF-----RRLQALMMECWDTKPEKRPLALSVVSQMKDPTFA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- VVEKNERLTIPSSCPRSFAELLHQCWEADAKKRPSFKQIISILESMSND 266
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AFR: 09/163,115
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27.9%; Pred. No. 3.1e-11;
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; NAME/KEY: VARIANT
; LOCATION: (154)...(
; OTHER INFORMATION:
US-09-904-389-2
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US-09-974-298-129
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Best Local Similarity
Matches 69; Conserv
                                                                                                                        APPLICANT: Chen, Hu
                                                                                                                                                              Sequence 129, Application US/09974298 Patent No. US20020156263A1
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 60/238,331
PRIOR FILING DATE: 2000-05-10
                                                                                  TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER FILE REFERENCE: PA-0037 P
                                                                                                                                                                                                                                                                                                             189 LS-KGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQMKDPT 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  617 NEFLREVAIMKSLRHPNIVLFMGAVTKPPNLSIVTEYLSRGSLYRLLHK----SGVKDID 672
                                                                                                                                                                                                                                                                                      788 VGFKGKR--LDIPRDVN-PKLASLIVACWADEPWKRPSFSSIMETLKPMT 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                    673 ETRRINMAFDVAKGMNYLHRRDPPIVHRDLKSPNLL-----VDKKYTVKVCDFGLSRLKA 727
                                                                                                                                                                                                                                                                                                                                                                    728 RTFLSSKSAAGTPEWMAPEVLRDEPSNEKSDVYSFGVILWELATLQQPWCNLNPAQVVAA 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 SEFRQEASMLHALQHPCIVALIGISIHP--LCFALELAPLSSLNTVLSENARDSSFIPLG 72
                                                                                                                                                                                                                                                                                                                                                                                                          HE--GALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLSGQRPALGHHQLQIAKK 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMLTQKIAYQIASGLAYLHKKN--IIFCDLKSDNILVWSLDVKEHINIKLSDYGISRQSF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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735
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                                                                                                                                                                                                                                                                       47
                                                                                                                                                                                                                                                                                                                                           2 LRHLRATDAMKNESEFRQEASMLHALQHPCIVALIG--ISIHPLC-----
                                                                                                           YGMVLYELLS-GQRPALGHHQLQIAKKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPE 221
                                                                                                                                                                                                                                                                   LELAPLSSLNTVLSENARDSSFIPLGHMLTQKIAYQIASGLAYLHKKNIIFCDLKSDNIL 106
RRPRFKDIHVRLRSWEGLSSHTSSTTPSGGNATTQTTSLSASPVSNLSNPRYPNYM----
                                                                         FGVVLWEIFSFGLQPYYGFSNQEVIEMVRK--RQLLPCSEDCP-PRMYSLMTECWNEIPS
                                                                                                                                                   ----IGEQLHVKISDLGLSREIYSADYYRVQSKSLLPIRWMPPEAIMYGKFSSDSDIWS
                                                                                                                                                                                         VWSLDVKEHINIKLSDYGISRQSFHEGALGVEGTP----GYQAPEIRPRIVYDEKVDMFS 162
                                                                                                                                                                                                                               IMRSPHSDVGCSSDEDGTVKSSLDHGDFL--HIAIQIAAGMEYLSSHFFVHKDLAARNIL
                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                     -----LALSVVSQMKDPTFATFMYELC
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                                                                                                                                                                                                                                   622
                                       246
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US-09-974-298-129

FEATURE:
NAME/KEY: misc\_feature ORGANISM: Homo sapiens

OTHER INFORMATION: Incyte ID No. US20020156263A1 1331526CD1

Query Match

Local Similarity

25.3%;

Score 238; DB 9; Pred. No. 2.1e-10;

Length 937;

10

NUMBER OF SEQ ID NOS: 19
SOFTWARE: PERL Program
SEQ ID NO 129
LENGTH: 937
TYPE: PRT

ID NOS: 194

US-09-977-261-6

Query Match

Local Similarity es 75; Conserv

Conservative.

49;

6.4%; 30.5%;

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240 TEMYEL

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FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
OTHER INFORMATION: kinase 3
5-09-977-269-6
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PRIOR FILING DATE: 1994-04-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
15Q ID NO 6
LENGTH: 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/977, 269
CURRENT FILING DATE: 2001-10-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 VDNEDIYESRHEIKLPVKWT----APEAIRSNKFSIKSDVWSFGILLYEIITYGKMPYSG 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327 -HLTQQVDMAAQVASGMAYLESRNYIHRDLAARNVL----VGEHNIYKVADFGLARVFK 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LICANT: SURES, IRMINGARD
LE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 NDFLREAQIMKNIRHPKLIQLYAVCTLEDPIYIITELMRHGSLQEYL-QNDTGSKI---- 326
                                                                                                                                                                                                                                                                                                                                               15 SEFRQEASMLHALQHPCIVALIGISI--HPLCFALELAPLSSLNTVLSENARDSSFIPLG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 HMLTQKI--AYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKLSDYGISR--- 127
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                                     MTGAQVIQMLAQNYR - - LPQPSNCP - QQFYNIMLECWNAEPKER - -
                                                                          HHQLQIAKKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQMKDPTFA 239
                                                                                                                                                                                                              -HLTQQVDMAAQVASGMAYLESRNYIHRDLAARNVL-----VGEHNIYKVADFGLARVFK 380
                                                                                                                                                                                                                                                          HMLTQKI--AYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKLSDYGISR--- 127
                                                                                                                                                                                                                                                                                                      NDFLREAQIMKNLRHPKLIQLYAVCTLEDPIYIITELMRHGSLQEYL-QNDTGSKI---- 326
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                                                                                                                                                    -----OSFHEGALGVEGTPGYQAPEIRPRIVYDEKYDMFSYGMYLYELLS-GQRPALG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLS-GQRPALG 179
                                                                                                                                                                                                                                                                                                                                                                                       Score 243.5; Db ...
Pred. No. 3.3e-11;
Pred. No. 77;
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Pred. No. 3.
                                                                                                                        APEAIRSNKFSIKSDVWSFGILLYEIITYGKMPYSG 436
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                                                                                                                                                                                                                                                                                                                                                                                              Indels 45;
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                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 30.5%;
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                                                                                                                                               327
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                                                     381 VDNEDIYESRHEIKLPVKWT----APEAIRSNKFSIKSDVWSFGILLYEIITYGKMPYSG 436
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                                                                                                                                                                                                                                                                               15 SEFRQEASMLHALQHPCIVALIGISI--HPLCFALELAPLSSLNTVLSENARDSSFIPLG 72
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FILING DATE: 1996-MAY-23
APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/ÄGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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HHQLQIAKKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQMKDPTFA 239
                                                                                                                                                                      HMLTQKI--AYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKLSDYGISR--- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Genentech,
                                                                                                                                          -HLTQQVDMAAQVASGMAYLESRNYIHRDLAARNVL-----VGEHNIYKVADFGLARVFK 380
                                                                                                                                                                                                                                   NDFLREAQIMKNLRHPKLIQLYAVCTLEDPIYIITELMRHGSLQEYL-QNDTGSKI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 40,378 REFERENCE/DOCKET NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/982,610 FILING DATE: 17-Oct-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lee, Wendy M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES R OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION DATA:
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                                                                                            -QSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLS-GQRPALG 179
                                                                                                                                                                                                                                                                                                                        Conservative
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Goeddel, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         William
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                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
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Pred. No. 3.3e-11;
9; Mismatches 77;
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482 240

TLRWKL 487 TEMYEL 245

US-09-977-269-6

Sequence 6, Application US/09977269 Patent No. US20020082037A1

APPLICANT: ULLRICH, AXEL

GISHIZKY, MIKHAIL

2001-10-

INFORMATION:

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327

73

381

272

Query Match

6.4%;
Local Similarity 30.5%;
es 75; Conservation

49;

ORGANISM: Unknown Organism

133-	
; Sequence 2, Application US/10143133 ; Publication No. US20020197658A1	
<pre>; GENERAL INFORMATION: ; APPLICANT: Yoganathan, .Thillainathan</pre>	
ICANT: Del	Protein Kinase and Its Use
CURRENT APPLICATION NUMBER: US/10/143 CURRENT FILING DATE: 2002-05-09	,133
APPLICATION NUMBER: 6 FILING DATE: 2001-05-	
FastSE	4.0
; LENGTH: 847 ; TYPE: PRT ; ORGANISM: Homo saplen rs.10-143-133-2	
ry Match t Local Simi	260.5; DB 9; Length 847; No. 3e-12;
es 162; Conservative 84;	ches
18	DSSFIPLGHML
TOO MUNICIPAL MATERIA	44
Qy 76 TQXIAYQIASGLAYLHXXNIIFCDLXSDNILVW-	
130 FH	1 1
275	HKTTQMSAAGTYAWMAPEVIKASTFSKGSDVWSFGVLLWELL/TGEVPYRGIDCLAVAYGV 334
QY 187KKLSKGIRPVLGQPEEVQFRRLQALM	KKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQMKDPTFATFMYE 244
AVNKLTLPIPSTCPEPFA	w
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QY 304 QRSLWTATEDQKIYIYTLKGMCPLNTPQC	LWTATEDQKIYIYTLKGMCPLNTPQQALDTPAVVTCFLAVPVIKKNSYLVLAGLADG 363
Db 421 EEELTRAAREORSQA	EQLRREHLLAOW 448
Qy 364 LVAVFPVVPVVRGTPK	RGTPKDSCSYLCSHTANRSKFSIADE 397
398	AMEVVNSGSEVWYSNGPGLLVID
Db 497 DFKHRITVQASPGLDRRRNVFEVGPGDSPTFPRFRAIQLEPAEPG	PRFRAIQLEPAEPG-QAWGRQSP 549
COC TRANSPORT	ACWAWGFSSFRFGEAQNGRRRSRMLEAIW
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25 SIADVSIMYSEELGTQILIHQESLT	SYSSSPPRQAARSPSSLPSSP
Db 645 LLRGTALLASLGLGRDL	-QPPGGPGRERGESPTTPPTPTPAPCPTEP 690
QY 577 ASSSSVPFSTDCEDSDMLHTP	GAASDRSEHDLTPMDGETFS 617
Db 691 PPSPLICFSLKTPDSPPTPAPLLIDLGII	VCOBCAKCBBEFFBBCCTVCBBBCTCBC 748

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OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
OTHER INFORMATION: kinase 3
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OTHER INFORMATION: Description of Unknown Organism: Megakaryocyte
                                                                                                                                                                                                                                                                                URRENT APPLICATION NUMBER: US/09/977,261
                                               DRGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                             PLICANT: SURES, IRMINGARD
TLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
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TLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES
                                                                                                    ENGTH: 505
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lication No. US20030054527A1
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Pred. No. 3.3e-11;
9; Mismatches 77;
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PRIOR APPLICATION NUMBER: US 09/345,473
PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 82
SOFTWARE: FastSFQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 394
TYPE: NOT-20
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US-09-862-027-19
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                                                   : ORGANISM: Homo US-09-862-027-19
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                                                                                                                                                                                                                           Sequence 19, Application US/09862027 Patent No. US20020142428A1 GENERAL INFORMATION:
 Best Local Similarity 31.3 Matches 78; Conservative
                           Query Match
                                                                                                                                                                                       APPLICANT: Hodge, Martin R.
TITLE OF INVENTION: NO. US20020142428A1el Kinases and
FILE REFERENCE: 35800/234862
                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/862,027 CURRENT FILING DATE: 2001-05-21
                                                                          LENGTH: 39
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                               SDRSEHDLTPMDGETFSQHLQAVKILAVRDLIWVPRRGGDVIVIGLEKDSEAQRGRVIAV
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            7.2%;
42;
Score 275.5; DB 10 Pred. No. 6.6e-14; 2; Mismatches 92;
                        DB 10;
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; NAME/KEY: VARIANT
; LOCATION: (1)...(1036)
; OTHER INFORMATION: Xaa
US-10-014-882-2
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US-10-014-882-2
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.9%; Score 263; DB 12; Best Local Similarity 32.4%; Pred. No. 2.6e-12; Matches 81; Conservative 42; Mismatches 91
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TITLE OF INVENTION: No. USZO20107384A161
FILE REFERENCE: LEX-0279-USA
CURRENT APPLICATION NUMBER: US/10/014,882
CURRENT FILING DATE: 2001-12-11
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TYPE: PRT
ORGANISM: homo
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PRIOR FILING DATE: 2000-12-11
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PSFALILEQL 398
                                PLALSVVSQM 233
                                                                        ELLTGEVPYRGIDGLAVAYGVAVNKLTLPIPSTCPEP--
                                                                                                                                                                                  EHINI-----KLSDYGISRQSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLY 168
                                                                                                                                                                                                                      DPRAPGPRRARRIP-PHVLV-NWAVQIARGMLYLHEEAFVPILHRDLKSSNILL--LEKI
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                                                                                                           ELLSGQRPALGHHQLQTA----KKLSKGTRPVLGQPEEVQFRRLQALMMECWDTKPEKR
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-132-382-8
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US-10-132-382-8
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                                                                                                                               Query Match
                                                                                                                                                                                                                               SEQ ID NO 8
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS FILE REFERENCE: SCH-1811
                                                                                                                                                                                                                                                                                                                                               APPLICANT: WEISS,
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                                                                                                               Local Similarity
                                                             1 MLRHLRATDAMKNESEFRQEASMLHALQHPCIVALIGISIHPLCFALELAPLSSLNTVLS 60
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ENARDSSFIPLGHMLTQKIAYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKL 120
                              MLRHLRATDAMKNFSEFROEASMLHALQHPCIVALIGISIHPLCFALELAPLSSLNTVLS 1386
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                                                                                                              94.5%;
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                                                                                              Score 3574.5; DB 9;
Pred. No. 1.3e-274;
0; Mismatches 1;
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1 MLRHLRATDAMKNFSEFRQEASMLHALQHPCIVALIGISIHPLCFALELAPLSSLNTVLS 60

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                                           ; TYPE: PRT; ORGANISM: H
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US-10-132-382-4
                                                                                      TITLE OF INVENTION: MEMBRANE RECEPTORS FOR FILE REFERENCE: SCH-1811 CURRENT APPLICATION NUMBER: US/10/132,382 CURRENT FILING DATE: 2002-04-26 NUMBER OF SEQ ID NOS: 26 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 4
                                                                                                                                                                     Sequence 4, Application US/10132382
Publication No. US20030045699A1
GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
         Query Match
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Best Local Similarity 94.5
Matches 687; Conservative
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CURRENT APPLICATION NUMBER: US/10/132_382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 2013
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                             Sequence 2, Application US/10132382
Publication No. US20030045699A1
GENERAL INFORMATION:
APPLICANT: WEISS, BERTRAM
TITLE OF INVENTION: MEMBRANE RECEPTORS
FILE REFERENCE: SCH-1811
                                                                                 Query Match 93.5%;
Hest Local Similarity 94.5%;
Matches 687; Conservative
                                           1326
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                                        EACTRKR 727
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                                                                                 Score 3574.5; DB 9;
Pred. No. 1.3e-274;
0; Mismatches 1;
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Sequence 30, Appli
Sequence 4, Appli
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Sequence 25, Appl
Sequence 26, Appl
Sequence 27, Appl
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Sequence 4, Appl
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Sequence 18, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 19, Appl
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Sequence 9, Appl
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Match Length
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.: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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.: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
.: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
.: /cgn2_6/ptodata/1/pubpaa/USU8_PUBCOMB.pep:*
.: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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                                                                                         SUMMARIES
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US-09-836-392-21

ALIGNMENTS

Sequence 21, Application US/09836392 Patent No. US20020173458A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.

TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptic TITLE OF INVENTION: Antibodies
FILE REFERENCE: PT020P1
CURRENT APPLICATION NUMBER: US/09/836,392
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: PT7/US00/28066
PRIOR FILING DATE: 2001-01-11
PRIOR PILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 60/159,542
PRIOR FILING DATE: 1999-10-15
PRIOR FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/165,914
PRIOR APPLICATION NUMBER: 60/165,914
PRIOR APPLICATION NUMBER: 60/189,027
PRIOR APPLICATION NUMBER: 60/189,027

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Sequence 235, App	Sequence 197, App	Sequence 5, Appli	Sequence 29, Appl	Sequence 129, App	Sequence 2, Appl1	Sequence 5, Appli	Sequence 20, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 19, Appl	Sequence 4, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 6, Appli	Sequence 21, Appl		Description	•	
Db 121 SDYGISRQSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLASGQRFALGH 100		Qy 121 SDYGISRQSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLSGQRFALGH 100		Db 61 ENARDSSFIPLGHMLTQKIAYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIAL 140		Qy 61 ENARDSSFIPIGHMLTQKIAYQIASGLAYLHKKNIIFCDLKSUNILVWSLUVKEHININL 140		Db 1 MLRHLRATDAMKNESEFRQEASMLHALQHPCIVALIGISIHFLCFALELAFLSSUNIVLS OV		Qy 1 MIRHIRATDAMKNE'SEFRQEASMHALQHE'CIVALIGISIHELCE ALELIAFISISHIY VIS		Matches 728; Conservative 0; Mismatches 0; indets 0; waps	Best Local Similarity 100.0%; Pred. No. /e-295;	Query Match 100.0%; Score 3822; DB 3; Length /20;		US-09-836-392-21	; ORGANISM: Homo sapiens	; TYPE: PRT	; LENGTH: /28	; SEQ ID NO 21	; SOFTWARE: PatentIn Ver. 2.0	; NUMBER OF SEQ ID NOS: 34

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35774.5 35774.5 35774.5 2774.5 2774.5 2443.5 263

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Kinase; SH3 domain.
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SEQUENCE 1066 AA;
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PKINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase; 1.
ProDom; PD00066; SH3; 1.
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SMART; SM00219; TYTKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50002; SH3; 1.
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InterPro; IPRO01245; Tyr_pkinase.
                                                                                                                                                                                                          231 GDLSNKI-LKITDFGLAREWHRTTKMSAAGTYAWMAPEVIRASMFSKGSDVWSYGVLLWE 289
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343 SFTNILDQL 351
                                                                                                                                        170 LLSGQRPALGHHOLQIA-----KKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRP 224
                                                                                                                                                                                                                                             111 -DVKEHINIKLSDYGISRQSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMYLYE 169
                                                                                                                                                                                                                                                                                                                    182 -----GKRIPPDILVNWAVQIARGMNYLHDEAIVPIIHRDLKSSNILILQKVEN 230
                                                      225 LALSVVSQM 233
                                                                                                       290 LLTGEVPFRGIDGLAVAYGVAMNKLALPIPSTCPEP--
                                                                                                                                                                                                                                                                                                                                                     61 ENARDSSFIPLGHMLTQKI----AYQIASGLAYLHKK---NIIFCDLKSDNILVWSL--- 110
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Search completed: April 8, 2003, 10:25:30 Job time : 111 secs

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PRESULA RESULA                                                                                                                                                                                                                                                STRAIN=CV. COLUMBIA;

MEDDINE=20083487; PubMed=10617197;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldbyum T.V.,

RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,

RA Cronin L.A., Shen M., Vanaken S.E., Umáyam L., Tallon L.J., Gill J.E.,

RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,

RA Salzberg S.L., Fraser C.M., Venter J.C.;

RT "Sequence and analysis of chromosome 2 - "

RI thaliana.";
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Matches 78
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfan; PF00069; pkinase; 1.
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01-JAN-1998 (
01-MAY-2000 (
01-MAR-2002 (
                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eddicotyledons; core eu
eurosids II. Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PS50011; PROTEIN_KINASE_DOM;
PROSITE; PS00108; PROTEIN_KINASE_ST; 1
SEQUENCE FROM N.A
                                                                    Submitted
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                                                                                                                                                                                                                                         Nature 402:761-768(1999).
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(TEMBLIEL. 13, Last sequence update)
(TEMBLIEL. 20, Last annotation updat)
1 61.5 kDa protein.
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45958 MW; 54F986CED934353B
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Pred. No. 1e-1
38; Mismatches
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                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Pr
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                             Q9H2N5;
                                       McNee J.J., Dower S.K., Guesdon F.;
"cDNA sequence and gene organisation of mixed
submitted (APR-2000) to the EMBL/GenBank/DDBJ
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; AF251442; AAG44591.1;
HSSP; P29355; 1SEM.
                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
Mixed lineage kinase MLK1 (Fragment).
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Prodom; PD000001; Euk_pkinase; 1.

SMART; SM00221; STYKC; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM;

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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Yamamura Y., Yu G., Yu S., Bowser L., Carninci P., Chen H.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-New
Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M.,
Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., So
Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-2001) to the EMBL/GenBank/DDBJ-1-SIMILARITY: BELONGS TO THE SER/THR FAMILY
                                                                                                                                                                                        SEQUENCE FROM N.A.
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  InterPro;
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IPR000719;
IPR002290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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AAL49781.1; -.
                                                                                                                                                                                                                                                          Chordata;
Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61509 MW; E74F30F60D91F426 CRC64;
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.S., Quach H.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ACT.
; Euk_pkinase.
; Ser_thr_pkinase.
; STY_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene At2g17700 (GI:15227883).";
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                                                                                                                                                                                                                                                             Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chang E.,
L., Tang (
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Kamiya A., Karlin-Neumann
                                                                                                                                                                                                                                                          Vertebrata;
1; Hominidae;
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C., Toriumi
                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                 lineage kinase
databases.
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OF PROTEIN
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                                                                                                                                                                                                                                                                                   Euteleostom1;
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RESULT
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Best Local S
Matches 88
Q95UN8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mixed lineage kinase.

MLK2 OR DMLK OR CG2272.

Drosophila melanogaster (Fruit Tly).

Drosophila melanogaster (Fruit Tly).

Eukaryota; Metazoa; Arthropoda; Tracheata; He

Pterygota; Neoptera; Endopterygota; Diptera;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD000001; Euk_pkinase; 1.
ProDom; PD00066; SH3; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
PROSITE; PS50002; SH3; 1.
ATP-binding; Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sathyanarayana P., Tzivion (Submitted (AUG-2001) to the EMBL; AF416233; AAL08011.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           436
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Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interPro; IPR002290; Ser_thr_pkinase.interPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lyBase; FBgn0030018; Mlk2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CBI_TaxID=7227;
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                                                                                                       286
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Local Similarity 29.0%;
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                                                                                                       ΕVQ
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                                                                             RVQ
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                                                                                                                                                          KDPTFATFMYELCCGK----
                                                                                                                                                                                                              QRPALGHHQLQIAKKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQM
                                                                                                                                                                                                                                         QQKTLKITDFGLAREMYNTQRMSAAGTYAWMPPEVISVSTYSKFSDVWSYGVLLWELITG
                                                                                                                                                                                                                                                               ---NIKLSDYGISRQSFHEGALGVEGTPGYQAPEIRPRIVYDEKVDMFSYGMVLYELLSG
                                                                                                                                                                                                                                                                                                                                                IAHQTGEDDMQRMRDNVLQEAKLFWALKHENIAALRGVCLNTKLCLVMEYARGGSLNRIL
                                                                                                                                                                                    ETPYKGFDPLSVAYGVAVNTL-TLPIPKTCP-ETWGALMKSCWQTDPHKRPGFKEILKQL
                                                                                                                                                                                                                                                                                           AGK-----IPPDVLVNW--AIQIARGMNYLHNEAPMSIIHRDLKSSNVLIYEAIEGNHL
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                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -SIACSKFTLTPQESFHYMQECWRKEIAGVLHDLREKEKE--LRNKEEQLL
                                                                                                                                 SIACSKFTLTPQESFHYMQECWRKEIAGVLHDLREKEKE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tzivion G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase.
127511 MW;
                                                                                                                                                           QTAFFSSQ--
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EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                Score 288.5;
Pred. No. 3.
               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       66A7D7A6E75E116C CRC64;
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               1161
                                                                                                                                                           GQEYTVVFWDGKEESRNYTVVNTEKGLM
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a; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana A.;
databases.
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                 LRNKEEQLL
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Q94C42
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Best Local S
Matches 88
                                                                094C42;
094C42;
01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stronach B.E., Perrimon N.;

"Activation of the JNK pathway during dorsal crequires the mixed lineage kinase, slipper.";

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; AY045717; AAK98795.1;

FlyBase; FBgn0030018; Mlk2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel 19, C
01-DEC-2001 (TrEMBLrel 19, L
01-MAR-2002 (TrEMBLrel 20, L
01-MAR-2002 (TrEMBLrel 20, L
Mixed lineage protein kinase.
MLK2 OR SLPR OR CG2272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
PROSITE; PS50002; SH3; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 1161 AA; 128960 MW; DD6C7ABAC08ED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly)
                        Serine/thronine protein kinase.
Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Strep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ProDom; PD000001; Euk_pkinase; ProDom; PD000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00069; pkinase; 1. Pfam; PF00018; SH3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ephydroidea;
  Spermatophyta; Magnoliophyta; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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les 88; Conserv
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                                                                                                                                                                                                                                                         KDPTFATFMYELCCGK----'QTAFFSSQ---GQEYTVVFWDGKEESRNYTVVNTEKGLM
                                                                                                                                                                                                                                                                                                                       QRPALGHHQLQIAKKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQM
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                                                                                                                                                                                                                                                                                                                                                                                                                   SENARDSSFIPLGHMLTQKIAYQIASGLAYLHKK---NIIFCDLKSDNILVWSLDVKEHI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAHQTGEDDMQRMRDNYLQEAKLFWALKHENIAALRGVCLNTKLCLVMEYARGGSLNRIL
                                                                                                                                                                                                                                                                                               ETPYKGFDPLSVAYGVAVNTL-TLPIPKTCP-ETWGALMKSCWQTDPHKRPGFKEILKQL
                                                                                                                                                                                                                                                                                                                                                 QQKTLKITDFGLAREMYNTQRMSAAGTYAWMPPEVISVSTYSKFSDVWSYGVLLWELITG
                                                                                                                                                                                                                                                                                                                                                                                                     AGK-----IPPDVLVNW--AIQIARGMNYLHNEAPMSIIHRDLKSSNVLIYEAIEGNHL
                                                                                                                                                                                       451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FBgn0030018; Mlk2.
IPR000719; Euk_pkinase.
IPR002290; Ser_thr_pkinase.
IPR001452; SH3.
                                                                (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence up
(TrEMBLrel. 20, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophilidae; Drosophila
                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                           SIACSKETLTPQESFHYMQECWRKEIAGVLHDLREKEKE--LRNKEEQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128960 MW; DD6C7ABAC08EDA24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.0%;
               Streptophyta; Er
yta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 288.5;
Pred. No. 3.7
                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                 Embryophyta; Tracheophyta;
a; Poales; Poaceae; Pooideae;
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                                                                   on update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1161;
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C STRAIN-BERKELEY:

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

A Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,

A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

A Sutton G.G., Fortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

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A Sutton G.G., Fortman J.R., Jandell G., Nelson C.R., Miklos G.L.(

RA Haradoon R.C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.(

RA Haradoon R.C., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Berns B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra
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CG2272 protein
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Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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era; Muscomorpha;
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Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lux N., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McHison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinseck G.M., Weissenbäch J.,
RA Zheng X.H., Zhong F.N., Zaveri J.S., Zhan M., Zhang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhon X., Zhu S., Zhu X., Smith H.O.,
The genome sequence of Drosophila melanogaster.*;
CC --- SIMILARITY: BELONGS TO THE SEP/Mus
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Best Local S
Matches 88
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PRINTS; PR00109; TYRKINASE; 1.
PRODOM; PD000001; EUK_PK1NASE; 1.
PRODOM; PD000066; SH3; 1.
SMART; SM00325; SH3; 1.
SMART; SM00221; STYKC; 1.
SMART; SM0021; PROTEIN_KINASE_DOM; 1.
PROSITE; PS000108; PROTEIN_KINASE_ST; 1.
PROSITE; PS000108; PROTEIN_KINASE_ST; 1.
PROSITE; PS000108; SH3; 1.
ATP-binding; SH3 domain; Serine/threonin
SEQUENCE 1020 AA; 113701 MW; D48FDB9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0030018; Mlk2.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001452; SH3.
InterPro; IPR004040; STY_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00069; pkinase; Pfam; PF00018; SH3; 1.
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                  234
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                                                                                                                                                                                                                                                                                LRHLRATDAMKNESE-FRQEASMLHALQHPCIVALIGISIH-PLCFALELAPLSSLNTVL
                 KDPTFATEMYELCCGK--
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                                                                  SENARDSSFIPLGHMLTQKIAYQIASGLAYLHKK---NIIFCDLKSDNILVWSLDVKEHI 116
                                                                                                                QOKTLKITDFGLAREMYNTQRMSAAGTYAWMPPEVISVSTYSKFSDVWSYGVLLWELITG
                                                                                                                                                                                                                                                 IAHQTGEDDMQRMRDNVLQEAKLFWALKHENIAALRGVCLNTKLCLVMEYARGGSLNRIL
                                                                                                                                                                                                                                                                                                                88; Conser
                                               PYKGFDPLSVAYGVAVNTL-TLPIPKTCP-HTWGALWKSCWQTDPHKRPGFKEILKQL
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                 IPPDVLVNW -- AIQIARGMNYLHNEAPMSIIHRDLKSSNVLIYEAIEGNHL
                                                                                                                                                                                                                                                                                                                            7.5%;
                                                                                                                                                                                                                                                                                                                                                                                 ain; Serine/threonine-protein 113701 MW; D48FDB9C6639A08F
Qfaffssq---gqeytvvfwdgkeesknytvvntekglm
                                                                                                                                                                                                                                                                                                                58;
                                                                                                                                                                                                                                                                                                              Score 288.5;
Pred. No. 3e-1
58; Mismatches
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DOMAIN.
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S., Gelbart W.M., Glasser K.,
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                                                                                                                                                                                                                                                                                                              37;
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Dunn
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A Goldsmith A.D., Jiang P.X., Lee J.M., Ondera C.S., Quach H.L.,
A Tang C., Toriumi M., Yu G., Yu S., Bowser L., Carninci P., Chen H.,
A Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J.,
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A Kariin-Neumann G., Kawai J., Kim C., Koesema E., Lam B., Lin J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J., Kim J
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Best Local :
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 412 AA; 46083 MW; 644F35A90210D488 CRC64;
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ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00221; STYKC; 1.
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01-MAY-1999 (TIEMBLTel. 10, Cr
01-JUN-2002 (TIEMBLTel. 21, La
01-JUN-2002 (TIEMBLTel. 21, La
Hypothetical 46.0 kDa protein.
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Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen
Barnstead M.E., Mason T.M., Bowman C.L., Ronn
Carrera A.J., Creasy T.H., Buell C.R., Town C
Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82; Conservative
PD000001; Euk_pkinase; 1.; PS50011; PROTEIN_KINASE_DOM; 1.
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21, Last sequence up
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Pred. No. 4.4e-18;
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udicots; Rosidae;
                                                                                                                                                                                                                                                                       Tracy S.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00326; SH3; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00220; TyrKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
PROSITE; PS50002; SH3; 1.
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                             R--APGPRRARRIPPQVLVNWAVQIARGMLYLHEEAVVPILHRDLKSSNILL--LEKIEH
                                                                                                                                       SFIPIGHMLTQKI-----AYQIASGLAYLHKK---NIIECDLKSDNILVWSLDVKEH 115
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IPR002290; Ser_thr_pkinase.
IPR001452; SH3.
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)069; pkinase; 1.
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Pred. No. 5.3e
12; Mismatches
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1.5e-15;
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RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegvam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegvam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu K., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Nelson D.R., Nelson K., Sunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F. N., Zhong W., Zhong S., Yao Q.A.,
RA Zheng X.H., Zhong F. N., Zhong W., Zhang G., Zhao Q., Zheng L.,
RA Spier E., Spradling A.C., Shan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F. N., Zhong W., Zhong S., Yao Q., Zheng L.,
RA Zheng X.H., Zhong W., Zhong W., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong W., Zhong W., Zhong S., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Zhong W., Zhu X., Smith H.O.,
RA Spier E., Spradling A.C., Shan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Zhong W., Zhong Y.,
RA Zheng X.H., Zhong W., Zhong W., Zhong Y.,
RA Zheng X.H., Zhong W., Zhong W., Zhong Y.,
RA Zheng X.H., Zhong W., Zhong W., Zhong Y.,
RA Zheng X.H., Zhong W., Zhong W., Zhong Y.,
RA Zheng X.H., Zhong W., Zhong W., Zhong Y.,
RA Zheng X.H., Zhong W., Zhong W., Zhong Y.,
RA Zheng X.H., Zhong W., Zhong W., Zhong Y.,
RA Zheng Y., Ra Zhong Y., Zhong Y., Zhong Y.,
RA Zheng Y., Zhong Y., Zhong Y., Zhong Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50088; ANK_REPEAT; 1.
PROSITE; PS50197; ANK_REP_REGION; 2.
PROSITE; PS001017; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1
ANK repeat; ATP-binding; GTP-binding; Repeat;
Serine/threonine-protein kinase; Transferase.
Serine/threonine-protein kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodom; PD000001; Euk_pkinase;
SMART; SM00370; LRR; 5.
SMART; SM00370; LRR; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G. Wan J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
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Sutton G.G., Wortman J.R., Y
Brandon R.C., Rogers Y.-H.C.
Wan K.H., Doyle C., Baxter E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00449; RASTRNSFRMNG.
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George R.A., Lewis S.E.,
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IPR001806; Ras_trnsfrmng.
IPR002290; Ser_thr_pkinase.
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IPR000719; Euk_pkinase.
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92; LRR_out.
                                                                                                                                                                                                                                                                                               9.5%;
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Pred. No. 3.9e
99; Mismatches
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3.9e-21;
.ches 243;
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                                   EU Arabidopsis sequencing project;
Submitted (WAR-2000) to the EMBL/GenBank/DDBJ
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY
EMBL; AL161578; CAB79835.1; -
HSSP; P08631; 1AD5.
                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eu

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Lennard N., Quail M.,
Mewes H.W., Lemcke K.
                                                                                                                                                                                                                                                                            AT4G31170
                                                                                                                                                                                                                                                                                       Protein kinase-like
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                            nterPro;
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531; 1AD5.
IPRO00719; Euk_pkinase.
IPR002290; Ser_thr_pkir
IPR004040; STY_pkinase.
                                                                                                                                     (MAR-2000)
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation updat
ase-like protein.
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Ser_thr_pkinase
STY_pkinase.
                                                                                                                                   Harris B., Rajandream, Mayer K.F.X.;
to the EMBL/GenBank/DDE
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01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Similar to hypothetical protein FLJ23119.
Homo sapiens (Human).
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Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TTEMBLTel. 13, 01-OCT-2001 (TTEMBLTel. 18, 01-MAR-2002 (TTEMBLTel. 20, Hypothetical 130.7 kDa prote T27C10.5.
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Mammalia; Eutheria;
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                                                                    STRAIN-BRISTOL N2;
Zhu H.J., Graves T., Hawkins
The sequence of C. elegans
Submitted (OCT-1998) to the
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
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       SEQUENCE FROM N.A
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           "Genome sequence of the nematode C. elegans: a investigating biology. The C. elegans Sequencing Science 282:2012-2018(1998).
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Pred. No. 4.6e-79;
6; Mismatches 9
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Best Local S
Matches 123
                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodom; PD000001; Euk_pkinase; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00220; TyrKC; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

ATP-binding; Hypothetical protein; Transferase.

SEQUENCE 1175 AA; 130667 MW; F4BFBF44DDC1390C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JUL-2001) to the EMBL/GenBank/DDBJ EMBL; AF098504; AAK73897.1; -
                                                                                                                                             CG5483 protein.
                                                                                                                                                           01-JUN-2002
                                                                                                                                                                          01-MAY-2000
01-MAY-2000
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                                                                                                                                                                                                      Q9VDJ9;
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 MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A.,
                           STRAIN-BERKELEY;
                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001
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mes 123; Conservative
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Pred. No. 9.5e-25;
6; Mismatches 175;
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Gocayne J.D.,
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Q9H5S3;
01-MAR-2001 (TIEMBLIEL 16, C)
01-MAR-2001 (TIEMBLIEL 16, L)
01-DEC-2001 (TIEMBLIEL 19, L)
CDNA: FL/Z3119 fis, clone LNG
                                                                        Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606; [1]
TISSUE-LUNG;

Rawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumu Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Subayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";
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                                                                                      Chordata;
Primates;
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project.";
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                                                                                       Craniata; V
Catarrhini;
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on update)
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Suzuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (APR-2002) to the
EMBL; BC027199; AAH27199.1;
Hypothetical protein.
SEQUENCE 252 AA; 28042 MV
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                                                                                                                                                  ELGTQILIHQESLTDYCSMSSYSSSPPRQAARSPSSLPSSPASSSSVPFSTDCEDSDMLH 595
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Rodentia;
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Pred. No. 2.8e
10; Mismatches
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Pred. No. 7.7e
0; Mismatches
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Sciurognathi; Muridae;
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.7e-104;
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1: sp_archea:*
2: sp_bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-836-392-21
3822
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Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        April 8, 2003, 10:19:44; Search time 98 Seconds (without alignments) 1530.636 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
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Maximum Match 100%
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sp_bacteriap:*
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Q9AWA6
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                                                                                                 Q9w3i3 drosophila
Q95wf6 drosophila
Q95wn8 drosophila
                                                                                                                                                                                                                                                              Q9bs11 homo sapien
Q9tzm4 caenorhabd1
Q9vdj9 drosophila
                                                                                                                                                                                                                                                                                                                                                                        Q96jn5 homo sapien
Q9h5s3 homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                             Q9m085 arabidopsis
Q9zq31 arabidopsis
Q8vdg6 mus musculu
                   Q94c42 triticum ae
O22558 arabidopsis
9h2n5 homo sapien
                                                                                                                                                                                                                                                                                                                                                  Q8r085 mus
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Q8wwn1 homo sapien	TNAMBÖ	4	1036	6.6	254	Ç
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		10	777		S	ถ
		10	763		255.5	F
		10	765		57	5
arab		10	525		259	9
	Q9JJ15	11	850		259.5	8
		10	545		259.5	37
		10	1248		260.5	ڣ
	o	4	847		260.5	ŭ
Q91u16 arabidopsis		10	378		262	4
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	n	رح.	527		263	õ
Q8ry96 arabidopsis		10	483		263	39
	0	σ	422		263	8
Q8t219 dictyosteli		Ġ	1553		264	7
Q8t7z1 caenorhabdi	0	ப	978		266	8
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## ALIGNMENTS

RESULT 1 Q96JN5

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PRELIMINARY;

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Best Local Similarity
Matches 728; Conserv
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SEQUENCE 1369 AA
                                                                                                                                       Prodom; PD000001;
PROSITE; PS00037;
PROSITE; PS50011;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                    -1- SIMILARITY: CONTAINS 1 WD REPEAT (TRP-ASP DOMAIN) EMBL; AB058693; BAB47419.1; -.
                                                                                                                                                                                                                                                                                Nagase T., Nakayama M., Nakajima D., Ki
"Prediction of the coding sequences of
The complete sequences of 100 new cDNA
for large Proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIAA1790 protein (Fragment)
                                                                                                                                                                                                     InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                             CBI_TaxID=9606;
                                                                                                                                                                                          fam; PF00069;
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 1 MLRHLRATDAMKNFSEFRQEASMLHALQHPCIVALIGISIHPLCFALELAPLSSLNTVLS 60
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                                                                                             1369 AA;
                               100.0%; silarity 100.0%; F
                                                                                                                                       Euk_pkinase; 1.
MYB_1; UNKNOWN_1.
PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                PubMed-11347906;
                                                                                             153626 MW; AE90CE09C88370D9 CRC64;
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Last annotation update)
                               Score 3822; DB 4
Pred. No. 6e-314;
); Mismatches 0
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of unidentified human genes. XX.
VA clones from brain which code
                                                            DB 4;
                                  0;
                                                              Length
                                  Indels
                                                                 1369;
                                0
                                Gaps
                                  0
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CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 7015
TYPE: DNA
ORGANISM: Homo sapiens
US-10-132-382-5
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Best Local Similarity 94.6%;
Matches 2065; Conservative
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                  GAGAAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAGCTGCCAG 900
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Pred. No. 0;
0; Mismatches 2;
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9865	TTATCGTCATTGGCCTGGAGAASGATTCTGGCGCCCAGCGGGCCGAGTCATTCCCGT	5927	фb
0861	GTEATCGTCATTGGCCTGGAGAAGGATTCTGAAGCCCAGCGGGGCCGAGTCATTGCCGTC	1921	у
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0261	AGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCCAGGCGCGGTGGAGA	1861	00
8	TCCGACAGGTCTGAGCATGACCCCCCATGGACGGGGGAGACCTTCAGCAGAGACCTG	80	40
0981	CCGACAGGTCTGAGCATGACCTGACCCCCATGGAUGGGGAGACCTTCAGUUAGUACC	1801	ov Ov
5806	AGTGTGCCTTTCTCCACCGACTGCGAGGACTCAGACATGCTACATACGCCCGGTGCTGCC	5747	ф
1800	GTGTGCCTTTCTCCACCGACTGCGAGGACTCAGACATGCTACATACGCCCGGTGCTGC	1741	Qγ
5746	CACCCCGCCAGGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTCCCCAGCAAGTTCTTCC	5687	Дb
1740	CACCCGCCAGGCTGCCAGGTCCCCCTCAAGCTTCCCCAGCTCCCCAGCAAGTTCTTC	1681	Qy
5686	ACTCCTCATC	5627	. dd
1680	TCCTGATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCT	1621	Qy
5626	CTGAGGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCAG	5567	Дb
1620	CTGAGGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGC	1561	Qy
5566	CCCGTGCGGCCTTGGACACGGAACCCCCGGCAGCCACACGGCCAACCCAAAGGTG	5507	DЪ
1560	CCGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCAGCCA	1501	Qy
5506	ACCTACCAGCTGTGTGCCCGGGTACTTCTGCGGGGTCCCCAGCCCCCTCAGGGACATGTTT	5447	Дb
1500	CTACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCAGCCCCCTCAGGGACATGTT	1441	Qy
5446	GAGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACTCCACC	5387	рb
1440	AGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACTCC	1381	Qy
5386	GAGCCCTACATGGCCCCCTCCATGGTTACGTCAGTCGTGCAGGCTCTGAGGGCAGAGGG	5327	Db
1380	AGCCCTACATGGCCCCCTCCATGGTTACGTCAGTCGTGTGCAGCTCTGAGGGCAGAGG	1321	Qy
5326	AGCAATGGGCCGGCCTTGTCATCGACTGTGCCTCCCTGGAGATCTGCAGGCGGCTG	5267	Db
1320	GCAATGGGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCTGGAGATCTGCAGGCGGCT	1261	Qy
5266	CAGAACCCCTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTAC	5207	В
1260	AGAACCCCTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTA	1201	Qy
5206	GTGCTCACACAGCCAACAGGTCCAAGTTCAGCATCGCGATGAAGA	5147	Db
1200	ACCTGTGCTCACACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATGAAGACGCACG	1141	Qy
5146	AGCTGCTC	5087	В
1140	CCGATGGCCTTGTGGCTGTGTTTTCCCGTGGTGCGGGGCACCCCAAAGGACAGCTGCT	1081	Ŋ
5086	다.	5058	рb
1080	TACCTGGTCTTAGCGGGCC	1021	Qy
5057		5058	Дb
1020.	CTCAAGGGCATGTGCCCCTTAAACACACCCCAACAGGCCTTGGATACTCCAGCTGTCGTC	961	Qy
5057	CTCCAGGTCCAGAGATCCCTGTGGACAGCCACCG	5024	DЬ
960	TCCAGGTCCAGAGATCCCTGTGGACAGCCACCGAGGACCAGAAAATCTACATCTACACC	901	Qy

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Sequence 1, Application US/10132382
; Publication No. US20030045699A1
; GENERAL INFORMATION:
   APPLICANT: WEISS, BERTRAM
; TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STIFILE REFERENCE; SCH-1811
; CURRENT APPLICATION NUMBER: US/10/132,382
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; SEQ ID NO 1
; LENGTH: 7093
; TYPE: DNA
; ORGANISM: Homo sapiens
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                                                                           TACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTG
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                             CCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTAGATATG
                                                GGCTGGGGGCCCAGGGAGTTCGACATTTTCTACCAGTCCTACGAGGAGCTGGGCCGGCTG
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                     CCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGGAAGGTAGATATG
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CCTGAGGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCAG
                                                                                                ACCTACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCAGCCCCCTCAGGGACATGTTT
                                                GAGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACTCCACC
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RESULT 4
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; Sequence 7, Application US/10132382
; Publication No. US20030045699A1
; GENERAL INFORMATION:
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TITLE OF INVENTION: MEMBRANE RECEPTORS FOR STEROIDS AND STEROLS
FILE REFERENCE: SCH-1811
CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7
LENGTH: 7229
TYPE: DNA
ORGANISM: Homo sapiens
US-10-132-382-7
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H - H	GAGAAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAGC 	841 5178	Db 5	
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	GAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGACACTA	601 938	Qy Db 4	
	CACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGC	541 878	Db A	D 10
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RESULT 5
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; Sequence 3, Application US/10132382
; Publication No. US20030045699A1
; GENERAL INFORMATION;
; APPLICANT: WEISS, BERTRAM
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CURRENT APPLICATION NUMBER: US/10/132,382
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
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                                   TACACCGTGGTGTTTTTGGGATGGAAAAGAGGGAGTCCAGGAACTACACGGTGGTGAACACA
                                                                                   TTCATGTATGAACTGTGCTGTGGGAAGCAGACAGCCTTCTTCTCATCCCAGGGCCAGGAG
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                            CAGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCCAGGCGCGGTGGAGAT
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                                                                  ATCCTGATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCTACTCCTCATCC
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         GTTATCGTCATTGGCCTGGAGAAGGATTCTGAAGCCCAGCGGGGCCGAGTCATTGCCGTC
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GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from
TITLE OF INVENTION: Compositions Isolated from
TITLE OF INVENTION: And Their Use in the Modi
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: U$/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR RILING DATE: 1999-01-01
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-01-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR RILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR RILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 149
LENGTH: 515
TYPE: DNA
ORGANISM: Eucalyptus grandis
US-10-101-464A-149
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; Sequence 149, Application US/10101464A
· Publication No. US20030046728A1
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GENERAL INFORMATION:
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Best Local Similarity
Matches 130; Conserv
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nilarity 51.8%;
Conservative
                               523
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pred. No. 9.9e-07;
0; Mismatches 121;
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, LENGTH: 1383
; TYPE: DNA
; ORGANIEM: Homo sapiens
US-09-935-464-2
                                                                                                                                                                                                                                                                                                                                                                                  US-09-935-464-4
                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09935464 Publication No. US20030027153A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 168; Conserv
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                                                            SEQ ID NO 4
                                                                                            APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/1H702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILLING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA FILE REFERENCE: 3322/11702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEO ID NOS: 90
NUMBER OF SEO ID NOS: 90
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APPLICANT: Barrin
APPLICANT: Parker
                                                                               SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                           APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Ma
APPLICANT: Parker, Alexa
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                       TYPE: DNA
ORGANISM: Homo
                                       ENGTH: 1738
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49.9%;
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Pred. No. 1.1e-05;
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                CAGGTTACTTGTCCCCTGAGGTCTTGAGGAAAGATCCCTATGGAAAACCTGTGGATATCT
                                       CTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTAGATATGT
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Query Match 2.4%;
Best Local Similarity 47.4%;
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APPLICANT: YE, Jane et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/10096960 Patent No. US20020132325A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2002-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN FITTLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2061.
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/800,960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: CL001158DIV
                                                                                                                                                                                                                                             540 CCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGC 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          420 TCCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAAGGTAGATAT 479
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  TTGGCCTAGCCATCGAAGTACAGGGAGGAGCAGCAGGCTTGGTTTTGGTTTTGCTGGCACCC
                                                  CTGACTACGGGATTTCGAGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACTC 421
                                                                                                       AGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTAT 361
                                                                                                                                                                                                              ATCAGATTCTGGAGAGTGTTAACCACATCCACCAGCATGACATCGTCCACAGGGACCTGA 524
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RESULT 11
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CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 227
LENGTH: 3705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Olga Bandman
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                                                                                                                                                                                             Sequence 3, Application US/09749956 Patent No. US20020068271A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Incyte ID No. US20020137081A1 327567.50-10-044-090-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED FILE REFERENCE: PA-0028 US
                                                                                                      ENBRAL INFORMATION:
APPLICANT: LA JOLIA Institute For Allergy
APPLICANT: Altman, Amnou
APPLICANT: Coudronniere, No. US20020068271Alwenn
CURRENT APPLICATION NUMBER: US/09/749,956
CURRENT FILING DATE: 2000-12-27
                                      TITLE OF INVENTION: METHODS FOR IDENTIFYING AGENTS CAPABLE TITLE OF INVENTION: THETA (PKC?) ACTIVITY FILE REFERENCE: 051501/0276390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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; SEQ ID.NO 3
; LENGTH: 2698
; TYPE: DNA
; ORGANISM: Human
US-09-749-956-3
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US-09-749-956-1
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Best Local Similarity
Matches 183; Conserv
                                                                                      Query Match 2.
Best Local Similarity 47.
Matches 183; Conservative
                                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 2705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09749956 Patent No. US20020068271A1
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                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS FOR IDENTIFYING TITLE OF INVENTION: THETA (PKC?) ACTIVITY FILE REFERENCE: 051501/0276390
                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/749,956
CURRENT FILING DATE: 2000-12-27
                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin version
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/173,171 PRIOR FILING DATE: 1999-12-27
                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: La Jolla Institute For Allergy
                                                                                                                                                                                                                      TYPE: DNA
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                                             256
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                           GGCCTGGCCTACCTGCACAAGAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATL 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTCTGCAGITCCTTCATTCCAAAGGAATAGTCTACAGGGACCTGAAGCTAGATAACATC 1551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coudronniere, No. US20020068271A1wenn
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Pred. No. 0.00049;
                                                                                      Score 48.8; DB 10;
Pred. No. 0.00049;
0; Mismatches 192;
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; TYPE: DNA; Homo sapiens
; ORGANISM: Homo sapiens
US-09-964-824A-119
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US-09-964-824A-119
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SOFTWARE: PatentIn v
SEQ ID NO 119
LENGTH: 2754
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GENERAL INFORMATION:
APPLICANT: Horrigan, Stephen
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PRIOR FILING DATE: 2000-09-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
    1796
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                                                                                                                                             436
                                                                                                                                                                                                                                                                                                                                                                                                          256 GGCCTGGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATT 315
                                                                                                                                                                                                                                 376 TCGAGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACTCCTGGCTACCAGGCC
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                                          GTGCTCTACGAGTTGCTGTCAGGACAGCGCCCTGCACTGGGCCACCACCAGCTCCAGATT 555
                                                                                                                                     CCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTAGATATGTTCTCCTATGGAATG 495
                                                                                                                                                                                                                                                                                CTG-----TTAGACAAAGATGGACATATCAAGATCGCGGATTTTGGAATGTGCAAG 1675
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CTCCTTTATGAAATGCTGATTGGTCAGTCGCCTTTCCACGGGCAGGATGAGGAGGAGCTC
                                                                                      CCAGAGATCTTGCTGGGTCAGAAATACAACCACTCTGTGGACTGGTGGTCCTTCGGGGTT
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Pred. No. 0.00049;
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-5
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US-09-712-363-5
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Best Local 9
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Patent No. US20020164588A1
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CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
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APPLICANT: Marcotte, Edward
TITLE OF INVENTION: DITERMINING THE FUNCTIONS
TITLE OF INVENTION: INTERACTIONS OF PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
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                 406 CACCGTGACGTCAAGCCGGCGAACATCATGATCAGCGCGACCAATGCAGTAAAAGGTGATG
                                               289 TICTGTGACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATC
                                                                                                                                                                                                                                                                                                                                              109 GGCATCAGCATCCACCCGCTCTGCTTCGCCCTGGAGCTCGCGCCGCTCAGCAGCCTCAAC 168
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                                                                                                                                                                                                                                                   169 ACCGTGCTGTCCGAGAACGCCAGAGATTCTTCCTTTATACCCCTGGGACACATGCTCACC 228
                                                                                                                                                                                                                                                                                                    226 GACACCGGTGAAGCCGAAACGCCCGCCGGGCCATTGCCCTACATCGTCATGGAATACGTC 285
                                                                                                                                                                                                                                                                                                                                                                                                166 TICCGGCGTGAGGCGCAAAACGCCGCGGCATTGAACCACCCTGCAATCGTCGCGGTCTAC 225
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FILING DATE: 1999-02-01
APPLICATION NUMBER: 60/126,593
FILING DATE: 1999-03-26
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                                                                                                                                                       CAAAAAATAGCCTACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAAAAACATCATC 288
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for Windows Version
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556 GCCAAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGCAGCCGGAGGAAGTGCAGTTC
Score 48.2; DB 9;
Pred. No. 0.00065;
0; Mismatches 373;
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BY COMPARATIVE ANALYSIS
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; ORGANISM: Mouse
US-09-823-038A-58
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US-09-823-038A-58
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Best Local Similarity 51.7%;
Matches 166; Conservative
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SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 58
LENGTH: 3503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 58, Application US/09823038A Patent No. US20020058335A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
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703 GTGTCGGCGGCAGTATGATGCGCGTGTGGACCTCTGGTCTGTGGGGGGTGATCCTGTACGA 762
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                               GCCTCGCATTGYATATGATGAGAAGGTAGATATGTTCTCCTATGGAATGGTGCTCTACGA 50t
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Kumble, Anand
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Pred. No. 0.00078;
0; Mismatches 143;
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밁 ρy 507 GTTGCTGTCAGGACAGCGCCC 763 AGCCCTCTTTGGGCAGCCCCC 783 527

Search completed: April 15, 2003, 07:05:58 Job time : 416 secs

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Result
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## ALIGNMENTS

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Region 310315	Region 267274		Region 218223		Region 6267		Region 1520	Key Location/Qualifiers		Homo sapiens.	:	behavioural disorder; renal disorder.	musculo-skeletal disorder; Parkinson's disease; autoimmune disorder;	gene therapy; nephrotic syndrome; glomerulonephritis; allergy; neoplasm;	blood coagulation disorder; trauma; cerebrovascular disorder; tendonitis;	neurodegenerative disorder; gastrointestinal disorder; cancer; lymphoma;	multiple sclerosis; Alzheimer's disease; vascular dementia; thrombosis;	hyperproliferative disorder; atherosclerosis; brain disorder; leukaemia;	cardiovascular disorder; severe combined immunodeficiency; SCID; vaccine;	<pre>antifungal; antiparasitic; sarcoidosis; inflammation; asthma; arthritis;</pre>	Human; protein tyrosine kinase receptor; PTK; antibacterial; antiviral;		Human protein tyrosine kinase receptor (PTK) from clone HDPSB68.		02-JUL-2001 (first entry)		AAE00669;		AAE00669 AAE00669 standard; Protein; 728 AA.	

Human

kinase PKIN

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14-MAR-2000; 2
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Albumin fusion protein; therapeutic protein x; human albumin; human serum albumin; HSA; cancer; reproductive disorder; disorder; disorder; fumune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder; protestatic; antiinfertility; antiinflammator; antiulcer; contestic; anti-HTV; antidabetic; haemostatic; nouropineuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                     Human albumin
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                                                                                                                                                                               ABG64871 standard;
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osteopathic; antiarthritic.

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Best Local S
Matches 706
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25-APR-2000; 2000US-199384P.
21-DEC-2000; 2000US-256931P.
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les 706; Conservative
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CSHTANRSKFSIADEDARQNPYPVKAMEVVNSGSEVWYSNGPGLLVIDCASLEICERLEP
                                                                                                                                                                            VQFRRLQALMMECNDTKPEKRPLALSVVSQMKDPTFATFMYELCCGKQTAFFSSQGQEYT
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                                              GMCPLNTPQQALDTPAVVTCFLAVPVIKKNSYLVLAGLADGLVAVFPVVRGIPKDSCSYL
                                                           GMCPLNIPQQALDTPAVVTCFLAVPVIKKNSYLVLAGLADGLVAVFPVVRGTPKDSCSYL 382
                                                                                                   VVFWDGKEESRNYTVVNTEKGLMEVQRMCCPGMKVSCQLQVQRSLWTATEDQKIYIYTLK
                                                                                                                     VVFWDGKEESRNYTVVNTEKGLMEVQRMCCPGMKVSCQLQVQRSLWTATEDQKTYIYTLK
                                                                                                                                                             VQFRRLQALMMECWDTKPEKRPLALSVVSQMKDPTFATFMYELCCGKQTAFFSSQGQEYT
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fused to a therapeutic protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 1564-1566;
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100.0%; Pr
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                                                                  Rosen
Moore
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Wei P, Ebner R,
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Shi Y,
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WPI; 2002-304113/34 N-PSDB; AAD33718.

An isolated nucleic acid molecule (I) comprising a polynucleotide

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cc amount of the new protein in a sample or by determining the presence of comutations in the new genes. Specific uses are described for each of the claim genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of commune or autoimmune diseases e.g. AIDS (acquired immune deficiency comparison), asthma, anaemia and rheumatoid arthritis, breast neoplasia cand breast cancer, neurological diseases e.g. Alzheimer's disease, and breast cancer, huntington's disease, Tourette syndrome, companies, demyelinating disease, peripheral neuropathies, neoplasia, crauma, congenital malformations, spinal cord injuries, toxic trauma, congenital malformations, spinal cord injuries, multiple clerosis, ischaemia and infarction, haemorrhages, schizophrenia, mania, congenital, depression, panic disorder, learning disabilities, ALS, caltered behaviours e.g. disorders in feeding, sleep patterns, balance and perception, encephalitis, disorders in feeding, sleep patterns, balance and perception, encephalitis, disorders in behavioural disorders and hyperproliferative disorder. The present sequence represents a human conservation providers and the present sequence represents a human conservation providers and the present sequence represents a human conservation providers and the present sequence represents a human conservation providers and the present sequence represents a human conservation and the present sequence represents a human conservation and the present sequence represents a human conservation and the present sequence represents a human conservation and the present sequence represents a human conservation and the present sequence represents a human conservation and the present sequence represents a human conservation and the present sequence represents a human conservation and the present sequence represents a human conservation and the present sequence represents a human conservation and the present sequence represents a human conservation and the presen
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                          therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and disgnosing disorders such as cancer, reproductive disorders, disease, ulcerative colitis), immune disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin fusion proteins of the invention.
                                                                                                                                                                                                                               The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum
                                                                                                                                                                                                                                                                                  Claim 1;
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immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
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                                                                                                                                                                                                                                                                                                               fusion protein for treating disease e.g. diabetes comprises whin fused to a therapeutic protein -
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Human; secreted protein; immune disorder; antiallergic; antirheumatic; rheumatoid arthritis; breast neoplasia; breast cancer; antiarthritic; neurological disease; Alzheimer's disease; Parkinson's disease; trauma; Tourette syndrome; encephalitis; cytostatic; haemostatic; anaemia; mania; antinflammatory; ophthalmalogical; dermatological; immunostimulatory; immunomodulatory; immunosuppressive; antibacterial; antipsoriatic; gene therapy; autoimmune disease; Huntington's disease; meningitis; demyellnating disease; peripheral neuropathy; congenital malformation; spinal cord injury; peripheral neuropathy; ischaemia; perception; multiple sclerosis; infarction; haemorrhage; schizophrenia; dementia; depression; panic disorder; learning disability; ALS; feeding disorder;
                                                                                                                                                                                                                                                                                                                           Human
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hyperproliferative disorder; sleep pattern; cardiovascular disorder; reproductive disorder; digestive system disorder; behavioural disorder
Homo sapiens.
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Location/Qualifiers

Protein Peptide /label= 25..706 note-"Human mature Signal\_peptide secreted

protein"

WO200216390-A1

28-FEB-2002

17-JAN-2001; 2001WO-US01435

18-AUG-2000; 2000US-226282P (HUMA:) HUMAN GENOME SCI INC

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Moore PA, Wei P, Komatsoulis GA, Ebner **7**2 Baker Duan DR, Birse ( Cho1 Soppet oi GH, Fiscella Olsen :

HS;

N-PSDB; 2002-304113/34. DB; AAD33695.

An isolated nucleic acid molecule (I) comprising a polynucleotide which encodes a polypeptide useful in the diagnosis and treatment of disorders e.g. immune disorders -

Claim 11; Page 472-474; 534pp; English

CC AADJ33692-AADJ3736 represent cDNAs corresponding to 21 human secreted CC protein genes, and AAEZ1191-AAEZ1235 represent the proteins they encode. AAEZ1236-AAEZ1280 represent human secreted protein fragments. The genes CC and their corresponding secreted proteins are useful for preventing, CC treating or ameliorating medical conditions, e.g., by protein or gene CC therapy. Pathological conditions can be diagnosed by determining the CC amount of the new protein in a sample or by determining the presence of CC indictions in the new genes. Specific uses are described for each of the CC 19 genes, based on the tissues in which they are most highly expressed, CC indictions of the CC immune or autoimmune diseases e.g. AIDS (acquired immune deficiency CC syndrome), asthma, anaemia and rheumatoid arthritis, breast neoplasia CC and breast cancer, neurological diseases. Tourette syndrome, CC trauma, congenital malformations, spinal cord injuries, toxic celerosis, ischaemia and infarction, haemorrhages, schizophrenia, mania, CC celerosis, ischaemia and infarction, haemorrhages, schizophrenia, mania, CC dementia, depression, panic disorders in feeding, sleep patterns, balance and perception, encephalitis, disorders in cardiovascular, neural/CC sensory, reproductive and digestive systems, behavioural disorders and constants a human constants and infarctive and secuence represents a human constants. hyperproliferative disorder . secreted protein of the inver rder. The present sequence invention.

Sequence 706 AA;

밁 Q Ş Best Loc Matches Query Match 83 23 Local Н MLHALQHPCIVALIGISIHPLCFALELAPLSSLNTVLSENARDSSFIPLGHMLTQKIAYQ IASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKLSDYGISROSFHEGALGVEGTPG 705<sub>i</sub>; Similarity Conservative 96.98; Score 3705; D Pred. No. 0; 0; Mismatches 0 BB 23; ۲, Length Indels 0; Gaps 142 60 82

0

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120

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RESULT 6
AAG677395
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29-MAR-2000; 2000US-0193404.
13-NOV-2000; 2000US-0247013.
                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                           infection; ocular disease; migraine; pain; sexual dysfunction; mood disorder; attention disorder; cognition disorder; hypoten hypertension; psychotic disorder; dyskinesia; transplant rejec
                                                                                                                                                                                                                                                                                                                                                                         peripheral nervous system disease; amyotrophic lateral infection; ocular disease; migraine; pain; sexual dysf
                                                                                                                                                                                                                                                                                                                                                                                                                Human; protein kinase; cancer; immune disease; cardiovascula
brain disease; neuronal disease; Alzheimer's disease; chromo
Parkinson's disease; multiple sclerosis; metabolic disorder;
                                                                                                                                                    02-MAR-2001;
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of tissues and cancers of hematopoietic origin), immune-related disea and disorders, cardiovascular disease, brain or neuronal associated diseases (e.g. Alzheimer's disease, brain or neuronal associated diseases (e.g. Alzheimer's disease, parkinson's disease, multiple sclerosis), metabolic disorders, peripheral nervous system diseases, amyotrophic lateral sclerosis, viral infections, infections caused by prions, infections caused by bringi, ocular diseases, migraines, pain, sexual dysfunction, mood disorders, attention disorders, pain, sexual dysfunction, mood disorders, psychotic disorders, dyskinesias, and organ transplant rejection. Ninase inhibitors are useful for treating diseases and disorders
                                                                                                                                                                                                                located on chromosome 15. The kinase polypeptides are useful for diagnosing a disease or disorder selected from cancers (e.g. cancers of tissues and cancers of hematopoietic origin), immune-related dise
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and neuronal-associated diseas
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Query Match Best Local : Best Local Sin Matches 688; Similarity Conservative 93.7%; 0 Score 3579.5; DB 2 Pred. No. 1.4e-312; Mismatches 22; Length Gaps ۲.

Sequence

2014 AA;

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RESULT 7
AAE24137
ID AAE2
20-OCT-2000;
27-OCT-2000;
03-NOV-2000;
09-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis; development; hepatitis; cardiovascular; hypertension; drug screening; myocardial infarction; Goodpasture's syndrome; lipid disorder; growth; fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic; hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hIV; neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic;
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hyperlipidaemia; enzyme.
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                   New human kinase polypeptide, for diagnosing, preventing and treat cancer, immune system disorders, growth and development disorders, cardiovascular disorders and lipid disorders
                                                                                                    Thangavelu K, Khan
                                                                                                                            Gandhi AR,
                                                                                                                                                                                                                                                                                                                  25-APR-2002.
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22-NOV-2000;
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                                                                               2002-454603/48
                                                                                         an R, Dunny, Park, Ramkumar J, Dan, Ramkumar J, Dan, Burrou.
AR, Lu Y, Yue H, Burrou.
AR, Lu DAM, Borov
                                                                                                                                                                          INCYTE GENOMICS INC.
                                                                    AAD38851
                                                                                                                                                                                              2000US-242410P.
2000US-244068P.
2000US-245708P.
2000US-247672P.
2000US-249565P.
2000US-252730P.
2000US-250807P.
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Ding L, Tang YT, Hafalia AJA, Nguyen DB
He H, Burford N, Bandman O, Tribouley CM;
Lu DAM, Borowsky ML, Thornton M, Swarna
                                                                                                                                                                                                                                                                                                                                                                "Transmembrane
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acquired immune deficiency syndrome (AIDS), Addison's disease, allergy, acquired immune deficiency syndrome (AIDS), Addison's disease, allergy, affecting growth and development (e.g., arteriosclerosis, cirrhosis, chepatitis), cardiovascular disorder (e.g., hypertension, myocardial) infarction, Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver, Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia, besity), and for assessing the effects of exogenous compounds. Anti-PKIN antibody is useful in a diagnostic test for a condition or a disease associated with the expression of FKIN in a biological sample. A composition comprising PKIN or an agonist or antagonist of PKIN is useful for treating a disease or condition associated with decreased or increased expression of functional PKIN. Sassociated with decreased or increased expression of functional PKIN. The proteome of a tissue or cell type. PKIN DNA is useful human diseases, those who was a supple of the proteome of a tissue or cell type. PKIN DNA is useful human diseases, and the proteome of the proteome of a tissue or cell type. PKIN DNA is useful human diseases, and the proteome of the proteome of a tissue or cell type. PKIN DNA is useful human diseases, and the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteome of the proteom
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PKIN and its DNA are useful for diagnosing, treating and preventing cancer, an immune system disorder (e.g., and its action of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control o
in somatic or germline gene therapy. The present sequence is
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Sequence 2014 AA;

Query Match Best Local Similarity

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Score 3579.5; Pred. No. 1.46

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Length

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                    ILIHQESLTDYCSMSSYSSSPPRQAARSPSSLPSSPASSSSVPFSTDCEDSDMLHTPGAA
                                                                                                                  TYQLCARYFCGVPSPLRDMFPVRPLDTEPPAASHTANPKVPEGDS1ADVSIMYSEELGTQ
                                                                                                                                                               SNGPGLLVIDCASLEICRRLEPYMAPSMYTSVVCSSEGRGEEVVWCLDDKANSLVMYHST
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 LKARELTPHGVLYDAAVVAKDTVVCTEENENTEWCLAVWKGWGAREFDIFYOSYFELGRI.
                                                                                                        TYQLCARYFCGVPSPLRDMFPVRPLDTEPPAASHTANPKVPEGDSIADVSIMYSEELGTQ
                                                                                                                                                   SNGPGLLVIDCASLEICRRLEPYMAPSMVTSVVCSSEGRGEEVVWCLDDKANSLVMYHST
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Claim 1;

Page 147-152; 210pp; English

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RESULT 8
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Query Match
Best Local Sin
Matches 584;
                                                                                                                                                                                                                                                                                                                            The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnosatics. Generatics, came mapping, identification of mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2007
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                                                                                                                                                                 diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                  Sequence
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23-AUG-2000;
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food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences.
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DB; AAS72238.
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                                                                                             23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVLAGLADGLVAVFPVVRGTPKDSCSYLCSHTANRSKFSIADEDARQNPYPVKAMEVVNS
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Adams M,
                                                                                                                                                                                                                                                                                                                                                                                      developmental biology; cell signalling; insecticide;
                                                                                           2000US-191637P.
2000US-0614150.
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Li PWD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                   2062
                                                                                                                                                                                                                                                                               2008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO.11484; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 interactions
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      559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YRRSGAH--MGPHTFQTLVLQAARAIEYLHRRRIIYRDLKSENVLVWELPQPHTEDSPRN 1796
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                                                                                                                                                                                                                NCAFAEGSFVLTEICSGFVLHAACSVVVDGIYELWCGEIAGKINVFPLNENGVSGHQALC
                                                                                                                                                                                                                                                                          AYSTSTYAHLFS--YMLD-PNIKSAVISLVYMEKIA-RVAVGTHNG--RVFLVDATQMPS
                                                                                                                                                                                                                                                                                                                                                                     LMEVQRMCC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                KDPTFATFM-----YELCCGK-QTAFFSSQGQEYTVVFWDGKEESRNYTVVNTEKG- 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----GHE--SIKECILEGSRPALTQ-RETQFPTCCLDLMVLCWHEQPRRRPTASQIVSIL 1887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPALGHHOLQIAKKLSKGIRPVLGQPEEVQFRR-LQALMMECWDTKPEKRPLALSVVSQM 233
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DB; ABL05667.
   SSPPRQAARS
                               ISVFRPYENEIKSIITLSKDNVP---LIATIGRRY-RSLISRYVDSAESST----KSSAV 2277
                                                          V---RPLDTEPPAASHTANPKVPEGDSIADVSIMYSEELGTQILIHQESLTDYCSMSSYS
                                                                                              STAIDEHVNLIKG-
                                                                                                                                                     HSEEPNLIEDVKVARMCSNESHVFSCLYPGCMVYQWDVISKRIENKLDCSKLLPCSESLQ
                                                                                                                                                                                                                                            SCSY----ARQNPYP------
                                                                                                                                                                                                                                                                                                                                                                                                SAPECIHLLDVVAMPHSEKIVCGVFQSLVGMGDDERCGLELWLPSFGSRIDILDCSPSGS
                                                                                                                      PYMAPSMVTSVVCSSEGRGEEVVWCLDDKANSLVMYHSTTYQLCARYFCGVPSPLRDMFP
                                                                                                                                                                                                                                                                                                          IYTLKGMCPLNTPQQALDTPAVVTCFLAVPVIKKNSYLVLAGLADGLVAVFPVVRGTPKD
                                                                                                                                                                                                                                                                                                                                      LLQCNSISCSPQPQVAPPKTPENGANSRARSAQRLPKMNMLCCCLVGEAIWMGDV9GNLH
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Pred. No. 1.1e-22;
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                                                                                         -QISALAAHNSELY-IGTTWGCLIVAELHTLRP
                                                                                                                                                                                                                                                                                                                                                                  -PGMKVSCQLQVQRSLWTATEDQKIY 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
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RESULT 10
AAE16259
ID AAE16
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Human
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                                                                                             AAE16259;
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                                                                                                standard;
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                                                                                          entry)
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Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia; allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoporosis; Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris; cardiovascular disease; hypertension; vasculitis; myocarditis; obesity; congestive heart failure; ischaemic heart disease; lung tumour; gout; fatty liver; Niemann-Pick's disease; gene therapy. kinase; PKIN-5; cancer; leukaemia; adenocarcinoma; osteoarthritis; disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;

THOUS THOUSE CENTURE INC	07-JUL-2000; 13-JUL-2000; 25-AUG-2000;	15-JUN-2000;	14-JUN-2001; ;	20-DEC-2001.	WO200196547-A2.	DOMALII		Domain	Domain	Domain	Key Domain
CENTONICS THE	2000US-21551P. 2000US-21665P. 2000US-218372P. 2000US-228056P.	2000US-212073P. 2000US-213467P.	2001WO-US19444.			/label= Protein_kinase_domain	/label= Protein_kinase_domain	<pre>/note= "Eukaryotic protein kinase domain" 14252</pre>	/label= Protein_kinase_domain 14257	/habel- protein_kinase_domain 14. 197	Location/Qualifiers 13252

## (INCY-) INCYTE GENOMICS INC.

Gandhi AR, Triucus A Ramkumar J, Griffin JA, K Baughn MR, He A, Thorntor Lo TP, Khan F, Recipon S: Lal P, Bandman O, AR, Yao MG, Lu L., AR, Tribouley CM, Walla NK, Yao MG, Lu L., AR, Tribouley CM, Walla NK, Yao MG, Lu L., Nguyen DB, Tang x IT J, Griffin JA, Kearney L, Burford N, Nguyen DB, Tang x IT J, Griffin JA, Thornton M, Hafalia A, Patterson C, Gururajan MR, He A, Thornton MA, Azimzai Y, Policky JL, Ding L; Khan F, Recipon SA, Azimzai Y, Policky JL, Ding L; Filiott VS, Thangavelu K, Batra S, Ison CH; Yao MG, Lu man Greenwald SR;

## N-PSDB; 2002-090207/12 AAD26452

New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, diseases such as cancer, comprise human kinase polypeptides.

Claim Page 197pp; English

The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition containing PKIN agonist is useful for

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RESULT 11
AAU03554
ID 3554
ID 3554
ID 3654
ID 3703554
ID 3703554
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ID 12-SE
XX 12-SE
XX Human
XX Human
KW metab
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Matches 101
                                       metabolic disorder; immune related disease; neurological disorder neurodegenerative disorder; inflammatory Air-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's Syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis, bacterial, parasitic, fungal, viral, protozoal and helminthic infections) growth and development disorders (arteriosclerosis, cirrhosis, hepatitis, cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio vascular disease (arteriovenous fistula, hypertension, vasculitis, aneurysms, congestive heart failure, angina pectoris, myocarditis, ischaemic heart disease, chronie-bronchitis, lung tumours); lipid disorder (fatty liver, Fabry's disease, Niemann-pick's disease, hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity of a test compound and in gene therapy. The present sequence is human protest.
                                                                                                                                                                                                                                              AAU03554 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, atherosclerosis, anaemia, allergies, adult respiratory distress syndrome, autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease, osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
 Homo sapiens
                                                                                                                               Human protein
                                                                                                                                                                                                            AAU03554;
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                                                                                                                                                                       12-SEP-2001
                                     reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                        YCNSFSKQSKQKNFLLVGTADGKLAIF 404
                                                                                                                                                                                                                                                                                                                                                                              LAVPVIK -- KNSYLVLAGLADGLVAVF 368
                                                                                                                                                                                                                                                                                                                                                                                                              ADSRILCLAL - - - VHLPVEKESWIVSGTQSGTLLVINTEDGKKRHTLEKMTDS - - - VTCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AELYCLTRRILLPKNYIVECMVATHHNSRNASIWLGCGHTDRGQLSFLDLNTEGYTSEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTFATFMYELCCGKQT---AFFSSQGQEYTVVFWDG----KEESRNYTVVNTEKGLMEV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPNEFDELEIQGKLPDPVKEYGCAP----WPMVEKLIKQCLKENPQERPTSAQVFDILNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----HHQLQIAKKLSKGIRPVLGQPEEVQFRRLQALMMECWDTKPEKRPLALSVVSQMKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AS-----LTRTLQHRIALHVADGLRYLHSAMIIYRDLKPHNVLLETLYPNAAIIAKIADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDSSFIPLGHMLTQKIAYQIASGLAYLHKKNIIFCDLKSDNILVWSLDVKEHINIKLSDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMKNESE-----FRQEASMLHALQHPCIVALIGISIHPLCFALELAPLSSLNTVLSENA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                   --QRMCCPGMKVSCQLQVQRSLW--TATEDQKIYIYTLKGMCPLNTPQQALDTPAVVTCF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a disease or condition associated with decreased expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                     disorder
                                                                                                                                                                 (first entry
                                                                                                                             kinase #54.
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                                                                                                                                                                                                                                              Protein; 909
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26.1%; Pred. No. 3.1e-20;
tive 75; Mismatches 168
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                                                                       disorder;
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encoding protein kinases and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoietic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. parkinson's disease), inflammatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility). Additionally, polynucleotides encoding protein kinases may be used for gene therapy and as DNA probes in disgnostic assays. The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity.
Sequence
                                                                                                                                                                                                                                                              AAU03501-AAU03557 represent novel human protein kinases *1-0/. ....
novel protein kinases have been identified as members of the tyrosine
or serine/threonine kinase (PTK and STK) families. The polynucleotides
or serine/threonine kinases and the polypeptides may be used in the
                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections -
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Flanagan P,
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Query Match
8.6%; Score 327.5; DB 22; Length 909;
Best Local Similarity 26.1%; Pred. No. 5.3e-20;
Matches 101; Conservative 75; Mismatches 168; Indels 43; Gaps 13;

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Matches 82; Conservative .5%; ; Score 315; DB 21; ; Pred. No. 1.7e-19; 44; Mismatches 73; Indels 32; Gaps

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Query Match 8.2%;
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cDNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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/clone_lib="NIH_MGC_12"
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                  Homo sapiens cDNA FLJ25299 fis, cLono STMO: AK054028
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oligo capping; fis (full insert sequence). Homo sapiens stomach mucosa cDNA to mRNA, clone:STM07710.
Homo sapiens
 Eukaryota; Metazoa;
Mammalia; Eutheria;
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FLJ25299 fis,
 Chordata;
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 Craniata; Vertebrata; Catarrhini; Hominidae;
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MEDO human cDNA sequencing project supported by Ministry of MEDO human cDNA sequencing project supported by Ministry of Economy. Trade and Industry of Japan; cDNA full insert sequencing Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing: Institute of Medica Science, University of Tokyo, Laboratory of Genome Structure, Hu Genome Center; 3'-end one pass sequencing: RAB; clone selection full insert sequencing; RAB and Helix Research Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (24-OCT-2001) Sumio Sugano, Institute of Medical University of Tokyo, Laboratory of Genome Structure, Human Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Ja (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
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                                                                                                  Direct Submission

Submitted (04-7UL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RaB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'-6 3'-cnd one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: RAB, RAB; annotation: HRI and RAB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A. Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagano, Isogai, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oligo capping; fis (full insert sequence). Homo sapiens neuroglioma cell_line:H4 cDN/clone_lib_ENGH41 clone:BNGH41000104. Homo sapiens
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Homo sapiens cDNA FLJ30100 fis,
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Isogai, T., Otsuki, T.
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/db_xref="taxon:9606"
/clone="BNGH41000104"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="neuroglioma"
/clone_lib="BNGH41"
/note="cloning vector: pi
872 c 862 g 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_line="H4"
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Pred. No. 0;
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TORNEY/AGENT INFORMATION:

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US-08-946-994-12
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US-08-665-574C-12
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Best Local Similarity 47.9%;
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 371-25. INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                tent No.
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                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                    SOFTWARE: PatentIn Release #1.0,
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CLASSIFICATION:
RIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                            TLE OF INVENTION:
                                                      FILING DATE:
                                                                                                                                                                                       COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                         CITY: Washington STATE: D.C.
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                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                          SEQUENCES:
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1100 New York Avenue, Suite
                                                                                                                                                                                                                                                                                                                                                                                          Silvennoinen, Ollie
                                                                                                                                                                                                                                                                                                                                                            Quelle, Frederick W.
                                                                                                                                                                                                                                                                                                                                                                             Witthuhn, Bruce A.
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                                                                      US/08/946,994
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                                                                                                      Version #1.25
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US-08-755-728-1
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Best Local Similarity
Matches 134; Conserv
                                                                                                                                                                                                                                                                                                                     Sequence
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               quence 1, Application US/08755728 tent No. 5962312
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3068
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                                                                                                                                                                                                             TITLE OF INVENTION:
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REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 06
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                                                                      COUNTRY:
                                                                                         STATE:
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                                                                                                                                                          ADDRESSEE:
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                                                                                                    Los Angeles
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                                                                                                                        Suite 4700
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29-JUL-1993
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                                                                                                                                                                                                                                                            Gregory
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Pred. No. 0.076;
                    1.44 Mb
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Best Local Similarity
Matches 170; Conser
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Patent No.
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LOCATION: (81)..(1136)
NAME/KEY: unsure
LOCATION: 6
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
NAME: FOX, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656.0370000/SLF/GKT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT:
                                                                                        FILING DATE: 29-JULY-1994
CLASSIFICATION: 435
                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLICANT:
                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                              LE OF INVENTION:
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20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08097997A
                                                                                                                                                                                                                                                                                                   D.C.
                                                                                                                                                                                                                                                                                                                                        1100 New York Avenue,
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ork Avenue, Suite 600
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                                                                                                                                                                      Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Regulation of Cytokine
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US-08-097-997A-12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vatent No. 6136595
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3248
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                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/2:
FILING DATE: 29-JUL-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                      PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                    APPLICATION NUMBER: 08/0 FILING DATE: 29-JUL-1993
                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 18-JU
                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 20005-3934
APPLICATION NUMBER: 08/118,968 FILING DATE: 09-SEP-1993
                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                  SOFTWARE:
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Witthuhn, Bruce A.
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                                                                                                                                   08/282,012
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Pred. No. 0.076;
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LENGTH: 1732
TYPE: DNA
ORGANISM: Homo sapiens
JS-09-430-564-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application Patent No. 6372467 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 176; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 00246/506002
CURRENT APPLICATION NUMBER: US/09/430,564
CURRENT FILING DATE: 1999-10-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: P5486K AND P8586K GENES, PROTEINS,
TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                     TGTTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCTGCACTGGGCC
                                                                   CCATTGAGTACATGGCCCCTGAGATTCTGGTGCGCAGTGGCCACAACCGGGCTGTGGACT
                                                                                         CGGACAACATTCTGGTGGTGCCCTTGACGTCAAGGAGCACCATCAACATCAAGCTATCTG
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                                                                                                                                         ACTITIGUACICTGCAAGGAGTCTATCCATGAGGGCGCGTCACTCACACCTTCTGCGGCA
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Calvin J. Kuo
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US-09-429-322-3
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SEQ ID NO 3
LENGTH: 2754
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity 47.7%;
Matches 183; Conservative
NUMBER OF SEQ ID NOS:
SEQ ID NO 3
LENGTH: 2549
                                                                                                                                                                                              Sequence 3, Application US/09467082 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                              CURRENT APPLICATION NUMBER: US/09/467,082
CURRENT FILING DATE: 1999-12-17
                                                                                                      APPLICANT: Brett P. Monia
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF
FILE REFERENCE: RTS-0088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/429,322A CURRENT FILING DATE: 1999-10-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: RTS-0100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ANTISENSE MODULATION OF PROTEIN KINASE C-THETA TITLE OF INVENTION: EXPRESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: CDS
LOCATION: (95)
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ATTORNEY/AGENT INFORMATION:

Stephen A

REGISTRATION NUMBER:

38,609

2323-120A

/DOCKET NUMBER:

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                                                                                                                                                        ; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Human
US-09-800-960-1
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Best Local Similarity
Matches 154; Conserv
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                                                                                                                                                                                                                  SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                 CURRENT FILING DATE:
                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/800,960 CURRENT FILING DATE: 2001-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                           ENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                               TE REFERENCE:
                                                                                                                                                                                                                                                                                                            TLE OF INVENTION:
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 302 AGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTAT 361
                              465 ATCAGATTCTGGAGAGTGTTAACCACATCCACCAGCATGACATCGTCCACAGGGACCTGA 524
                                                            242 ACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTGA 301
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les 117; Conserv
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LOCATION: 96
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Pred. No. 0.00:
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0; Mismatches 1
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ENCODING HUMAN KI
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                                                                      US-08-966-316-10
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Query Match
Best Local Similarity
Matches 176; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mathur, Preete
TITLE OF INVENTION: SIGNAL PEPTIDE -
NUMBER OF SEQUENCES: 18
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                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                       TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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SOFTWARE: FastSEQ for Windows Version
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                                                                                  LIBRARY: SKINBIT01
CLONE: 1869688
                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                         LENGTH: 1637 base pairs
                                                                                                                                                                                                                                                            TELEFAX:
                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                               NAME: Billings, Lucy J
REGISTRATION NUMBER: 31
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
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nilarity 51.9%;
Conservative
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Murry, Lynn E.
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Score 49.8; DB 2;
Pred. No. 0.0093;
0; Mismatches 142;
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TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES
FILE REFERENCE: MNI-090
CURRENT APPLICATION NUMBER: US/09/948,802
CURRENT FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 09/387,212
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 18
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Best Local Similarity
Matches 513; Conser
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                GACTTTIGCCACCTICAIGTATGAACIGTGCTGTGGGAAGGCAGACAGCCTTCTTC-TCAT 766
                                                                                                                                                                                                                                                      GCACTGGGCCACCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCGGTT
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NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND PHOSPHATASE HOMOLOGUES AND USES THEREFOR
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98.5%;
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Pred. No. 1.4e-104;
); Mismatches 5;
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RESULT 4:
US-08-678-039A-41
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 41,
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Best Local Similarity
Matches 148; Conserv
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/
FILING DATE: 10-AUG-16989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 154,206
FILING DATE: 10-FEB-1988
                          SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/678,039A
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CORRESPONDENCE ADDRESS:
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                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Keating, Mark T.
APPLICANT: Morris, Colleen A.
TITLE OF INVENTION: Diagnosis
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FILING DATE: 1 CLASSIFICATION:
                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   MEDIUM TYPE:
                                                                                                                                                     COUNTRY: U
ZIP: 20004
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5 Thirteenth Street,
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eet, N.W., Suite 701
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Q
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40.8 40.8	41.2 41.2 40.8 40.8	42.4 42.4 41.6	43.4 42.6
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Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli	Sequence 9, Appli Sequence 35, Appl Sequence 37, Appl Sequence 37, Appli Sequence 3, Appli	Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 14, Appl Sequence 1, Appli	יוְבְּשִׁיִי
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## ALIGNMENTS

Qy 589 CTGGGGCAGCCGGAGGAAGTGCAGTTCCGGCGACTGCAGGGGCTCATGATGGAGTGCAGTGCTGG	529 246	Qy 469 Az 11 Db 186 Az	Qy 409 G1   1   Db   126 G1	Qy 349 AF Db 66 AF	Qy 289 TT Db 6 TC	Query Matc Best Local Matches 5	TYPE: DNA CORGANISM: HOMO FEATURE: OTHER INFORMAT US-09-387-212-10	SOFTWARE: P SEQ ID NO 10 LENGTH: 526	FILE REFE CURRENT A CURRENT F	GENERAL INFORMATION: APPLICANT: ROBISON TITLE OF INVENTION: TITLE OF INVENTION:	s-09-387-21 Sequence 1
reeecaecce	GCACTGGGCCACCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCGGTTGCCACTGGGCCACCACCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCGGTTGCCACGGCCACCAGCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCGGTT	AAGGTAGATATGTTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCT	GTGGAGGGCACTCCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAG 	AACATCAAGCTATCTGACTACGGGATTTCGAGGCAGTCATTCCATGAGGGCGCCCTAGGC	TTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATC.	Query Match 21.9 Best Local Similarity 98.9 Matches 513; Conservative	DNA ISM: Homo sapiens RE: INFORMATION: All -212-10	: SEQ 15 NOS: 1 : PatentIn Ver: 10 526	RENCE: PPLICAT ILING D	FORMATION: ROBISON, INVENTION: INVENTION:	US-09-387-212-10 ; Sequence 10, Application US/09387212A
AGGAAGTGCA	ACCAGCTCCAC	TCTCCTATGG	CTGGCTACCAC	CTGACTACGGC	AGTCGGACAA           AGTCGGACAA	dp dp	ens All occurences	Ver. 2.0		KEITH E. NUCLEIC ACII PHOSPHATASE	ion US/0938
CTGGGGCAGCCGGAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGG	BATTGCCAAGA/              BATTGCCAAGA/	ATGGTGCTCT!              ATGGTGCTCT!	GCCCCAGAGAT 	ATTTCGAGGCA              ATTTCGAGGCA	ATTCTGGTGTG           ATTCTGGTGTG	Score 477.6; DB 4; Pred. No. 1.4e-104; 0; Mismatches 5;	ces of n indicate		090 UMBER: US/09/387,212A 1999-08-31	ACID MOLECULES	7212A .
GCAGGCGCTC	AGCTGTCCAAGO	CGAGTTGCTG	CAGGCCTCGC	GTCATTCCATO	GTCCCTTGACO	DB 4; e-104; 5;	any		·	S ENCODING	
ATGATGGAGTG	GCATCCGCCC	PCAGGACAGCG	ATTGTATATGA            ATTGTATATGA	AGGGCGCCCT HIHHHHHH AGGGCGCCCT	TCAAGGAGCA           TCAAGGAGCA	Length 526; Indels 3;	nucleotide	.*	,	HUMAN KINASE THEREFOR	
CTGG 648	GGTT 588	CCCT 528	TGAG 468      TGAG 185	AGGC 408      AGGC 1:25	CATC 348 1111 CATC 65	Gaps	-			SE AND	

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                                                               AAGCCCAGCGGGGCCGAGTCATTGCCGTCTTAAAAGCCCGAGAGCTTGACTCCGCATGGGG 2011
                                                                                                                TCATTTGGGTCCCCAGGCGCGGTGGAGATGTTATCGTCATTGGCCTGGAGAAGGATTCTG 1951
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AGENCOURT_6854302 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5925776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l (bases 1 to 1072)
WIH-MGC http://mgc.nci.nih.gov/
Wational Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ssue Procurement: Lou Staudt
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Library."
331 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           using ZAP-cDNA synthesis kit (Stratagene) and Supe II RT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Gerald M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8kb. Library constructed by Ling Hong in the laboratory Gerald M. Rubin (University of California, Berkeley)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _xref="taxon:9606"
| lone="IMAGE:5925776"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        te="organ: lymph; Vector: poTBf; Site_1: XhoI; Site_2:
RI; cDA made by oligo-dT priming. Directionally cloned o EcoRI/XhoI sites using the following 5' adaptor:
ACGAG(G). Size-selected >500bp for average insert size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          one_11b="NIH_MGC_99"
                                                                                                                                                                                                                                                                                                                                                                  18.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ue_type="lymphoma, cell line"
host="DH10B (phage-resistant)"
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Pred. No. 1.3e-87;
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Search completed: April 15, 2003, 05:33:25 Job time: 2117 secs

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RESULT 14
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                                                                                                                                                                                                                                                             AGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTTCTGGTACAGCAATGGGCCGGGCCTCC
                                                                        CGGTACTTCTGTGGGGAACCCCAGTCTTCTCAGGGACACGCTTACC
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                                                                                                                   ATCGACGAGAACGGCCCATCGCTAACTGATGTACCAATCAGCACCTAACAGCTCCGTG-C
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Plate: LLAM9451 row: j column: 22
High quality sequence stop: 575.
  AW502376 465 bp mRNA
UI-HF-BROp-aka-f-03-0-UI.rl NIH_MGC_52
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/Strain="rvo/"
/db_xref="taxon:10090"
/clone="IMAGE:4164981"
/clone_lib="NCI_CGAP_SG2"
/lab_host="PH10B (Tl phage-resistant)"
/note="Organ: salivary gland; Vector: pcMV-SPORT6; Si NotI; Site_2: Sali; Cloned unidirectionally. Primer: dT. Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
a 302 c 241 g 156 t
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Pred. No. 4.1e-90;
D; Mismatches 116;
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Eukaryota; Me
Mammalia; Eut
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Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information
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National Institutes of Health, Mammalian
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Seq primer: M13 Forward.
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/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco R:
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco R:
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/tissue_type="lymph"
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/db_xref="taxon:9606"
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/cell_line="MGC85"
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Catarrhini;
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Mases 1 to 471)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan
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UI-HF-BNO-ak1-h-09-0-UI.r1 NIH_MGC_50 Hc
IMAGE:3077249 5', mRNA sequence.
AM500039
                                                                                            Email: cgapbs-r@mail.nlh.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution informe

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                              www-bio.llnl.gov/bbrp/image/image.html
                                                                  primer: M13 Forward
                                              Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BF301427
BF301427.1 GI
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Incyte Genomics, Inc.
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602029885F1_NCI_CGAP_SG2
                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, &
Unpublished (1999)
Contact: Robert Strausberg, Ph.1
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/lab_host="DHIOB (LTI)"
/note="Yector: pT7T3-Pac; Site_1: NotI; Site_2: Eco R
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/note="Yector: pT7T3-Pac; Site_1: NotI; Site_2: Eco R
/note="Yector: pT7T3-Pac; Site_1: NotI; Site_2: Eco R
/note="Yector: pT7T3-Pac; Site_1: NotI; Site_2: Eco R
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/cell_line="MGC85"
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/clone_lib="NIH_MGC_50
/tissue_type="lymph"
/cell_type="germinal c
                                                                                                                                                                                                                                                                                          Metazoa;
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Pred. No. 2.2e-90;
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                      Mammalian
                                                                                                                                                                                      Gene
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Computer-based methods for the mouse full-length cDNA

Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P.,

Sugahara

Hayashizaki,Y

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FEATURES
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TCAACAGCGGCTCTGAGGTCTGGTACAGCAATGGGCCGGGCCTCCTTGTCATCGACTGTG 1294
                                                                                                                                                                                                                                                                                                                                                             AGGCCTGGACACCCCAGCTGTCGTCACCTGTTTCTTGGCAGTACCTGTTATCAAAAAGA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGACCAGAAAATCTACATCTACACCCTCAAGGGCATGTGCCCCTTAAACACACCCCCAAC 994
                                                                                                                                                           TCAGCATCGCGGATGAAGACGCACGGCAGAACCCCTACCCAGTGAAGGCCATGGAGGTGG
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                                                                                                                                                                                                                                                                                                     ATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTTGTGGGCTGTTTTCCCGTGGTGC 1114
                                                                                                                                                                                                                                                                                                                                                                                                  AGGCCTTGGATACTCCAGCTGTCGTCACCTGCTTCTTGGCCGTGCCTGTTATTAAAAAGA 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                          AGGACCAGAAAATCTATATCTACAGCCTTAAGGGTATGTGCCCCATTAAGCGTGCCCCAGC 86
                                                                                                                    TCTGCATCCCGACGAAGATGCACGGCAGAACCCTTACCCAGTGAAGGCAATGGAAGTGG
                                                                                                                                                                                                   GGGGCACCCCAAAAGAAAGCTGCTCCTACCTGTGCTCCCACACAGCCAACAGGTCCAAGT : 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     further details
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Please visit our web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Computational Analysis of Full-Length Mouse cDNAs Compared with tuman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                was cloned into the XhoI and BamHI sites. Vector: modified pBluescript KS(+) after bulk excision from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Rik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="head"
/dev_stage="16 days
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="C130082A22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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                                 1092_TGTGGCTGTGTTTCCCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTCCTACCTGTGCTC 1151
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                                                                                                                   GGCAGTACCTGTTATCAAAAAGAACTCCTTCCTGGTGCTGGCAGGCCTGGCTGACGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.I
cDNA Library Preparation: Life Technolog
cDNA Library Arrayed by: The I.M.A.G.E.
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Plate: LLAM9815 row:
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National Institutes of Health, Mammalian
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       found through the I.M.A.G.E. Consortium/LLNL
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Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg,
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                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:4224922".
/clone_lib="NCI_CGAP_CO24"
/clone_lib="NCI_CGAP_CO24"
/lab_host="DH10B ('Tl phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1
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D; Mismatches 137;
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                                                                                          CTCCTTGTCATCGACCTGTGCCTCCCTGGAGATCTGCAGGCGCCTGGAGCCCTACATGGCC
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
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PM0-MT0202-090501-013-h11
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                              /note-"Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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/dev_stage="Adult"
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1 (bases 1 to 715)

Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.,
Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,H., Sasaki,A., Nomura,K., Ohno,H., Sasaki,A., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
                                                                               Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., 1t,
M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
gones. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuu
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                    Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2001)
Contact: Yoshihide Hayashizaki --
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                                                                   Hayashimaki,Y
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  RIKEN integrated sequence analysis (RISA) system 384-formut
requencing pipeline with 384 multicapillary sequencer. Genomo
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Plate: LLAM12269 row: c column: ??
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pec
Bovidae; Bovinae; Bos.
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/tissue_type="lymphoma, cell line"
/tissue_type="lymphoma, cell line"
/tlab_host="DH10B (phage resistant)"
/note="Organ; lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 323 c 271 g 180 t 1 others
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Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.1 Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called
v0.980904.e. Vector identified by crc
and .minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USDA, ARS, US Meat Animal PO Box 166, Clay Center, N Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTITTCCCAGTCAGCAGC
Plate: 82 row: F column: 5
Seg primer: ATTTAGGTGACACTATAG
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156 c 175 g 100 t
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/db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-res@gsc.riken.go.jp, *URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-607 (2000)
wag1,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
wayashiraki,Y.
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Konno,H., Fukunishiy., Shibata,K., Itoh,M., Carninci,P., Sugging and Britanishiy.
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/dev_stage="0 day neonate"
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/strain="C57BL/6J"
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        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
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Mammalia; Eutheria; Primates; Catarrhini;
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                                                                        Contact: Robert Straustry
Email: cgapbs r@mail.nih.gov
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llni.gov
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Plate: LLAM9957 row: k column: 12
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectonpublished (1999)
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/db_xref="taxon:9606"
/clone="IMAGE:4342403"
/clone_lib="NIH_MGC_85"
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Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 638)
Arakawa, T., Carninci,
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/lab_host="hBHOB (phage-resistant)"
/note="organ: lymph; Vector: pcMv-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
a 323 c 283 g 197 t
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                                                                                                                     638 bp mRNA RIKEN full-length enriched, 0 day cDNA clone 4832415J17 5', mRNA sec
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Rodentia;
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Sciurognathi; Muridae;
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les 49;
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REFERENCE

Fukuda,S.,

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                       GCTGCTCCTACCTGTGCTCACACACACACCACCACCACCTCCAAGTTCAGCATCGCGGATGAAG 1192
                                                                  CAGECCTGGCTGACGGACTCGTGGCTGTTTTCCTGTGGCACGGGGCACCCCAAAAGACA
                                                                                                                                                            CTACAGCCTTAAGGGTATGTGCCCATTAAGCGTGCCCCAGCTAGGCCCCTGGACACCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGGAGTACACTGTGGTGTTCTGGGATGGGAAGGAGGAGTCCAGGAATTACACGGTGGT
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://imagg.llnl.gov
Plate: LLAMI1115 row: 1 column: 20
H1gh quality sequence stop: 783.
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/clone_lib="NCI_CGAP_Kid14"
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1:
S1te_2: Sall; Cloned unidirectionally. Primer: Oll
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 243 c 252 g 178 t
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 al Similarity
546; Conser
                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information or through the I.M.A.G.E. Consortium/LLNL at: http://image.series: IRAL Plate: 20 Row: c Column: 22
This clone has the following problem: incomplete process
                                                                                                                                                                                                                                                                                                                                                                                              Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Shevchenko,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Broo
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Karlins,E., Legas
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legas
Lim,M., Maduro,O.L., Masiello,C., Mastrian,S.D., McCloskey,J.
McDowell,J., Pearson,R., Snyder,B., Stantipop,S., Thomas,P.J
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (07-DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens,
BC018934
                                                                                                                                                                                                                                                                                                                                                                              Zhang, L.-H. and Green, E.D.
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Tissue Procurement: ATCC
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Contact: MGC help desk
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                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4120491"
/tisshe_type="Muscle, rhabdomyosarcoma"
/clone=lib="NIH_MGC_17"
/lab_host="DH10B-R"
/noten "vector: poTB7"
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clone IMAGE:4120491,
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Primates;
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Pred. No. 8.5e
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                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution: MGC clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 611)
NH+MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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603022572F1 NIH_MGC_114
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Plate: LLAM11483 row: o column:
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/lab_nostr______/
/note-*Organ: brain; Vector: pCMV-SPORT6; bite_1. ______/
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dr
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
range 1-3 kb. Library is normalized by C. Gruber
                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:5193448"
/clone_11b="NIH_MGC_114"
                                                                                                                                                                                                                                                     location/Qualifiers
                                                                                                                                            'lab_host="DH10B"
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BASE COUNT
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TITLE
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BI100538
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                             COMMENT
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Best Local Sim
Matches 606;
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 Email:
Tissue
                         NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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06; Conservative
                                                                                                                          Mus musculus
                                                                                  Mammalia; Eutheria;
1 (bases 1 to 863)
                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                      BI100538.1 GI:14551431
                                                                                                                                          house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111
cgapbs-r@mail.nih.gov
Procurement: Jeffrey 1
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this is a NIH_MGC Library."
1 · 213 c 169 g 118 t
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99.3%;
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Rodentia;
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 [F]
                                                                                               Craniata; Vertebrata;
Sciurognathi; Muridae;
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musculus
  Green,
  3
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Best Local Similarity
Matches 2074; Conser
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AGGCCAGGAGTACACCGTGGTGTTTTGGGATGGAAAAGAGGAGTCCAGGAACTACACGG
                                                                      CTTTTGCCACCTTCATGTATGAACTGTGCTGTGGGAAGCAGACAGCCTTCTTCTCATCCC
                                                                                                                                                               ACACTAAGCCAGAGAAGCGACCGCTGGCCCTGTCGGTGAGGCCAGATGAAGGACCCGA
                                                                                                                                                                                                                                       TGGGGCAGCCGGAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGG
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                                                                                                                                            ACACTAAGCCAGAGGAGCGACCGCTGGCCCTGTCGGTGAGCCAGATGAAGGACCCGA
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This clone has the following problem: no 5' EST match.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, ) A:M.,Holloway, M., Telford, B, Hodgson, A., Bouck, J., 1 Muzny,D.M., Gunaratne, P., Yoon, V., Kowis, C., Martin; Lawrence, S., Richards, S., Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            810
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/db_xref="taxon:9606"
/clone="IMAGE:3463102"
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994 c 953 g 752 t
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/clone_lib="NIH_MGC_12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'lab_host-"DH10B"
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93.3%;
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Pred. No. 0;
0; Mismatches
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J., Yu, W.,
rtin; R.,
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1909	850 GCCAGCACCTGCAGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCCAGGC	Qy
1740	681 CCGGTGCTGCCTCCGACAGGTCTGAGCATGACCTGACCCCCATGGACGGGGAGACCTTCA	Db
1849	GGTGCTGCCTCCGACAGGTCTGACCATGACCTGACCCCCATGGACGGGGAGACCTTCA	Qy
1680	730 CAAGTTCTTCCAGTGTGCCTTTCTCCACCGACTGCGAGGACTCAGACATGCTACATACGC	da A
N	561 ACTCCTCATCCCCACCCGCCAGGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTCCCCAG	, B
1729	70 ACTCCTCATCCCCACCCCCCCAGGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTCCCCAG	γQ
5	501 TGGGCACGCAGATCCTGATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCT	Db
1669	610 TGGGCACGCAGATCCTGATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCT	Qy
G O	550 ACCCAAAGGTGCCTGAGGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGC	Оγ
1440	381 GGGACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCAGC	В
1549	490 GGGACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCAGC	Qy
æ		Db
80	430 ACCACTCCACCACCTACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCAGCCCCCTCA	Qy
3 2		₽,
-	3GCAGAGGGGAGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGT	γΩ
26	201 GCAGGCGGCTGGAGCCCTACATGGCCCCCTCCATGGTTACGTCAGTCGTGTGCAGCTCTG	В
w	310 GCAGGCGGCTGGAGCCCTACATGGCCCCCTCCATGGTTACGTCAGTCGTGTGCAGCTCTG	γQ
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∔ دس	250 AGGTCTGGTACAGCAATGGGCCGGGGCCTTCCTTGTCATCATCTATCT	ογ
1 4	081 AAGACGCACGAAAACCCCTACCCAGTGAAGGCCATGGAGGTGGTCAAACAGCGCTTTTG	<del>р</del>
1249	AGACGCACGGCAGAACCCCTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTC	Ωy
1189	1130 ACAGCTGCTCCTACCTGTGCTCACACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATG	Db Qy
1020	61 TAGC	В
1129	70 TAGCGGGCCTCGCCGATGGGCTTGTGGCTGTGTTTTCCCGTGGTGCGGGGCACCCCAAAG	Qy
960	901 CAGCTGTCGTCACCTGCTTCTTGGCCGTGCCTGTTATTAAAAAGAATTCCTACCTGGTCT	Db.
1069	10 CAGCTGTCGTCACCTGCTTCTTGGCCGTGCCTGTTATTAAAAAGAATTCCTACCTGGTC	Qy
	841 ACATCTACACCCTCAAGGGCATGTGCCCCTTAAACACACCCCAACAGGCCTTGGATACTC	DЬ
1009	50 ACATCTACACCCTCAAGGGCATGTGCCCCCTTAAACACACCCCCAACAGGCCTTGGATACT	Qy
4		dd
949	90 TGAGCTGCCAGCTCCAGGTCCAGAGATCCCTGTGGACAGCCACCGAGGACCAGAAAATC	Qy
œ		Db -
889 9	30 TGGTGAACACAGAGAAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAG	VΩ

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Title:
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                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                       1915.4
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2184
1 atgctgaggcacctgcgggc.....
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BC018934 Homo sapi
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## ALIGNMENTS

	REMARK COMMENT	AUTHORS TITLE JOURNAL	SOURCE ORGANISM REFERENCE	RESULT 1 BC020379 LOCUS DEFINITION ACCESSION VERSION VERSION
CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: villalon@bcm .tmc.edu.	USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC	Strausberg,R.  Direct Submission  Direct Submission  Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	Homo sapiens. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  1 (bases 1 to 3509)	BC020379 3509 bp mRNA linear HTC 03-JAN-2002 Homo sapiens, clone IMAGE:3463102, mRNA. BC020379 BC020379.1 GI:18042971

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c pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
c carcinomas, and cancers which may metastasise to the lungs, including
breast and prostate cancer. The reduction of the adenosine content of
the ONS reduces side effects. The A-containing ONS break down with the
release of deoxyadenosine which activates adenosine receptors causing
bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
nucleotide sequences given in the sequence listing from the present
invention, which correspond to SEQ ID NO:1 to 2815, but the sequences
differ from the previously named sequences. SEQ ID NO:11 to 1880
(AAA33233 to AAA3392) are specifically claimed ONS from the present
invention. N.B. Sequences given in the disclosure of the present
invention do not match up with their corresponding SEQ ID NO: sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.1
Best Local Similarity 55.9
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antisense oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, and instabliantic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired aliways, including lung diseases and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain, cystic asthma, impeded respiration, respiratory distress syndrome, pain, cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 1310-1311; 1343pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstriction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-205971/18.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
pulmonary hypertension; emphysema; pulmonary transplantation rejection;
                                                                                                                                 Disclosure;
                                                                                                                                                                                                                                       iow adenosine (A) content antisense oligonucleotides which
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                                                                                                                                 Page 1395-1396; 1592pp;
                                                                                                                                                                                                                                                                                                                                                                                                    EAST CAROLINA.
J W.
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Pred. No. 1
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Best Local S
Matches 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmitters, defensins, growth factors, vascattive peptides and receptors, binding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasconstriction, inflammation, allergies, asthma, impeded respiration, respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary hypertension, emphysema, chronic obstructive pulmonary disease (CODD), pulmonary transplantation rejection, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fragments and antisense oligonucleotides used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The antisense oligonucleotides and (I) can be used to down-regulate expression and or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, chemokines, endogenously produced specific and non-specific enzymes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    binding proteins, adhesion molecules and their receptors, cytokine and chemokine receptors, adenosine receptors, bradykinin receptors, central nervous system (CNS) and peripheral nervous and non-nervous system receptors, CNS and peripheral nervous and non-nervous system peptide
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157; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
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Pred. No. 1.2e-05;
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respiratory distress syndrome; pain; cystic fibrosis; emphysem:
pulmonary hypertension; chronic obstructive pulmonary disease;
                                                                                                                                                       phosphorothicate; impaired respiration; inflammation; allergy; allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
                                                                                                                                                                                                                                                                                                    Human adenosine receptor related polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA35295
                                                             antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
lung disease; ischaemic condition; pulmonary vasoconstriction; asthm
respiratory distress syndrome; pain; cystic fibrosis; emphysema;
                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2000
                                                                                                                                                                                                                                       adenosine receptor; low adenosine antisense
leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
carcinoma; metastasis;
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                                                                                                                                                                                                                                                                                                            SEQ
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NO:169.

asthma;

The present invention describes low adenosine (A) content antisense oligonuclectides and compositions (I) comprising them: In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,

sapiens

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RESULT 12
AAS72237
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  CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC polymucleotides are also used in diagnostics as expressed sequence tags CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. CC The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC diagnostic coding sequences of the invention. CC diagnostic coding sequences of the invention. CC diagnostic coding sequences of the invention. CC diagnostic coding sequences of the invention. CC diagnostic coding sequences of the invention. CC are the sequence data for this patent did not appear in the printed confiction, but was obtained in electronic format directly from WIPO at figure in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the printed confiction in the print
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food supplement; medical imaging; diagnostic; genetic disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide and encoded polypeptides, use diagnostics, forensics, gene mapping, identification of mresponsible for genetic disorders or other traits and to biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT, Liu
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23-AUG-2000;
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Sequence 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention
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DB; ABG08050.
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2000US-0649167.
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BP;
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88
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111 C;
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94 G;
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76 T; 0 other;
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Query Match Best Local :

Local Similarity

99.08;

Score Pred.

103.4; No. 6e-

.4; DB 23; 6e-14;

Length 369;

Sequence 1625 BP; 330 A; 491 C;

471 G;

333 T; 0 other

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RESULT 13
AAS87109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, uidiagnostics, forensics, gene mapping, identification of responsible for genetic disorders or other traits and to biodiversity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding novel
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                                                                                                                                                                                                                                                                                                                                                          polypeptide (II) sequences. (I) is useful as hybridisati polymerase chain reaction (PCR) primers, oligomers, and and gene mapping, and in recombinant production of (II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and
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                                 ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                Human; ss; protein kinase; mine32641human_s1; cytostatic; a hypotensive; cardiant; cardiovascular disorder; heart failu hypertension; atrial fibrillation; dilated cardiomyopathy; idiopathic cardiomyopathy; angina; proliferative disorder; melanoma; prostate cancer; cervical cancer; breast cancer; colon sarcoma; qene therapy.
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                                                                                                                                                                                                      Homo sapiens
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                                                  31-AUG-1999;
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r; heart failure;
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The invention relates to identifying a compound which binds to a Kinase CC (encoded by a nuclectide sequence of 1888, 403, 545, 361, 473, 3001, 526, 683 or 1448 base pair (bp) as given in the specification) comprising CC contacting the kinase with a test compound under suitable conditions for binding, and detecting binding of the compound to the kinase. CC The method is useful for identifying a compound which binds to the kinase. CC disorder characterised by aberrant kinase activity of the kinase. CC disorder characterised by aberrant kinase activity where the disorder includes cellular growth related disorders which includes a disorder, claim or a downregulation, of cellular growth, cellular growth CC deregulation or a downregulation, of cellular growth, cellular growth CC deregulation of cellular proliferation, cell cycle conditions callular differentiation and/or cellular hypertrophy, cc cardiovascular disorders such as heart failure, hypertension, atrial CC fibrillation, dilated cardiomyopathy, idiopathic cardiomyopathy, or candinal, proliferative disorders such as cancer (including melanoma, prostate cancer, cervical, breast, colon sarcoma). The kinases can antibodies raised against them are useful in one or more method composition as screening assays, predictive medicine and methods of treatment cand motopath (e.g. in gene therapy applications), to detect kinase and composition in a Kinase and phosphatase gene and to modulate kinase and phosphatase activity. The present can be composed to the composition of the composition of a composition of a composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition of the composition o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying compound which binds to a Kinase, useful for treating diseases e.g. cancer, by contacting kinase with test compound and detecting its binding to the kinase {}^{\circ}
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Sequence 526 BP; 115 A; 137 C; 160 G; 111 T; 3 other;

21.9%;

24;

Length

δÃ Db ρy дb ΩĄ В Š 8 δÃ 밁 9 밁 Š Query Match Best Local Similarity Matches, 513; Conserv 246 529 186 469 126 409 349 289 66 σ GCACTGGGCCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGAGGGCATCCGCCCGGTT AAGGTAGATATGTTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCT GTGGAGGGCACTCCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAG AACATCAAGCTATCTGACTACGGGATTTTCGAGGCAGTCATTCCATGAGGGCGCCCTAGGC TCCGGTGACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATC TTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATC CTGGGGCAGCCGGAGGAAGTGCAGTTCCGGCGACTGCAGGCGCT AACATCAAGCTATCTGACTACGGGATTTCGAGGCAGTCATTCCATGAGGGCGCCCTAGGC GTGGAGGGCACTCCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAG Conservative Score 477.6; DB 2 Pred. No. 5.5e-99; 0; Mismatches 5 <u>ن</u> Indels ω •• Gaps 468 65 425 707 365 588 245 528 185 125 w ..

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2001US-0259678.
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Rosen CA, Barash .SC, Ruben MS

WPI; 2001-483426/52

metastasis Nucleic acids encoding useful for preventing, preventing, human immune/hematopoietic diagnosing and/or treating cancers n polypeptides, and

Disclosure; CI DES NO 38919; 3071pp + Sequence Listing; English

cc amino acid sequences given in AAM82170 to AAM891921. (1) have cytostatic contivity, and can be used in gene therapy and vaccine production. (1) cc proteins and polynucleotides may be used in the prevention, diagnosis and ct treatment of diseases associated with inappropriate (1) expression. For ce example, they may be used to treat disorders associated with decreased complex they may be used to treat disorders associated with decreased complex they may be used to treat disorders associated with decreased complex the patients own production of (1). Additionally, (1) cc supplement the patients own production of (1). Additionally, (1) cc polynucleotides may be used to produce the secreted (1), by inserting complex the nucleic acids into a host cell and culturing the cell to express the complex and treat immune/haematopoietic-related diseases, especially concers and cancer metastases of haematopoietic antigen genomic concerns according to the present invention. AAK54921 to AAK87650 and AAM82169 concerns a con represent sequences ç AAK64702 used in encode the exemplification immune/haematopoietic antigen of the present invention E

Sequence 18287 B₽; 4371 ? 4858 C; 4942 <u>ი</u> 4116 T; 0 other;

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                                                                AGTTCAGCATCGCGGATGAAGACGCACGGCAGAACCCCTACCCAGTGAAGGCCATGGAGG
                                           881;
                                                                                            Similarity
                                                                                       Conservative
                                                                                           39.3%;
                                                                                     Score 858.8; pred. No. 3.2e 0; Mismatches
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3.2e-185;
hes 37;
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1292

GTGCCTCCCTGGAGATCTGCAGGCGGCTGGAGCCCTACATGGCCCCCTCCATGGTTACGT

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TCATTTGGGTCCCCAGGCGCGGTGGAGATGTTATCGTCATTGGCCTGGAGAAGGATTCTG
                                                              TGGACGGGGAGACCTTCAGCCAGCACCTGCAGGCCGTGAAGATCCTCGCCGTCAGAGACC
                                                                                                                                                                                     GCCTCCCCAGCTCCCCAGCAAGTTCTTCCAGTGTGCCTTTCTCCACCGACTGCGAGGACT
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                                            TGGACGGGGAGACCTTCAGCCAGCACCTGCAGGCCGTGAAGATCCTCGCCGTCAGAGACC
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hes 37;
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22-AUG-2000;
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cytostatic; gene therapy; vacc
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2000US-0209467.

2000US-0214886.

2000US-0215135.

2000US-0216647.

2000US-0217487.

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2000US-0217487.

2000US-0217496.
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2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
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ine; metastasis; ds.
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20-OCT-2000;
01-NOV-2000;
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08-NOV-20
08-NOV-20
08-NOV-20
08-NOV-20
08-NOV-20
AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, disgnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I)
                                                                                                                                                                 WPI;
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                                                                                                                         Nucleic acids encoding useful for preventing, metastasis -
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                                                                                                     Disclosure;
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                                                                                                                                                                                      CA,
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2000US-0249300.

2000US-0250160.

2000US-0250391.

2000US-0251930.

2000US-0251988.

2000US-0251988.

2000US-0251869.

2000US-0251869.

2000US-0251989.

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2000US-0249215.

2000US-0249216.

2000US-0249217.

2000US-0249218.

2000US-0249244.
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2000US-0246475.
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2000US-0246523
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                                                                                                                                   human immur
diagnosing
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                                                                                                                                   immune/hematopoietic antigen
osing and/or treating cancers
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08-SEP-2000; 08-SEP-2000;

08-SEP-2000 11-SEP-2000 11-SEP-2000 11-SEP-2000 11-SEP-2000 11-SEP-2000 11-SEP-2000 11-SEP-2000 11-SEP-2000 21-SEP-2000 21-SEP-2000 25-SEP-2000 25-SEP-2000 27-SEP-2000 27-SEP-2000 27-SEP-2000 29-SEP-2000 29-SEP-2000

2000US-0232080 2000US-023299 2000US-0232398 2000US-0232398 2000US-02333063 2000US-0233063 2000US-0233063 2000US-0233063 2000US-0233063 2000US-0234998 2000US-0234997 2000US-0235484 2000US-0235484 2000US-0235484 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0235836 2000US-0236367 2000US-0236367 2000US-0236367 2000US-0237038 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0237038 2000US-0237038 2000US-0237038 2000US-0237038 2000US-0237038 2000US-0237038 2000US-0237038 2000US-0237038 2000US-0237039 2000US-0237039 2000US-0237039 2000US-0241786 2000US-0241786

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Listing; English

polypeptides, and

05-SEP-2000; 05-SEP-2000; 06-SEP-2000; 06-SEP-2000;

2000US-0227009.
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2000US-0229344.
2000US-0229345.
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2000US-0229509.
2000US-0239509.
2000US-0239437.
2000US-0239437.
2000US-0231434.
2000US-0231443.
2000US-0231443.

01-SEP-2000; 01-SEP-2000;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54912 to AAK54950 and AAM82169 carefresent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoletic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and
metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 18286 BP; 4372 A; 4856 C; 4941 G; 4117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAK54951 to AAK64702 encode the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
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                                                                                                                                                   CCAACTCCTTGGTGATGTACCACTCCACCACCTACCAGCTGTGTGCCCGGTACTTCTGCG 1471
                                            CAGTCGTGTGCAGCTCTGAGGGCAGAGGGGAGGAGGTCGTCTGGTGCCTGGATGACAAGG 1411
                            CAGTCGTGTGCAGCTCTGAGGGCAGAGGGGGGGGGGTCGTCTGGTGCCTGGATGACAAGG
                                                                                                                                                                                                                                                                                                                                          AGAATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCCTTGTGGCTGTTTTCCCCGTGG 13583
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                                                                                                                                                                                                                                                                                                                                                                                                       881; . Conservative
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2000US-0251869.
2000US-0251989.
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2001US-0259678.
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96.0%;
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                                                                 18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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02-MAR-2000;
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04-FEB-2000;
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                     2000US-0189874.

2000US-0190076.

2000US-0198123.

2000US-0205515.

2000US-0209467.

2000US-0214886.

2000US-0215135.
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RESULT 5
AAK84104
ID AAK8
01-SEP
01-SEP
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                                                                                                                                                                                                                                                               Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
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23-AUG-
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2000US-0232398.
2000US-0232399.
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AAK54951 to AAK64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis ar treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the
                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                 Nucleic acids encoding useful for preventing, metastasis -
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                                                                                                                                                                                                        human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
                                                                                                                                                                           3071pp + Sequence Listing; English
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protein. (I) proteins and polynucleotides may be used to prevent, diagnose and trent immune/haematopoletic-related diseases, especially cancers and cancer metastases of haematopoletic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic

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immune/haematopoietic antigen genomic invention. AAK54942 to AAK54950 and AAM82169

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                                                 TCATTTGGGTCCCCAGGCGCGGTGGAGATGTTATCGTCATTGGCCTGGAGAAGGAT;CTG
                                                                             GCCTCCCCAGCTCCCCAGCAAGTTCTTCCAGTGTGCCTTTCTCCACCGACTGCGAGGACTGCCITCCCCCAGCTCCCCAGCAGTGTCTTCCAGTGTGCCTTTCTCCACCGACTGCGAGGACTGCCGAGCACTCTTCCCAGCCAACTGCGAGGACTGCAGGACTGCCCAGCCAACTGCCAAGTTCTTCCAGTGTGCCTTTCTCCACCGACTGCGAGGACT
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                                     TCATTTGGGTCCCCAGGTACGTTCCCGAGGTGAGGGCACCATCCAGGGCACGCCCACTG
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Pred. No. 3.2e-185;
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cytostatic; gene therapy; vaccine; metastasis; ds.
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04-FEB-2000;
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28-JUN-2000;
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Claim 5; Page 192-194; 210pp; English.

affecting growth and development (e.g., arteriosclerosis, cirrhosis, hepatitis), cardiovascular disorder (e.g., hypertension, myocardial infarction, Goodpasture's syndrome), and a lipid disorder (e.g., fatty liver, Gaucher's disease, Niemann-Pick's disease, hypercholesterolaemia, compounds. Anti-PKIN antibody is useful in a diagnostic test for a condition or a disease associated with the expression of PKIN in a biological sample. A composition comprising PKIN or an agonist or antagonist of PKIN is useful for treating a disease or condition associated with decreased or increased expression of functional PKIN. FKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN DNA is useful for creating knockin humanised animals or transgenic animals to model human diseases, and in somatic or germline gene therapy. The present sequence is human treating and preventing cancer, an immune system disorder (e.g., acquired immune deficiency syndrome (AIDS), Addison's disease, all asthma, atherosclerosis, multiple sclerosis, psoriasis), disorders nucleic acid sequences. PKIN and its DNA are useful for diagnosing, relates human kinases (PKIN) and their corresponding allergy,

Sequence 7093 BP; 1554 A; 2102 C; 2027 G; 1410 T; 0 other;

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16-NOV-2000;
22-NOV-2000;
01-DEC-2000;
                                                                                                                                                                                                                                                                                                                                               Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis; development; hepatitis; cardiovascular; hypertension; drug screening; myocardial infarction; Goodpasture's syndrome; lipid disorder; growth fatty liver; Gaucher's disease; Niemann-pick's disease; anorectic; hypercholesterolaemia; obesity; gene therapy; cytostatic; anti-hIV; neuroprotective; hepatotropic; hypotensive; cardiant; nephrotropic; hyperlipidaemia; enzyme; gene; ss.
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29-MAR-2000;
13-NOV-2000;
The present sequence encodes a human protein kinase. The gene is located on chromosome 15. The kinase polypeptides are useful for diagnosing a disease or disorder selected from cancers (e.g. cancers of tissues and cancers of hematopoietic origin), immune-related diseases and disorders, cardiovascular disease, brain or neuronal-associated diseases (e.g. Alzheimer's disease, Parkinson's disease, multiple
                                                                                                                                                                                                                                               Nucleic acids capable of encoding human polypeptides having a kinase or kinase-like activity, useful for diagnosing a disease selected from cancers, cardiovascular disease and neuronal-associated discuses (e.g. Alzheimer's disease)
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hypertension; psychotic disorder; dyskinesia; transplant rejection;
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1740	1681 CCACCCCGCCAGGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTCCCCAGCAAGTTCTTCC	Qy	
	1621 ATCOTGATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCTACTCCTCATCC	Оу	
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polypeptide (II) sequences. (1) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tays for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or treat disease states involving (II). (II) is useful for generating antihodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a rood supplement. (II) and its binding partners are useful for treating disorders involving abbrrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in
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AAD33692-AAD33736 represent cDNAs corresponding to 21 human secreted protein genes, and AAE21191-AAE21235 represent the proteins they encode. AAE21236-AAE212360 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of nutations in the new genes. Specific uses are described for each of the 21 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of immune or autoimmune diseases e.g. AIDS (acquired immune deficiency syndrome), asthma, anaemia and rheumatoid arthritis, breast neoplasia
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7	900 967	GAGAAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAGCTGCCAG 	841 908
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7	480 547	CCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATAAGAAAGGTAGATATG	421 488
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7	360 427	AAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTA	301 368
7	300 367	TACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTG	241 308
.7	240 307	GAGAACGCCAGAGATTCTTCCTTTATACCCCTGGGACACATGCTCACCCAAAAAATAGCC 	181 248
7 0	180 247	CACCCGCTCTGCTTCGCCCTGGAGCTCGCGCCGCTCAGCAGCCTCAACACCGTGCTGTCC	121 188
7 0	120 187	GCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATC	61 128
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	2160	GCTGGGGCGCCAGGGAGTTCGACATTTTTCTACCAGTCCTACGAGGAGCTGGGCCGGC	Qγ	
	2167	2108 GACACTGTTGTGTGCACCTTTGAAAATGAAAACACAGAGTGGTGCCTGGCCGTCTGGAGG	ΔQ	
	2100	ACACTGTTGTGTGCACCTTTGAAAATGAAAACACAGAGTGGTGCCTGGCCGTCTGG	Qy	
	2107	2048 TTAAAAGCCCGAGAGCTGACTÇCGCATGGGGTGCTGGTGGATGCTGCCGTGGTGGCAAAG	dg.	
	2040	TAAAAGCCCGAGAGCTGACTCCGCATGGGGTGCTGGTGGATGCTGCCGTGGTGGCAAA	Qy	
	2047	1988 GTTATCGTCATTGGCCTGGAGAAAGGATTCTGAAGCCCCAGCGGGGCCGAGTCATTGCCGTC	рь	
	1980	921 GTTATCGTCATTGGCCTGGAGAAGGATTCTGAÄĞCCCAGCGGGGCCGAGTCATTGCCGT	Qу	
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	1920	AGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCCAGGCGCGGTGGAGA	Qy	
	1927	1868 TCCGACAGGTCTGAGCATGACCTCCATGGACGGGGAGACCTTCAGCCAGC	DЬ	
	1860	CCGACAGGTCTGAGCATGACCTGACCCCCATGGACGGGGAGACCTTCAGCCAGC	Qy	
	1867	1808 AGTGTGCCTTTCTCCACCGACTGCGAGGGACTCAGACATGCTACATACGCCCGGTGCTGCC	ф	
	1800	GTGTGCCTTTCTCCACCGACTGCGAGGACTCAGACATGCTACATACGCCCGGTGCTGC	Qу	
	1807	1748 CCACCCCGCCAGGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTCCCCCAGCAAGTTCCTTCC	Дb	
	1740	CACCCCCCAGGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTCCCCAGCAAGTTCTTC	Qy	
•	1747	1688 ATCCTGATCCACCAGGAATCACTGACTGACTACTGCTCCATGTCCTCCTACTCCTCATCC	Db	
	1680	TCCTGATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCTACTCCTCATC	Qy	
	1687	1628 CCTGAGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCAG	ДD	
	1620	CTGAGGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCA	Qy	
	1627	1568 CCCGTGCGGCCTTGGACACGGAACCCCCGGCAGCCAGCCA	망	
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	1507	1448 GAGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACTCCACC	фd	
	1440	aggaggtcgtctggtgcctggatgacaaggccaactccttggtgatgtaccactccac	γQ	
	1447	1388 GAGCCCTACATGGCCCCCTCCATGGTTACGTCGTGTGCAGCTCTGAGGGCAGAGGG	В	
	1380	AGCCCTACATGGCCCCCTCCATGGTTACGTCAGTCGTGTGCAGCCCTGAGGGCAGAGG	Qy	
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      Human; secreted protein; immune disorder; antiallergic; antirheumatic; rheumatoid arthritis; breast neoplasla; breast cancer; antiarthritic; neurological disease; Alzheimer's disease; Parkinson's disease; trauma; Tourette syndrome; encephalitis; cytostatic; haemostatic; anaemia; mania; antiinflammatory; ophthalmalogical; dermatological; immunostimulatory; immunomodulatory; immunosuppressive; antibacterial; antipsoriatic; gene therapy; autoimmune disease; Huntington's disease; meningitis; demyelinating disease; peripheral neuropathy; congenital malformation; spinal cord injury; peripheral neuropathy; ischaemia; perception; spinal cord injury; peripheral neuropathy; ischaemia; dementia; dementia;
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Query Match Best Local S Matches 2184

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CC AAD33692-AAD33736 represent cDNAs corresponding to 21 human secreted CC protein genes, and AAE21191-AAE21235 represent, the proteins they encode. CC AAE21236-AAE21280 represent human secreted protein fragments. The genes CC and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene CC therapy. Pathological conditions can be diagnosed by determining the CC amount of the new protein in a sample or by determining the presence of CC amount of the new genes. Specific uses are described for each of the C1 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of CC immune or autoimmune diseases e.g. AIDS (acquired immune deficiency CC syndrome) asthma, anaemia and rheumatoid arthiltis, breast neoplasia CC and breast cancer, neurological disease, Tourette syndrome. CC meningitis demyelinating disease, peripheral neuropathies, mephasia, CC neuropathies induced by neurotoxins, spinal cord injuries, toxic celetrosis, ischaemia and infarction, haemorrhages, schizophrenia, mania, dementia, depression, panic disorders in feeding, sleep patterns, balance cand perception, encephalitis, disorders in cardiovascular, neural/CC sensory, reproductive and digestive systems, behavioural disorders and CC secreted protein-encoding cDNA of the invention.
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P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                syndrome); musculo-skeletal disorders (arthritis, trauma, tendonitis); renal disorders (nephrotic syndrome, glomerulonephritis); metastases of malignancies and related disorders (leukaemia, multiple myeloma); and infections caused by bacteria, viruses, fungi and parasities. PTK is also useful for screening therapeutic compounds. PTK is used as an antigen in a vaccine to raise an immune response against infectious disease. PTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   atherosclerosis); central nervous system disorders (multiple sclerosis) neurodegenerative disorders (Alzheimer's disease, Parkinson's disease); blood coagulation disorders (thrombocytopalenia); autoimmune disorders (billary cirrhosis, Crohn's disease); respiratory disorders (asthma, allergy); gastrointestinal disorders (inflammatory bowel disease); cerebrovascular disorders (thrombosis, wascular dementia); brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present cDNA sequence encodes human protein tyrosine kinase receptor (PTK) from clone HDPSB68.

The invention relates to human protein tyrosine kinase (PTK) receptors and their corresponding cDNA molecules. PTK receptors are useful in providing immunological probes for differential identification of the tissues or cell types present in a biological sample. PTK is used in methods for the diagnosis, prevention and treatment of various disorders related to PTK such as immune system disorders (severe combined immunodeficiency (SCID), inflammation); hyperproliferative disorders (neoplasm, sarcoidosis); cardiovascular disorders (arrhythmia, complasm, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorders (phenylketonuria); cancers (such as ovarian, lung, bladder, liver, breast and lymphomas); behavioural disorders (Tourette's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 265-266; 288pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid molecule for producing human protein tyrosine kinase receptor
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17-NOV-1999;
                                                                                                                                                                                                                                181 GAGAACGCCAGAGATICTTCCTTTATACCCCTGGGACACATGCTCACCCAAAAAATAGCC
     322
                     301 AAGTCGGACAACAITCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGGTA 360
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                                                                                                                             241 TACCAGATCGCCTCGGGCCTGGCCTGCACAAGAAAACATCATCTTCTGTGACCTG
                                                                                                                                                                                                        202 GAGAACGCCAGAGATTCTTCCTTTATACCCCTGGGACACATGCTCACCCAAAAAATAGCC
                                                                                                                                                                                                                                                                                                              142 CACCCGCTCTGCTTCGCCCTGGAGCTCGCGCCCGCTCAGCAGCCTCAACACCGTGCTGTCC
                                                                                                                                                                                                                                                                                                                                         121 CACCCGCTCTGCTTCGCCCTGGAGCTCGGCGCCCTCAGCAGCCTCAACACACCGTGCTGTCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATC 120
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NAGTCGGACAACATTCTGGTGTGGTCCCTYGACGTCAAGGAGCACATCAACATCAAGCTA
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1380 1401	1321 GAGCCCTACATGGCCCCCTCCATGGTTACGTCAGTCGTGTGCAGCTCTGAGGGCAGAGGG	oy Yo
1320 1341	1261 ACCAATGGGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCTGGAGATCTGCAGGGGGCTG	Db
1260 1281	)TGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTAC 	Qy Db
1200 1221	141 TACCTGTGCTCACACACGCCAACAGGTCCAAGTTCAGCATCGCGGATGAAGACGCACGG	D dy
1140 1161	81 GCCGATGGGCTTGTGGCTGTTTTCCCGTGGTGCTGGGGCACCCCAAAGGACAGCTGCTCC	β · 64
1080	1021 ACCTGCTTCTTGGCCGTGCCTGTTATTAAAAAGAATTCCTACCTGGTCTTAGCGGGCCTC	Оу
1020	61 CTCAAGGGCATGTGCCCCTTAAACACACCCCAACAGGCCTTGGATACTCCAGCTGTCGTC	Оу
960 981	01 CTCCAGGTCCAGAGATCCCTGTGGACAGCCAGCGAGGACCAGAAAATCTACATCTACACCC	dg V
900 921	41 GAGAAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAGCTGCCAG 	Db Oy
840 861	81 TACACCGTGGTGTTTTGGGATGGAAAAGAGGAGTCCAGGAACTACACGGTGGTGAACACA	ДУ
780 801	21 TTCATGTATGAACTGTGCTGTGGGAAGCAGACAGCCTTCTTCTCATCCCAGGGCCAGGAG	Db Qy
720 . 741	61 GAGAAGCGACCGCTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACC	g vy
660	01 GAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAGGCGTGGGACACTAAGCCA 	Db Qy
600 621	541 CACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGGCCGG	Db dy
540 , 561	81 TTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAGGGCCCTGCACTGGGCCAC	Оу
480 501	421 CCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTAGATATG	Db db
420 441	361 TCTGACTACGGGATTTCGAGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACT	Db Qy

GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Minimum DB
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Result No.	Score	Query Match Length DB	Length	:	Ħ	Description
سو	2184	100.0	3496	22	AAD03995	Human protein tyro
N	2184	100.0	3579	24	AAD33718	Human secreted pro
ω	2180.8	99.9	3564	24	AAD33695	Human secreted pro
4	2132.4	97.6	2652	23	AAS72238	DNA encoding novel
Çī	1936.8	88.7	6045	22	AAH77994	Nucleotide sequenc
6	1936.8	88.7	7093	24	AAD38851	Human kinase (PKIN
7	858.8	39.3	18286	22	AAK70889	Human immune/haema
80	858.8	39.3	18286	22	AAK84104	Human immune/haema
9	858.8	39.3	18287	22	AAK70892	Human immune/haema

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## ALIGNMENTS

RESULT 1 AAD03995

AAD03995 standard; cDNA; 3496 BP

AAD03995;

02-JUL-2001 (first entry)

Human protein tyrosine kinase receptor:(PTK) cDNA from clone HDPSB68.

neurodegenerative disorder; gastrointestinal disorder; blood coagulation disorder; trauma; cerebrovascular dis hyperproliferative disorder; atherosclerosis; brain multiple sclerosis; Alzheimer's disease; vascular de antifungal; antiparasitic; sarcoidosis; inflammation; asthma; cardiovascular disorder; severe combined immunodeficiency; SCI behavioural musculo-skeletal gene therapy; nephrotic syndrome; glomerulonephritis; Human; protein tyrosine kinase receptor; PTK; antibacterial; antiviral; disorder; disorder; Parkinson's disorder; ss. disease; autoimmune disorder; vascular dementia; ciency; SCID; vaccine; disorder; leukaemia; cancer; lymphoma; thrombosis; arthritis;

Homo sapiens.

CDS ocation/Qualifiers

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"Human PTK protein from clone HDPSB68"

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SUMMARIES

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## ALIGNMENTS

RESULT 1
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AB058693.1 GI:14017796
KEYNORDS
SOURCE
ORGANISM
Homo sapiens brain cDNA to mRNA, clone:fh24104.
CORRESTON
CORRESTON
AB058693.1 GI:14017796

KEYNORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelcostomi;
Mammualia; Eutheria; Primates; Catarrinii; Hominidae; Homo.

REFERENCE
AUTHORS
Prediction of the coding sequences of unidentified human qencs. XX.
The complete sequences of 100 new cDNA clones from brain which core

Pred. No.

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the number of results predicted by chance to have

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JOURNAL
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source
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Best Local Similarity
Matches 2184; Conserv
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                                                                               2106 GAGAACGCCAGAGATTCTTCCTTTATACCCCTGGGACACATGCTCACCCCAAAAAATAGCC
                      181 GAGAACGCCAGAGATTCTTCCTTTATACCCCTGGGACACATGCTCACCCAAAAAAATAGCC 240
                                                                                                                                                                                                                                                         for large proteins in vitro DNA Res. 8 (2), 85-95 (2001) 21245130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohara, O., Nagase, T. and Kikuno, R.
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AVKILAVRDLLWYPRRGGDVTVIGLEKOSEAQRGRVIAVLKARELTPHGYLVDAAVVA
KDTVVCTFENENTEWGLAVWRGWGAREFDIFYQSYEELGRLEACTRKRR"
1 1553 c 1502 g 1089 t
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SKFSIADEDARQNPYPVKAMEVVNSGSEVWYSNGPGLLVIDCASLEICRRLEPYMAPS
MVTSVVCSSEGRGEEVVWCLDDKANSLVMYHSTTYQLCARYFCGVPSPLRDMFPVRPL
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GYLSVESSDVNWKKKKSGGKKIVCQSEVRDFSAMAFITDHVNSLIDQWFPALTATESD
GTPLMEQYVPCPVCETARAEQHTDPSEKSEDVGYFDMEDCYLTAIERDFISCPRHPDLF
VPLQELVPELFMTDFPARLFILENSKLEHSEDEGSVLGQGGSCTVIYARRYQGQPVAVK
RFHIKKFKNFANVPADTMLRHLRATDAMKNFSEFRQEASMLHALQHPCIVALIGISIH
PLCFALELAPLSSLNTVLSENARDSSFIPLGHMLTQKIAYQIASGLAYLHKKNIIFCD
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WDTKPEKRPLALSVYSQMKDPTFATFMYELCCGKQTAFFSSQGQEYTVYFWDGKEESR
NYTYVNTEKGLMEVQRMCCPGMKVSCQLQVQRSLWTATEDQKIYIYTLKGMCPLNTPQ
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/protein_id="BAB47419.1"
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/db_xref="taxon:9606"
/clone="fh24104"
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1320 3245	61 AGCAATGGGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCTGGAGATCTGCAGGCGGCTG	Qy 12 Db 31	
1260 3185	01 CAGAACCCCTACCCAGTGAAGGCCATGGAGGTCGTCAACAGCGGCTCTGAGGTCTGGTAC	Qy 12 Db 31	
1200 3125	41 TACCTCTCTCTCACACACACACCCAACAGCTCCAAGTTCAGCATCGCGGATGAAGACGCACGG	Qy 11 Db 30	
1140 3065	81 GCCGATGGGCTTGTGGCTGTTTTCCCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTCC. 	Qy 10 Db 30	
3005	21 ACCIGCTTCTIGGCCGIGCCIGTTAITAAAAAGAATICCIACCIGGICTIAGCGGGCCIC:	Qy 10 Db 29	
1020	61 CTCAAGGGCATGTGCCCCTTAAACACACCCCAACAGGGCCTTGGATACTCCAGCTGTCGTC:	Qy 9 Db 28	
960 2885 ·	01 CTCCAGGTCCAGAGATCCCTGTGGACAGCCACCGAGGACAGAAAATCTACATCTACACC (	Qy 9 Db 28	
900	41 GAGAAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAGCTGCCAG (	Qy 8 Db · 27	
840 2765	81 TACACCGTGGTGTTTTGGGATGGAAAAGAGGAGTCCAGGAACTACACGGTGGTGAACACA (	Qy 7 Db 27	
780 2705	1 TTCATGTATGAACTGTGCTGTGGGAAGCAGACAGCCTTCTTCTCATCCCAGGGGCCAGGAG	Qy 7 Db 26	
720 2645	61 GAGAAGCGACCGCTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACC ;	Qy 6 Db 25	
660 2585	01 GAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGACACTAAGCCA (	Qy 6 Db 25	
600 2525	41 CACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGCAGCCG (	Qy 5 Db 24	
540 2465	81 TTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCTGCACTGGGCCCC :	Oy 4 Db 24	*
480 2405	21 CCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAAGGTAGATATG 4	23 4	
420 2345	61 TCTGACTACGGGATTTCGAGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACT 4	Qy 3 Db 22	
360 2285	01 AAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTA 3 	Qy 3 Db 22	
300	41 TACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTG 3 	Qy 2 Db 21	

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                            TCATTTGGGTCCCCAGGCGCGGTGGAGATGTTATCGTCATTGGCCTGGAGAAGGATTCTG
                                                         GGGTCCCCAGCCCCCCAGGGACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCGG 1531
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GCGCCCAGCGGGGCCGAGTCATTGCCGTCTTAAAAAGCCCGAGAGCTGACTCCGCATGGGG
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        AAGCCCAGCGGGCCGAGTCATTGCCGTCTTAAAAGCCCGAGAGCTGACTCCGCATGGGG
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/note="cloning vector:
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1651 102095 .	OY 1592 TCATGTACAGTGAGGAGCTGGGCACGCAGATCCTGATCCACCAGGAATCACTGACTG
1591 102155	OY 1532 CAGCCAGCCACAGGGCCAACCCAAAGGTGCCTGAGGGGGACTCCATCGCGGACGTGAGCA
1531 102215	QY 1472 GGGTCCCCAGCCCCTCAGGGACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCGG
1471 102275	QY 1412 CGARCICCTIGGIGAIGTACCACTCCACCACCTACCAGCIGITGIGCCGGIACTICIGCG
1411 102335	OY 1352 CAGTCGTGTGCAGCTCTGAGĞGCAGAGGGGAAGGTCGTCTGGTGCCTGGATGACAAGG
1351 102395	GCTGGAGCCCTACATGGCCCCCTCCATGGTTACGT 
1291 102455	OY 1232 TGGTCAACAGCGGCTCTGAGGTCTGGTACAGCAATGGGCCGGGGCTCCTTGTCATCGACT
1231 · · · · · · · · · · · · · · · · · · ·	OY 1172 AGTTCAGCATCGCGGATGAAGACGCACGGCAGAACCCCTACCCAGTGAAGGCCATGGAGG
1171 102575	OY 1112 TGCGGGGCACCCCAAAGGACAGGTGCTCCTACCTGTGCTCACACACA
1111	OY 1052 AGAATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTTGTGGCTGTTTTCCCGTGG :
ps 0;	Query Match 39.3%; Score 858.8; DB 2; Length 110000; Best Local Similarity 96.0%; Pred. No. 1.6e-149; Matches 881; Conservative 0; Mismatches 37; Indels 0; Gap
ens chromosome	RESULT 7 AL390202_01/c WPCOMMENT  Sequence split into 10 fragments LOCUS AL390202 Accession AL390202 Fragment Name Begin End AL390202 Accession AL390202 AL390202_00 100001 210000 AL390202_02 200001 310000 AL390202_03 300001 410000 AL390202_04 400001 510000 AL390202_05 500001 510000 AL390202_06 600001 710000 AL390202_07 700001 810000 AL390202_08 800001 988176 Continuation (2 of 10) of AL390202 from base 100001 (AL390202 Homo sapis
	OY 2132 ACCAGTCCTACGAGGAGCTGGGCCGGCTGGAGGCTTGCACTCGCAAGAGAAGG 2184
2131	QY 2072 ACACAGAGTGGTGCCTGGCCGTCTGGAGGGGCTGGGGCCGCAGGGAGTTCGACATTTTCT 2
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                                                                    GTGCCTCCCTGGAGAICTGCAGGCGGCTGGAGCCCTACATGGCCCCCCCCCATGGTTACGT 1351
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DeArellano,K., Dewar,K., Domino,M., Doyle,M., Fenestor,J.,
Ferreira,P., FitzHugh,W., Forrest.C., Gage,D., Galagan,J.,
Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
Landers,T., Lehoczky,J., Levine,R., Lieu,C., Liu,G., Locke,K.,
Macdonald,P., Marquis,N., McEwan,P., McGurk,A., McKernan,K.,
McDheeters,R., Meldrim,J., Meneus,L., Morrow,J., Maylor,J.,
McPheeters,R., Meldrim,J., Meneus,L., Morrow,J., Maylor,J.,
McDwan,C.H., O'Connor,T., O'Donnell,P., Olivar,T.M., Peterson,K.,
Plerre,N., Pisani,C., Pollara,V., Raymond,C., Riley,R., Rothman,D.,
Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thomann,N.,
Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Tirreil,A., Vassillev,H., Viel,R., Vo,A., Wu,X., Wyman,D., Ye,W.J., Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Bousslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Birren, B., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone RP11-424I19 Mammalia; Eutheria; Pr 1 (bases 1 to 178876) Eukaryota; Metazoa; Homo sapiens HTG; HTGS\_PHASE1; Unpublished AC019254.9 GI:22123259 IN PROGRESS (bases 1 to 178876) 178876 bp DNA linear chromosome 15 clone RP11-424I19 map 15, \*\*\*, 3 unordered pieces. HTGS\_FULLTOP; HTGS\_ACTIVEFIN Chordata; Primates; Craniata; Vertebrata; Catarrhini; Hominidae; Euteleostomi; HTG 06-AUG-2002 \*\*\* SEQUENCING

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Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 6, 2002 this sequence version replaced gi:21699484. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Birren, B., Nusbaum, C., Lander, E., Ali, A., Earnd, N., Bastien, V., Bloom, T., Boguslavk
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Homo sapiens chromosome 15 clone
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Abola,A.P., Bruno,D., Conn.
Federspiel,N., Glukhov,S.,
                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                     Homo sapiens
                          (bases 1 to 183401)
                                                                                 sapiens.
                                                                                            HTGS_PHASE1;
                                                                                                             GI:12831370
                                                                                                                                      unordered pieces.
                                                                                            HTGS_DRAFT;
             Conn, L., Dela Rosa, M., Faulkner, D.,
                                                                                                                                                    clone
                                        Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                               HTGS_FULLTOP
                                                                                                                                                    RP11-505E24,
                                                                                                                                                                   DNA
                                           Hominidae;
                                                                                                                                                                   linear
                                                                                                                                                       WORKING
                                                        Euteleostomi;
                                                                                                                                                                   HTG 15-FEB-2001
                                                                                                                                                      DRAFT
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Hansen, N.,

Herman, Z.S., Hyman, R.

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JOURNAL REFERENCE
                                                                            ORIGIN
                                                                                             BASE COUNT
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                                      Query Match
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2 (bases 1 to 183401)
Bruno,D., Conn,L., Dela Rosa,M., Federspiel,N., Foreman,P.,
Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R.,
Morehouse,A.J., Oefner;P., Palm,C.J., Ramirez,D., Wilhelmy,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rao,J., Lam,B., Marathe,R., Miranda,M., Morehouse,A.J., Nguyen,M., Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmy,J., Yu,S. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 9.8x in Q20 bases; agarose-fp Quality coverage: 9.3x in Q20 bases; sum-of-contigs. NOTE: This is a "working draft" sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                             49346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-primer; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178788 bases at least Q40
Consensus quality: 180438 bases at least Q30
Consensus quality: 181007 bases at least Q20
Insert size: 17416; agarose-fp
Insert size: 183101; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://sequence-www.stanford.edu/group/human/Contact: hum-infodsequence.stanford.edu
------ Project Information
Center project name: 754
 Conservative
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3534
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Chemistry: Dye-primer; 0% of reads
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                                                                                        /note "assembly_name:Contig20
clone_end:T7"
28960. ,183401
/note-"assembly_name:Contig21
clone_end:SP6"
a 42604.c. 44323 g 46782 t
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                                                                                                                                                                                                       /note="assembly_name:Contig19"
16758. .28859
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3534. .16657
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/chromosome="15"
                                                                                                                                                                                                                                                                                                 clone_lib="RPCI human"
                                                                                                                                                                                                                                                                                                                      /clone="RP11-505E24"
                                                                                                                                                                                                                                                                                                                                                                          ∕organism="Homo sapiens"
                     39.3%;
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3: gap of unknown length
7: contig of 13124 bp in length
7: gap of unknown length
9: contig of 12102 bp in length
9: gap of unknown length
9: gap of unknown length
1: contig of 154442 bp in length
Score 858.8; DB 2;
Pred. No. 1.5e-149;
0; Mismatches 37;
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Mus musculus, Sir
MGC:28646 IMAGE:
BC027199
BC027199.1 GI:20
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\GE:4224922,
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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genom

Sequencing Center
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Contact: MGC help desk
Email: cgapbs-r@mail.n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-Apr-2002) National Institutes Collection (MGC), Cancer Genomics (Institute, 31 Center Drive, Room 11A03,
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Eukaryota; Metazoa;
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/db_xref="01:20073185"
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/translation="MYHSATYQLCARYFCGDPNPLRDTFSVQPSVLETPGSHKTTSKG
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HGGDIIVIGLEKDSGAQRGRVIAVLKARELNRHGVLVDAAVVAKDTVVCGFANENTEM
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/clone_lib="NCI_CGAP_CO24"
/lab_host="DH10B"
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/db_xref="taxon:10090"
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/protein id="maky27199 1"
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oligo capping; fis (full insert
Homo sapiens human lung cDNA to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
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Sugano, S., Suzuki, Y., Ota, T., Obayashi, M.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
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/translation="mynstatyolcaryecgpsplrdaarspsslpspa
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RRGGDVIVIGLEKDSGAORGFORASDRAEHDLYPMGTFSQHLQAVKILAVRDLIWVP
RRGGDVIVIGLEKDSGAORGFORASDRAEHDLYBHGVLVDAAVVAKDTVVCTFENENTE
WCLAVWRGWGAREFDLFYQSYEELGRLEACTRKRR"

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/clone_lib="LNG"
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/db_xref="taxon:9606"
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No. 7.2e-134;
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                                                                                              Center: Washington University Gecenter code: WUGSC
Web site.http
                                                                                                                                                                       Submitted (11-AUG-2002) Genome Sequencing Center, 4444 Forest Parkway, St. Louis, MO 63108, USA on Aug 11, 2002 this sequence version replaced gi:21887033.
                                                                                                                                                                                                                                 Submitted (17-JUL-2002) Genome Se Parkway, St. Louis, MO 63108, USA 3 (bases 1 to 288428) McPherson, J.D. and Waterston, R.H.
                                                                          Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
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Chemistry: Dye-terminator Big Dye; 100% of re
Assembly program: Phrap; version 0.990319
Consensus quality: 283337 bases at least Q40
Consensus quality: 284790 bases at least Q20
Consensus quality: 284790 bases at least Q20
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SOURCE
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Best Local :
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                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 513;
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Choepel,Y., Colangelo,M.,
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1 (bases 1 to 526)

Robison,K.E.

Nucleic acid molecules encoding human kinase and phosphatase
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 178529)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                      AC090907 178529 bp Homc sapiens clone RP11-505E24,
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                         Unpublished
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Patent: US 6309849-A 10 30-CCT-2001,
Docation/Qualifiers
1. 526
                                                                         Birren, B., Linton, L., Nusbaum, C., Homo sapiens, clone RP11-505E24
                                                                                                                                                  Homo sapiens
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Pred. No. 1.6e-78;
0; Mismatches 5;
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COMMENT

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bp in length in length

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Research, 320 Charles Street, Cambridge, MA 02141, USA
CE 3 (bases 1 to 178529)
RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslawkiy, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collings, S., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewaz, K., Diaz, J.S., Dodge, S.,
Farreira, P., FitzGerald, M., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I.,
Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Narquis, N.,
Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Pollara, V., Raymond, C., Retta, R., Riebek, M., Riley, R., Rise, C.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Topham, K., Taravis, N., Trigillo, J.,
Voung, G., Zainoun, J., Zembek, L., Zimmer, A., and Zody, M.
Direct Subnission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 1, 2002 this sequence version replaced g1:16259005.
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Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L.,
Grand-Pierre,N., Hagos,B., Heaford,A., Horton,L., Hulme,W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,
MacLean,C., Macdonald,P., Marquis,N., Matthews,C., McCarthy,M.,
McEwan,P., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome
1 3608: contig of 3608 bp in length
3609 3708: gap of 100 bp
3709 51847: contig of 48139 bp in lengt
51848 51947: gap of 100 bp
51948 89661: contig of 37714 bp in lengt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (17-MAR-2001) Whitehead Institute/MIT Center for Genome 320 Charles Street, Cambridge, MA 02141, USA
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REFERENCE AUTHORS JOURNAL TITLE

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Page 1
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BASE COUNT
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Search completed: April 15, 2003, 05:21:35 Job time: 5379 secs
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                                                                                                                                                                                                                                                                                                                18671 GGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTA 18629
                                                                                                                                                                                                             18731 GATTTCGAGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACTCCTGGCTACCA 18672
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                                                                                                                                        432 GGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTA 474
                                                                                                                                                                                                                                           372 GATTTCGAGGCAGTCATTCCATGAGGGGCGCCCTAGGCGTGGAGGGCACTCCTGGCTACCA 431
                                                                                                                                                                                                                                                                                                                                                                312 CATTCTGGTGGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGG 371
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/db_xref="taxon:9606"
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.78529: contig of 805 bp in length.
.ion/Qualifiers
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Length: Matches: 168 Conservative: 89 Mismatches: 257 Indels: 236
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euTyrArgAla 707	8 rgGlyGlySerArgAlaGlySerGln-	Db 68	
1548	7	Qy 152	_
yThrSerGlyA 688	œ	Db 66	
1525	4 GTGCGGCCCTTGGACACGGAACC	0у 150	
399 Id	3 rSerProAspSerProGlyGlyAlaLysGlyGluProProPro	Db 65	
⋛	8 TGCG	Qy 146	
ProGlySerth 653	33 ySerProProProAlaArgGlyAspThrProProSerGluGlySerAlaP	E9 4D	
CCGGTACTT	AACTCCTTGGTGATGTACCACTCCACCTACCAGCTGTG	QY 140	
GlyA	lyAla	Db 61	
ATGAC 1407	SCTCTGAGGGCAGAGGGAGGAGGTCGTCTGGTGCCTGG	Qy 135	
SerProAspLe 613		Db 59	
CA 1353	7	Оу 134	
CysProProAl 593	erProGlyGlyLeuGlyGlyGlyProSerAlaTrpGluAla	Db 57	
	GGCTGGAGCCCTACATGGCCC	Qy 131	
GluProGlyGl 573	53 sGlySerCysGlyAspLeuProGlyLeuArgThrAlaValProProHis	Db 55	
GAGATCTGCAGG 1314	GTACAGCAATGGGCCCGGGCCTCCTTGTCATCGACTGTGCCTCCCTG	Qy 125	
  AlaSerAlaLy 553	45 rArgHisArgLys	Db 54	
GCTCTGAGGTC 1254	95 GCACGGCAGAACCCCTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCG	ΩУ 119	
ArgGly	ysProLysAlaProProSerProGlyArgSerArg	Db S	
CGGATGAAG	TACCTGTGCTCACACACAGCCAACAGGTCCAAGTTCAGCATCG	Qy 113	
527		Db 52	
CAAAGGACAGC 1134	5 GGCCTCGCCGATGGGCTT	Qy 107	
LeuAspAlaAl 521	Ĺуs	Db 51	
ACCTGGTCTTAGCG 1074	15 GTCGTCACCTGCTTCTTGGCCGTGCCTGTTATTAAAAAAGAATTCCT	Qy 101	
spIleLeuLysAl 511	94 nValProGlnAsnLeuSerProHisSerGlnArgProAsp	Db. 49	
ATACTCCA	55 TACACCCTCAAGGGCATGTGCCCCTTAAACACACCCCCAACAGGCCTT	Qу 95	
  LysLysArgAs 494	::: GlyLeuLeuHisGlyAsnThrMetGluLysLeuIle	Db 4:	
ATCTACAT	95 TGCCAGCTCCAGGTCCAGAGATCCCTGTGGACAGCCACCGAGGACCAG	Ωу 89	
:: .euLeuLys-Pr 474	gArgCysProGlyL	Db 4:	
	44 AAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGG	0у 8	
 	35 ArgAlaAsnAsnLeuTyrMetGluLeuAsnAlaLeuMetLeuGlnLeuG	Db 4:	
GAG 843	23	Qy 8:	
rgLysLeuGlu 434	15 ArgArgGluGluLeuArgHisAlaLeuAspIleArgGluHisTyrGluA	Db 4:	
822	05AAAGAGGAGTCCAGGAA	Qу 80	
LeuValMetArg 414	::: 95 GluLysIleLysSerGluGlyThrCysLeuHisArgLeuGluGluGlu	Db 39	
804	84 ACCGTGGTGTTTTGGGATGGA	Qy 71	

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-QB-Issued_patents_AA -QFMT-fastan -SUFFIX=n2p.rai -MIMMATCH-0.1 -LOOPCI-0
-LOOPEXT=0 -UNITS-blts -START=1 = END-1 - MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -QUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
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equence 24	equence 11, Ap	equence 8, App	equence 27, App	equence 10, Ap	equence 107, Ap	equence 7, Appl	equence 2,	equence 29, Ap	quence 15, Ap	equence 4,	equence 23, Ap	equence 23, Ap	equence 2, App	quence 2, App	equence 2, Appl	equence 2, Appl	quence 5, Appl	equence 5, App	equence 5, Appl	equence 5, Appl	equence 21, App	equence 6, App	equence 6, App	equence 5, App	nce 5, Appl	e 5, Appl	e 5, Appl	equence 5, Appl	equence 5, Appl	equence 5, Appl	quence 5, App	equence 5, Appl

## ALIGNMENTS

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US-08-395-580-2
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CLASSIFICATION: 514

PRIOR APPLICATION NUMBER: 08/205,018

APPLICATION NUMBER: 08/205,018

FILING DATE: 01-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Rebecca L. Ralph (formerly Gaumond)

REGISTRATION NUMBER: 35,152

REFERENCE/DOCKET NUMBER: CH-0488

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 720
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Usharani R. Reddy, David Pleasure and the Children's APPLICANT: Hospital of Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                     APPLICATION NUMBER: U:
FILING DATE: herewith
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Philadelphia
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18 TEGET SET TO THE TERM TO TH	luProValAlaAlaValValProValAlaLeuAlaProProLeuValGlyAlaGlyGlyH 993		ProProSerSerProSerLeuSerProHisHisSerSerG 973	GATTCTGAAGCCCAGCGGGGCCGAGTCATTGCCGTCTTAAAAGCCCGAGA 1994	erSerProProLeuH1sAlaArgSerGlnTrp959	AGAGACCTCATTTGGGTCCCCAGGCGCGGTGGAGATGTTATCGTCATTGGCCTGGAGAAG: 1944	oProGlnLeuAlaAlaAla-AlaProLeuAlaSerArgArgHisThrArgArgS 949	CCCATGGACGGGGAGACCTTCAGCCAGCACCTGCAGGCCGTGAAGATCCTCGCCGTC 1884	Propro	GACTCAGACATGCTACATACGCCCGGTGCTGCCCTCCGACAGGTCTGAGCATGACCTGACC 1827	aAlaLeuHisHisAsnGluTrpAlaLeuAlaGlyGlnCysLeuThrProPro 928	CCAGCAAGTTCTTCCAGTGTGCCATTTCTCCACCGACTGCGAG 1767	eValAlaAlaAlaProSerAspArgArgLeuGlyProProGlnIleAlaAlaAlaAlaAl	CCCCACCCGCCAGGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTCC 1725	gAlaProSerAspArgArgArgArgLeuLeuSerSerProProProProProGlnI1 891	ATCCTGATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCTACTCCTCAT 1678	gCysArgSerHisLysSerAlaProProAr 872	CCTGAGGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGGCACGCAG 1620	ProArgGlnLeuGlyAlaThrAlaProThrAlaArgAr 862	STGNGCCCTTGGACACGGAACCCCCGGCAGCCAGCCACACGGCCAACCCAAAGGTG 1560	sHisHisArqCysSerSerSerSerSerSerSerProSerPro		gLeuIleTyrProAlaAlaThrGlySerThrAlaCysThrProProTrpProGluLeuHi 835	

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492 612 512	NTYPheProAspTrpIleTyrAspHis CTTCTGGGGCAGCCGGAGGAAGTGCAG                 : :   ValThrSerGluValGluGluIleAla	568 493	dy dy
6 7 2	AGGTAGATATGTTCTCCTATGGAATGGTGCTCTACGAGTTGCTGAGGACAGCGCCCT 5	55 44 45 52 55 65	dy Qy
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84 321 141 341 341	GATGCCATGAAGAACTTCTCCCGAGTTCCGGCAGGAGGCCAGCATGCTGCACGCGCTGCAG 8     :::	25 302 85 322	2 9 7 9 7 0
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	SEQUENCE FROM N.A.  STRAIN=CV. NIEPONBARE; SABAKI T., Matsumoto T., Yamamoto K.; SABAKI T., Matsumoto T., Yamamoto K.; SABAKI T., Matsumoto T., Yamamoto DNA, chromosome 1, PAC clone:P0443D08 "; Clone:P0443D08 "; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AP003250; BABB4138 1; InterPro; IPR0002561; EGF-11ke. InterPro; IPR000279; Sertthr_pkinase. InterPro; IPR000290; Sertthr_pkinase. Pfam; PF00069; pkinase; 1. Pfon; PF000091; Euk_pkinase; 1. SMART; SM00181; EGF; 1. SMART; SM00181; EGF; 1. PROSITE; PS00107; PROTEIN_KINASE_DOW, 1. PROSITE; PS00101; PROTEIN_KINASE_TOW, UNKNOWN_1. ATP-binding; Kinase; Receptor; Transferase. SEQUENCE 1267 AA; 136583 MW; 062F0C27C5490D75 CRC64;	• '	RP RP RC RC RA RT RT DR RT DR DR DR DR DR DR DR DR COR SOW

1444 Ar 815	1393 TGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACCTCCACCACCT	Ωy
Se 800		В
<b>L</b>	39 TCCATGGTTACGTCAGTCGTGTGCAGCTCTGAGGGCAGAGGGGAGGAG	Ωy
C 1338		P Qy
78	764 -	Db
TC 1278	GGTCAACAGCGGCTCTGAGGTCTGGTACAGCAATGGGCCGGGCC	Qy
	744 lAlaAspProAla	Db
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1171	1147 TGCTCACACACAGCCAACAGGTCCA	Qγ
11 724	704 rSerSerLeuSerLeuLeuThrGlyGlyGlyAlaArgGlyArgArgLeuArgProThrHi	망
rG 1146	1087 GGGCTTGTGGCTGTTTCCCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTCCTACCTG	Qy
se 704	684 uAlaGlyAlaCysTrpGlyArgGluArgArgProValLeuPheAlaThrAlaSerSerSe	Βb
T 1086	TGTTATTAAAAAGAATTCCTACCTGGTCTTAGCGGGCC	Qy
31 684	:::: 664 lLysAlaIleGlyProLysValArgArgThrAlaAlaAlaHisProArgArgLysThrGl	Db
1036	1009 CCAGCTGTCGTCACCT	Qy
7a 664	644 sLeuHisGlyPheArgValValValLeuPheGlyCysGlyGlyArgTyrAlaTrpAlaVa	Дb
1008	CTTGGAT	Qy.
11 644	::: 624 rProAlaThrGluLeuTrpProValThrAlaMetAlaAlaAlaArgArgAlaLeuArgHi	Вb
985	CCCTCAAGGGCATGTGCCCCCTTAAACA	VΩ
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C 957	CCCTGTGGACAGCCACCGAGGACCAGAAAA	Qy .
/a 604	588AsnSerProSerAlaAspLeuThrAlaValIleThrGluProAspArgVa	ДЬ
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S88	829 GTGGTGAACACAGAGAAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAG	Qy
- 582	566 uAsnAlaGluSerThrSerSerAlaThrAspLysAlaTyrAlaSerPro	Db·
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e 566	551 oLysGlnSerPheCysGluSerLeuGluHisProValHisLysLe	ф
769	GCTGTGGGAAGCAGACAGCCTTCTTCTC	Qy
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1254	GCACGGCAGAACCCCTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTC	1195	δÃ
541	ysProLysGlyProProSerProGlyAr	528	D
1194	CTACCTGTGCTCACACACACACCCAACAGGTCCAAGTTCAGCATCGCGGATGAA	1135	ρ
527	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	521	DЬ
1134	CGCCGATGGGCTTGTGGCTGTTTCCCCGTGGTGCGGGGCACCCCAAAG	1075	οy
521	rGluSer	511	뮻
1074	CTGCTTCTTGGCCGTGCCTGTTATTAAA	1015	Qy
511	ValProGlnLysLeuSer	494	皮
1014	TGCCCCTTAAACACACC	955	δ
494		474	뭥
954	cctgtggacagccaccgaggaccagaaaatctac	895	04
474	ArgGluLeuLeuArgArgGluGlnAlaLeuGluArgArgCysProGlyLeuLeuLys-Pr	455	망
894	AGGGCCTCATGGAGGTGCAGAGGATGTGC	844	Qy
454	AsnAsnLeuTyrMetGluLeuAsnAlaLeuMetLeuGlnLeu	435	Дb
843	TGGTGAACACA	823	Qy
434		415	₽.
822		805	Qy.
414	hrCysLeuHisArgLeuGluGluG	395	å
804		784	Qy
394	;::  nAlaGluTrpArgGluGluVa	375	B
783	AAGCAGACAGCCTTCTTCTCATCCCAGGGCCAGGAGTAC	745	Qy
374	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	366	Db
744	GTGGTGAGCCAGATGAAGGACCCGACTTTGCCACCTTCATGTATGAACTGTGCTGTGGG	685	γO
365		346	В
684		643	Qy
345	ProValProSerSerCysProAspGlyPheLysIeLeuLeuArgGln	330	В
642	CCGGTTCTGGGGCAGCCGGAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAG	583	, V
329	<pre>!::   :::    ::    ::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    :::    ::    :::    ::    ::    :::    :::    :::    :::    :::    :::    :::    :::    ::</pre>	319	D
582	GCACTGGGCCACCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGC	529	Qy
318	ValLeuTrpGluLeuThrGlyGluIleProTyrLysAspValAspSerSerAlaIle	299	D <sub>O</sub>
528	GTGCTCTACGAGTTGCTGTCAGGACAGCGCCCT	496	VQ.
298	ProGluValIleArgAsnGluProValSerGluLysValAspIleTrpSerPheGlyVal	279	d
495 ,	CCAGAGATCAGGCCTCGCATTGTATATGATGAGAGAGGTAGATATGTTCTCCTATGGAATG	436	γQ
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w	AUGCAGTCATTCCATGAUGGCGCCCTAGGCGTGGAGGGCACTCCTGGCTACCAGGCC	379	0
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270	<b>ひまぶに そりりりしゃ ふしゃりょうにゃ ふうじゃ せんしゅん</b>	110	<b>)</b>

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                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative receptor serine/threonine kinase.
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1860 GCAGGCCGTGAAGATCCT-CGCCGTCAGAGACCTCATTTGGGTCCCCAGGCGCGGTGGAG 1918	544 ySerGlnLeuGlnThrHisAlaGlnAlaSerMetAsnGluAlaTrpArgAlaThrTy 563	1800 CTCCGACAGGTCTGAGCATGACCCTGACCCCCATGGACGGGGGAGACCTTCAGCCAGC	1/44GIGCCITECICCACCGACTGCGACGGACTCAGACATGCTACATACGCCCGGTGCTGC 1799	512 oGlnArgValAlaProGluAlaLeuProAlaAlaGlyAlaArgProThrSerAlaHisAl	GGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCCAGCAAGTTCTTCCAGT 1 :::    :::	496 sAlaLysGlyValIleTyrGlyGlyProGlnAspSerGlyProArgPr 512	1632 CCAGGAATCACTCACTGACTACTCCTCCATGTCCTCCTACTCCTCATCCCCACCCCGCCA 1691	477 AsnAsnValGluArgAlaGlnGlnValGlnAlaAsnAlaHisAlaGlyArgMetAsp-Hi 496	1581GGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCAGATCCTGATCCA 1631	1542 CACGGCCAACCCAAAGGTGCCTGAGGGGGGACTCCATCGC	437 ProArgGlySerProTyrAlaGlnGlnGlnArgGlyTyrAsnGlyTyrGlyGlyAspPro 456	1515 GGACACGGAACCCCC	422TyrSerProProGlnProTyrGlyHisGlnGlnGlnDroSer 436	1455 TGCCCGGTACTTCTGCGGGGGTCCCCAGCCCCCTCAGGGACATGTTTCCCCGTGCGGCCCTT 1514	421 421	1395		Ω	385 AspHisProPheSerLeuProGlyGlyGlnGlnAlaProProTyrGlyAlaTyrProSer 404	1281 TGTCATCGACTGTGCCTCCCTGGAGATCTGCAGGCGGCTGGAGCCCTACATGGC 1334		1221 GGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTACAGCAATGGGCCGGGCCTCCT 1280	argproGlySer	1161 CAACAGGTCCAAGTTCAGCATCGCGGATGAAGACGCACGGCAGAACCCCCTACCCAGTGAA 1220	352 ProSerProHisSerProTyrProTyrGlnGlnGlyGlnIleProTyrLeuProHisGln 371			AATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTTGTGGCTGTGTTTTCCCGTGGT-		ひゃんゃん ないはないはいしょうじゅうしょうじゅうしゅうしゅうしゅうしゅうしゅうしゅうしゅうしゅうしゅうしゅうしゅうしゅうしゅ	934 GAGGACCAGAAAAFCTACATCTACACCCTCAAGGGCATGTGCCCCTTAAACACCACCCCAA 993 	GInProAlaSerAlaLys	
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am; PF00069; pkinase; 1.
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ART; SM00220; S_TKC; 1.
ART; SM00219; TYYKC; 1.
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enomic Structure and Promoter Characterization of the Homo sapiens p3K12 Gene.";
p3K12 Gene.";
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mmalia; Eutheria; Primates;
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-MAR-2002 (TrEMBLrel. 20, Last sequence update)
-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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	; ;	in cell cycle progression and microtubule severing during deflagellation."; J. Cell Sci. 0:0-0(2002).	감압
	h roles	SEQUENCE FROM N.A.  Mahjoub M., Montpetit B., Zhao Quarmby L.M.;  "The FA2 Gene of Chlamydomonae	RA RA
	is.	Chlamydomonas reinhardtii. Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocale Chlamydomonadaceae; Chlamydomonas. NCBI_TaxID=3055; [1]	88888
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874 TGCCCTGGGATGAAGGTGAGCTGCCAGCTCCAGGTCCAGAGATCCCTGTGGACAGCCACC 933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kilmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Llang Y., Lin X., Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Mcriu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Murphy B., Murphy L., Murny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pattman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pattman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pattman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pattman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pattman G.S., Pan S., Pollard J., Puri V., Reese M.G., Palazzolo M., Pattman G.S., Pan S., Pollard J., Puri V., Reese M.G., Pan S., Pollard M., Pattman G.S., Pan S., Pollard J., Puri V., Reese M.G., Pan S., Pollard M., Pattman G.S., Pan S., Pollard M., Pattman G.S., Pan S., Pollard M., Pattman G.S., Pan S., Pollard M., Pattman G.S., Pan S., Pollard M., Pattman G.S., Pan S., Pollard M., Pattman G.S., Pan S., Pollard M., Pattman G.S., Pan S., Pollard M., Pattman G.S., Pan S., Pollard M., Pattman G.S., Pan S., Pollard M., Pattman G.S., Pan S., Pollard M., Pattman G.S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan S., Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS: PRO0452; SH3DOMAIN.
PRINTS: PRO0109; TYRKINASE.
ProDom: PD0000001; Euk_pkinase; 1.
ProDom: PD000066; SH3; 1.
SMART; SM00326; SH3; 1.
SMART; SM00321; STYKC; 1.
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"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50002; SH3; 1.
ATP-binding; SH3 domain; Serine/threonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003443; AAF46344.1;
HSSP; P11362; 1FGK.
FlyBase; FBgn0030018; Mlk2.
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Dodson K., Doup L.E., Downes M., Dugan-Rocha S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00069; pkinase; Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES 1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
178 TCCGAGAACGCCAGAGATTCTTCCTTTATACCCCTGGGACACATGCTCACCCAAAAAATA 237
                                                                197
                                                                                                                      121 CAC---CCGCTCTGCTTCGCCCTGGAGCTCGCGCCGCTCAGCAGCCTCAACACCGTGCTG 177
                                                                                                                                                                                                                                                                                                       157 IleAlaHisGlnThrGlyGluAspAspMetGlnArgMetArgAspAsnValLeuGlnGlu 176
                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                             4 CTGAGGCACCTGCGGGCCACCGATGCCATGAAGAACTTCTCCGAG---TTCCGGCAGGAG
                                                                                                                                                                                                                                             GCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATC 120
                                                         AsnThrLysLeuCysLeuValMetGluTyrAlaArgGlyGlySerLeuAsnArgIleLeu
                                                                                                                                                                AlaLysLeuPheTrpAlaLeuLysHisGluAsnIleAlaAlaLeuArgGlyValCysLeu 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000719; Euk_pkinase.
IPR002290; Ser_thr_pkinase.
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IPRO01245; Tyr_pkinase.
0069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 domain; Serine/threonine-protein kinase; Transferase
AA; 113701 MW; D48FDB9C6639A08F CRC64;
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299.50
40.42%
25.41%
7.38%
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Conservative:
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	1648	9 AGATCCTGATCCACCAGGAATCACTCACTG	1619	Qy
	801	LeuLeuGlyAspProSer	785	В
	1618	TGCCTGAGGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGC	1559	Ωy
	784	ArgProArgArgSerThrSerProProSerArgLysLe	765	망
	1558	AACCCCCGGCAGCCAGCC	1523	Q
	764	:::         ProGluProProAlaArgGluGluLysLysArgArgGluGLyLeuPheGlnArgSerS	745	요 .
		CCCCAGCCCCTCAGGGACATGTTTCCCCGTGCGGCCCTTGGACA	7 1	Q (
	744	ThrGlvLeuGlvPheAspLeuLeuGluAlaGlvLvsCvsGlnL	725	물 :
	1475		1475	Q
	724	7 HishisArgArgCysGluValAlaLeuLeuGlyCysGlyAlaValLeuAlaAla	707	B &
	706	ArgGlyGlyAla	703	₽
	1436	AGGGGAGGAGGTCGTCTG	1377	Qy
	702	ProThrProValAsnSerAlaThrSerThr	683	뮹
	1376	GGCCCCCTCCATGGTTACGTCAGTCGTGTGCAGCTCTGAGGG	1332	Ŷ
	82		σn ·	당
	1331	CTCCCT	1296	Q
	1295 662	5 CAACAGGGGCTCTGAGGTCTGGTACAGCAATGGGCCGGGCCTCCTTGTCATCGACTGTGC :::	1236 649	β Q
	648	SerTrpValValProIleAspIleGluGluAspGluAspSerGluGlyProGlySerGly	629	D <sub>D</sub>
	1235	AGTGAAGGCC	1215	ΩУ
	628	ArgSerSerProAlaLeuProGlyPheThrSerLeuMetGluMetAlaLeuLeuAlaAla	609	В
	1214	CGCACGGCAGAACCCCTACCC	1194	οy
	809	Ser Leu Val Asp Gly Tyr Lys Gln Trp Ser Ser Ala Pro Asn Leu Val Lys Gly Property Control of the Control of th	589	В
	1193		1193	Qγ
	588	luLysAlaAsnGlyLeuSerThrProSerGluSerProHisPhe-HisLeuGlyLeuLys	569	B
	1193	CTGCTCCTACCTGTGCTCACACACAGCCAACAGGTCCAAGTTCAGCATCGCGGGATGAAGA	1134	ν
•	569	roGlyThrLeuGlyGlnLysGluLeuAlaSerGlyAspGluGlySerProGlnArgArgG	549	В
	1133	CTGTGT9T9TCCCGTGGTGCGGGGCACCCCAAAGGACAG	1097	οy
	549	ysGluGluGluGluGluGluLysArgAlaProLysLysGlyArgThrTrpGlyP	529	Ф
	1096	GGCTTGTGG	1088	δ
	529	leGlnLeuThrProGlyGluSerSerLysThrTrpGlyArgSerSerValValProL	510	B
•	1087	TT	1056	Ϋ́
	510	GeATACTICAGCTGTCGTCACCTGCTCTTCGCCGTGCCTGTTTATAAAAAAAA	490	β 5
	490	erAspPheGlnHisLysPheThrValGlnAlaSerProThRMetAspLysArgLysSetL	470	₽
	1001	CAAGG	963	, S
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                                                                                                                                                                                                 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Manantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-BERKELEY;
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01-MAR-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt IleSerGluCysAsnSerThrArgSerLeuLeuArgSerAspSerAspGluIleValVal}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuVal Asn Val Arg Val Glu Arg Phe Lys Arg Asp Pro Asn Gln Ser Leu Thr Pro Through Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnArgGlnArg---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AsnSerSerSerThrGluThrProSer 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTTCGACATTTTCTACCAGTCCTACG 2143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGACTCCGCATGGGGTGCTGGATGCTGCCGTGGTGGCAAAGGACACTGTTGTGTGCA 2056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {\tt AspSerThrLeuGluArgProLysThrLeuGluPheLeuProArgProArgProSerAlar}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -AGGATTCTGAAGCCCAGCGGGCCGAGTCATTGCCGTCTTAAAAGCCCCGAGAGC 1996
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450 ysGlyLysPheArgLysSerArgLeuLysLeuLysAspGlyAsnArgIleSerLeuProS 470	Db		The control of the
947TCTACATCTACACCCT 962	Qy		7 おびのつかいつではついっています。 マー・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・・
430 rgGluLeuAsnTleTleHesGlnLeuCysGlnGluLysProArgValLysLysArgL 450	Δþ		2N5 (1-1066
917	Qy		/ Match: 7.43% Indels:
Ģ	DD dd		Local Similarity: 21.87% Conservative:
7 GATGTGCTGCCCTGGGATGAAGGTGAGCTGCCAGGTCCCAGAGAT	2 04		d. No.: 7.82e-14 Length: re: 301.50 Matches: 0.00 Matches:
391 GluLeuArgThrTrpGluGluGluLeuThrArgAlaAlaLeuGlnGlnLysAsnGlnGlu 410	дb		Alignment Scores:
843 GAAGGGCCTCATGGAGGTGCAGAG 866	Qy		FT NON_TER 1 1 1 SQUENCE 1066 AA; 118463 MW; EDD08EBEE7482723 CRC64;
371 GlnAspAsnTrpLysHisGluIleGlnGluMetPheAspGlnLeuArgAlaLysGluLys 390	Db		PROSITE; PS50002; Kinase; SH3 domain
792 GTTTTGGGATGGAAAAGAGGGGTCCAGGAACTACACGGTGGTGAACACAGA 842	Оу		PS50011; PROTEIN_KINASE PS00108; PROTEIN_KINASE
351 LeuThrThrIleGluGluSerGlyPhePheGluMetProLysAspSerPheHisCysLeu 370	. 06		<pre>SMART; SM00219; Tyrkc; 1. PROSITE; PS00107; PROTEIN_KINASE_ATP;</pre>
733 CTGTGCTGTGGGAAGCAGACAGCCTTCTTCTC-ATCCCAGGGCCAGGAGTACACCGTGGT 791	Qy		SMART; SM00326; SH3; 1. SMART; SM00220; S_TKC;
342ProSerPheThrAsnIleLeuAspGln 350	Db		ProDom; PD000001; ProDom; PD000066;
673 CTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACCTTCATGAATGA	Qy	-	PRINTS; PRO045;
326PheAlaLysLeuMetGluAspCysTrpAsnProAspProHisSerArg 341	DЬ		Pfam; PF00069; pkinase; 1 Pfam; PF00018; SH3; 1.
613 TTCCGGCGACTGCAGGGCGCTCATGATGGAGTGCTGGGGACACTAAGCCAGAGAAGCGACCG 672	VΩ		<pre>InterPro; IPR001452; SH3. InterPro; IPR001245; Tyr_pkinase.</pre>
310 AlaMetAsnLysLeuAlaLeuProIleProSerThrCysProGluPro 325	Db		InterF InterF
559AAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGGAGGAAGGGGAAGTGCAG 612	Qy		EMBL; AF251442; AAG44591 HSSP; P29355; 1SEM.
290 LeuLeuThrGlyGluValProPheArgGlyIleAspGlyLeuAlaValAlaTyrGlyVal 309	Db		e EMBL/GenBank/DDBJ databases.
508 TTGCTGTCAGGACAGCGCCCTGCACTGGGCCACCACCAGCTCCAGATTGCC 558	Qy		<pre>McNee J.J., Dower S.K., Guesdon F.; "cDNA sequence and gene organisation of mixed</pre>
270 ArgAlaSerMetPheSerLysGlySerAspValTrpSerTyrGlyValLeuLeuTrpGlu 289	Дb		SEOU!
448 CCTCGCATTGTATATGATGAGAAGGTAGATATGTTCTCCCTATGGAATGGTGCTCTACGAG 507	νg		<pre>Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID-9606;</pre>
250 HisArgThrThrLysMetSerAlaAlaGlyThrTyrAlaTrpMetAlaProGluValIle 269	Db		Homo sapiens (Human). Eukaryota; Metazoa; Chordata;
388 TTCCATGAGGGCGCCCTAGGCGTGGAGGCCACTCCTGGCTACCAGGCCCCAGAGATCAGG 447	Qy		01-JUN-2002 (TrEMBLrel. 21) Last Mixed lineage kinase MLK1 (Fragme
231 GlyAspLeuSerAsnLysIleLeuLysIleThrAspPheGlyLeuAlaArgGluTrp 249	ДD		01-MAR-2001 01-MAR-2001
331GACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCAGTCA 387	Qy .		ID 09H2N5 PRELIMINARY; PRT; 1066 AA. AC 09H2N5.
	Db .		RESULT 11
280 AACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTT 330	Qy .		Db 383 LeuLeuGlu 385
	Дb		QY 694 CAGATGAAG 702
тсееесстеесст	Qy		Db 363 MetThrArgCysTrpAspAlaAsnProGluValArgProCysPheValGluValValLys 382
182	Ф	٠	Qy 634 ATGATGGAGTGCTGGGACACTAAGCCAGAGAAGCGACCGCTGGCCCTGTCGGTGGTGAGC 693
181 GAGAACGCCAGAGATTCTTCCTTTATACCCCTGGGACACATGCTCACCCAAAAAATA 237	Qy		Db 346 GlyValArgProThrValProAsnAspCysLeuProValLeuSerAspIle 362
	DЬ		
CTCTGCTTCGCCCTGGAGCTCGCGCCCCCAGCAGCCTCAACACCGTGCTGTCC	Oy .		
:::	₽ ;		517 GGACAGCGCCCTGCACTGGGCCACCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAG
67 ATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCCG 126	Q <sub>y</sub>		::::

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OSZO31 PRELIMINARY; PRT; 411 AA.
OSZO31; Q94AIO;
O1-MAY-1999 (TTEMBLrel. 10, Created)
O1-JUN-2002 (TTEMBLrel. 21, Last sequence upda
O1-JUN-2002 (TTEMBLrel. 21, Last annotation up
Hypothetical 46.0 kDa protein.
ATGZ4350.
ATGGZ4350.
Eukaryota; Viridiplantae; Streptophyta; Embryo
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ATP-binding; Kinase;
SEQUENCE 412 AA;
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GTATATGATGAGAAGGTAGATATGTTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCA
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C.M., Benito
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	л	7	1577	Ş
	4	euLe	634	da d
	1576	9TGCCTGAGGGGGACTCCA	1559	Ĝ
	634	9ProGluProGluGluProArgArgAlaGlyProThrGluArgGlyA	619	Db
	1558	3 CGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCAGCCACACGGCCAACCCAAAGG	1503	δ
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	1502	CTACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCC	1443	VΩ
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	1442	GGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCC	1383	φ
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	568	8 nSerPro-ArgArgLeuGluAspSerSerAsnGlyGluArgArgAlaCysTrpAlaTrpG	548	뭥
	1322	TGGGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCTGGAGATCTGCAGGCGGCTG	1266	Ş
	548	oArgPheArgAlaIleGl	529	뭥
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	529		510	뭥
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	1184		1128	Ş
	489	7 ArgAspGly	487	В
	1127	8 CTTAGCGGGCCTCGCCGATGGGCTTGTGGCTGTGTTTCCCGTGGTGCGGGGCCACCCCAAA	1068	Ş
	486	7 ArgGluArgProHisValArgArgArgArgGlyThrPheLysArgSerLysLeuArgAla	467	B
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	466	7 AlaGlnTrpGluLeuGluValPheGluArgAspValThrLeuLeuGluGlnValAsp	447	B
	1016	CCTCAAGGGCATGTGCCCCCTTAAACACACCCCCAACAGGCCTTTGGATACTCCCAGCTGT-	960	Q
	446	7 ArgAlaAlaArgGluGlnArgSerGlnAlaGluGlnLeuArgArgArgGluHisLeuLeu	427	日
	959	GCTCCAGGTCCAGAGATCCCTGTGGACAGCCACCGAGGACC	900	Ş
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	899	AGAGAAGGGCCTCATGGAGGTGC	840	Ş
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	839	GTTTTGGGATGGAAAAG	792	δ
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ing project; to the EMBL/GenBank/DDBJ database S TO THE SER/THR FAMILY OF PROTE UK_PKInase. ber_thr_pkinase. yr_pkinase. yr_pkinase. yr_pkinase. j. i. pkinase; 1. i. fil_KINASE_DOM; 1.	RESULT 9 Q9M085 Q9M085; PRELIMINARY; PRT; 412 AA.  AC Q9M085; DT 01-OCT-2000 (TrEMBLrel. 15, Created) DT 01-OCT-2000 (TrEMBLrel. 20, Last sequence update) DT 01-OCT-2000 (TrEMBLrel. 20, Last annotation update) DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) DE Protein kinase-like protein. GN AT4G31170. CN AT4G31170. CS Arabidopsis thaliana (Mouse-ear cress). CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; CC Eukaryota; Viridiplantae; Streptophyta; Core eudicots; Rosidae; CC Eukaryota; Magnoliophyta; eudicotyjedons; core eudicots; Rosidae; CC Spermatophyta; Magnoliophyta; eudicotyjedons; core eudicots; Rosidae; CC NCBI_TAXID=3702; RN [1] RP SEQUENCE FROM N.A. RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G., RA Mewes H.W., Lencke K., Mayer K.F. X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.	QY       1884 CAGAGACCTCATTTGGGTTCCCCAGGCGCGGTGGAGATGTTATCGTCATTTGGCCTTGAGAA       1943	Qy 1653 CTGCTCCATGTCCTCCTACTCCTCATCCCCAGCCCGCCAGGCTGCCAGGTCCCCCT

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Q9JJ15;
Q1-CCT-2000 (TrEMBLrel. 15, C
Q1-CCT-2000 (TrEMBLrel. 15, I
Q1-MAR-2002 (TrEMBLrel. 20, I
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STRAIN=129/OLA;
STRAIN=129/OLA;
MEDLINE=20354997; PubMed=10894943;
MEDLINE=20354997; PubMed=10894943;
Saridaki A., Ferraz C., Demaille J., Scherer G.,
Saridaki A., Ferraz C., Demaille J., Scherer G.,
"Genomic sequencing reveals the structure of the
"annes and their close vicinity to the Sipal gene
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                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
Euk_pkinase.
Ser_thr_pkinase.
                                                                  89:85-88(2000).
S TO THE SER/THR FAMILY
NS 1 SH3 DOMAIN.
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Kcnk6 and
on mouse
                                                                                     PROTEIN KINASES
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; Murinae; Mus
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Best Local Similarity:
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InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
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SMART; SM00219; TYTKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00452; SH3DOMAIN.
PRINTS; PR00109; TYRKINASE.
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   673
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 CTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACCTTCATGTATGAA
                                                                                                     AlaValAsnLysLeuThrLeuProIleProSerThrCysProGluPro---
                                                                                                                                                                      LeuLeuThrGlyGluValProTyrArgGlyIleAspCysLeuAlaValAlaTyrGlyVal
                                                                                                                                                                                                      TTGCTGTCAGGACAGCGCCCTGCACTGGGCCACCACCAGCTCCAGATTGCC-
                                                                                                                                                                                                                                          LysAlaSerThrPheSerLysGlySerAspValTrpSerPheGlyValLeuLeuTrpGlu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Val---AsnTrpAlaValGlnIleAlaArgGlyMetHisTyrLeuHisCysGluAlaLeu
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                                                                  TTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGACACTAAGCCAGAGAAGCGACCG
                                                                                                                                     ---- AAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGCAGCCGGAGGAAGTGCAG
                                                                                                                                                                                                                                                                                                            HisLysThrThrGlnMetSerAlaAlaGlyThrTyrAlaTrpMetAlaProGluValIle
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                                                                                                                                                                                                                                                                                                                                                                                                 -GACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS50011; PROTEIN_KINASE_DOM; PS00108; PROTEIN_KINASE_ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        850
                                 -PheAlaGlnLeuMetAlaAspCysTrpAlaGlnAspProHisArgArg---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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Indels:
Gaps:
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Matches:
Conservative:
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Best Local Similarity:
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ProDom; PD000001; Euk_Dkinase; 1.
ProDom; PD000066; SH3; 1.
SMART; SM00219; TYPIKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50002; SH3; 1.
PROSITE; PS50002; SH3; 1.
PROSITE; PS50002; SH3; 1.
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Pfam; PF00018; SH3; 1.
613 TTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGGACACTAAGCCGAGAGAAGCGACCG
                                                                                                                                                                                       508 TTGCTGTCAGGACAGCGCCCTGCACTGGGCCACCACCAGCTCCAGATTGCC------
                                                                                                                                                                                                                                   295 LysAlaSerThrPheSerLysGlySerAspValTrpSerPheGlyValLeuLeuTrpGlu
                                                                                                                                                                                                                                                                            448 CCTCGCATTGTATATGATGAGAAGGTAGATATGTTCTCCTATGGAATGGTGCTCTACGAG
                                                                                                                                                                                                                                                                                                                        275 HisLysThrThrGlnMetSerAlaAlaGlyThrTyrAlaTrpMetAlaProGluValIle 294
                                                                                                                                                                                                                                                                                                                                                             388 TTCCATGAGGGGGGCCCTAGGCGTGGAGGGCACTCCTGGCTACCAGGGCCCCAGAGATCAGG 447
                                                                                                                                                                                                                                                                                                                                                                                                      328 CTTGACGTCAAGGAGCACCATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCAGTCA 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 Val---AsnTrpalaValGinileAlaArgGlyMetHisTyrLeuHisCysGluAlaLeu
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                                                               335 AlaValAsnLysLeuThrLeuProIleProSerThrCysProGluPro-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 AACACCGTGCTGCCGAGAACGCCAGAGATTCTTCCTTTATACCCCCTGGGACACATGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 ValCysLeuGluGluProAsnLeuCysLeuValMetGluTyrAlaAlaGlyGlyProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 ATCAGCATCCACCCG-----CTCTGCTTCGCCCTGGAGCTCGCGCCGCTCAGCAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 ArgGlnGluAlaArgLeuPheAlaMetLeuAlaHisProAsnIleIleAlaLeuLysAla 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 ---AACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGG------TCC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 CGGCAGGAGGCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGC
                                                                                                        -----AAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGCAGCCGGAGGAAGTGCAG
                                                                                                                                             LeuLeuThrGlyGluValProTyrArgGlyIleAspCysLeuAlaValAlaTyrGlyVal 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCCAAAAAATAGCCTACCAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerArgAlaLeuAlaGlyArgArg-------ValPro---ProHisValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               847 AA; 92687 MW; AFB6E930EA281C15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.51e-16
337.50
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Db 676 ThrThrProProThrProThrP
128
Db 656 GlyLeuGlyArgAspLeuGlnProProGlyGlyProGlyArgG
Qy 1283
oz Lysargerovaleroalagiuargglys oy 1223 CCATGGAGGTGGTCAACAGCGGCTCTGA
1163
Qy 1106 CCGTGGTGCGGGGCACCCCAAAGG
 587 GluAlaThrTrpTyrL
Db 567 GlyProSerSerProLysProGlyGlu  Qy 1055 ATTCCTACCTGGTCTTAG
, 1010 C
:::::: 556 SerAsnGl
TACACCCTCAAGGGCATGTGC
Qy 923GGACAG           Db 536 GluProAlaGluProGlyGlnAlaTrpG
516 ValPheGluV
Qy 897ccagcrccaggrccag
Qy 879 TGGGATGAAGGTGAGCTG       Db 496 LeuAspPheLysHisArgIleThrValG
476 GlyThrPheLysArgSerLysLeuA
855
Qy 840
9
Db 416 GluLeuLeuSerArgGluGluGluLeuThrArgAl
Оу 818
Db 396 GlnGluGlyTrpLysArgGluIleGlnGlyLeuPheAs
Qy 792 GTTTTGGGATGGAAAAGAGGAGTCCAG
376 LeuGl
733 CTGTG-C
367
Qy 673 CTGGCCCTGTCGGTGAGCCAGATGAAGG
Db 351PheAlaGlnLeuMetAlaAspCysTrpAlaGlnAspProHisArgAr

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1284	TCTGAGGTCTGGTACAGCAATGGGCCGGGCCTCCTTGTC	1246	δĀ
2141	HisSerGluGluProAsnLeuIleGluAspValLysValAlaArgMetCysSerAsnGlu	2122	₽
1245	- ହି	1216	Ϋ́
2121	GlyLysIleAsnValPheProLeuAsnGluAsnGlyValSerGlyHisGlnAlaLeuCys	2102	ф
1215	GCACGGCAGAACCCCTACCCA	1195	δÃ
2101	HisAlaAlaCysSerValValAspGlyIleTyrGluLeuTrpCysGlyGluIleAla	2082	B
1194	CGCGGATGAAGAC	1165	γ
2081	asnCysAlaPheAlaGluGlySerPheValLeuThrGluIleCysSerGlyPheValLeu	2062	B
1164	GCTGCTCCTACCTGTGCTCACACACAGCCAAC	1132	Qy
2061	ValGlyThrHisAsnGly····-ArgValPheLeuValAspAlaThrGlnMetProSer	2044	Dβ
1131	·Ή	1072	Qy
2043	AsnIleLysSerAlaVallleSerLeuValTyrMetGluLysIleAlaArgValAla	2025	日
1071	AATTCCTACCTGGTCTTA	1012	Š
2024	:::     :::	2008	윰
1011	TACTO	952	γO
2007		1988	Ф
951	GACAGCCACCGAG	892	οy
1987	ProGluAsnGlyAlaAsnSerArgAlaArgSerAlaGlnArgLeuProLysMetAsnMet	1968	В
891		877	QΥ
1967	LeuLeuGlnCysAsnSerIleSerCysSerProGlnProGlnValAlaProProLysThr	1948	В
876	AGGTGCAGAGGATGTGCTGC	850	Qγ
1947	LeuTrpLeuProSerPheGlySerArgIleAspIleLeuAspCysSerProSerGlySer	1928	Д
849	TTTTGGGATGGAAAAGAGGAGTCCAGGAACTACACGGTGGTGAACACACAGAGAAGGGGC	793	VΩ
1927		1908	B
792	AGCCTTCTTCTCATCCCAGGGCCAGGAGTACACCGTGGTG	736	δ
1907	SerAlaProGluCysIleH1sLeuLeuAspValValAlaMetProH1sSerGluLysIle	1888	В
735	AAGGACCCGACTTTTGCCACCTTCATGTATGAACTG	700	δĀ
1887	:::       ::: erGlnIleValSerIleLeu	83	용 :
699	GACCGCTGGCCTGTCGGTGAGCCAGATG	640	٥
1867		1849	В
639	CCGGCGACTGCAGGCGCTCATGATG	583	Ş
1848	GlyH1sGluSerIleLysGluCysIleLeuGluGlySerArg		요 :
582	CGCCCTGCACTGGGCCACCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCCATCCGC	523	٥ V
1834	Asn	1834	B
522	TGAGAAGGTAGATATGTTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAG	463	Ş
1833		1817	용

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                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

MEDLINE-94253068; PubMed-8195146;

MEDLINE-94253068; PubMed-8195146;

Meallo K.A., Mark M.R., Scadden D.T., Wang Z., Gu Q., Godowski P.J.;

"Identification and characterization of SPRK, a novel src-homology domain-containing proline-rich kinase with serine/threonine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-94239754; PubMed-8183572;
Ing Y.L., Leung I.W., Heng H.H., Tsui L.C., L
"MLK-3; identification of a widely-expressed
SH3 domain and a leucine zipper-basic region
oncogene 9:1745-1750(1994).
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01-NOV-1996 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Protein kinase (Similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                          Biol.
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Last annotation update)
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RESULT 6
RA Adams M.D. (Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., RA George R.A., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Ra Borkova D., Debtchan M.R., Bouck J., Brokstein P., Brottler P., Ra Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Glasser K., RA Horstin D., Houston K.A., Howland T.J., Wei M.-H., Ibaywam C., RA Lasko P., Lei Y., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A. RA Lasko P., Lei Y., Levitsky A.A., Li J., Wei M.-H., Ibaywam C., RA Mount S.M., Nolson K., Molarny C., Morris J., Moshrefi A., RA Mount S.M., Nolson K.A., Howland T.J., Wei M.-P., McPherson D. L., RA Mount S.M., Nolson K., Molarny C., Morris J., Moshrefi A., RA Reinert K.A., Nixon K., Nusskern D.R., Pacleb J.M., Pall Z., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Resse M.G., Stapleton M., Skupski M.P., Smith T., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen H., Shen 
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
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InterPro; IFR000719; Euk_p)
InterPro; IFR001611; LRR.
InterPro; IFR003592; LRR_ou
InterPro; IFR003592; LRR_ty
InterPro; IFR003591; LRR_ty
InterPro; IFR002290; Ser_ty
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PROSITE; PS50088; ANK_REP_REGION; 2.

PROSITE; PS50297; ANK_REP_REGION; 2.

PROSITE; PS500107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

ANK repeat; ATP-binding; GTP-binding; Repeat;

Serine/threonine-protein kinase; Transferase.

Serine/threonine-protein kinase; CE36F007E79D5D0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    1684 LeuGlnHis----
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                                                                                                                                                                                                                                                                                                                                     124
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                                                                                                                                                                                                                                                                       184
                                                                                                                                                                                                                                                                                                                                                                                                   64 AGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CTGAGGCACCTGCGGGCCACCGATGCCATGAAGAACTTCTCCGAGTTCCGGCAGGAGGCC
                                                                                                                                                                                                                                                                                                                                                                 AlaValLeuLeuThrLeuLysHisProAsnIleValProLeuValGlyIleCysIleLys 1718
                                LeuValHisTleLysIleAlaAspTyrGlyIleSerArgGlnThrAlaProSerGlyAla
                                                       CACATCAACATCAAGCTATCTGACTACCGGGATTTCGAGGCAGTCATTCCATGAGGCGCCC
                                                                                                GlnAlaAlaArgAlaIleGluTyrLeuHisArgArgArgIleIleTyrArgAspLeuLys
                                                                                                                                                                                              CAGATCGCCTCGGGCCTGGCCTACCTGCACAAGAAAAAACATCATCTTCTGTGACCTGAAG
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CTAGGCGTGGAGGGCACTCCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATAT 462
                                                                                                                                   TCGGACAACATTCTGGTGTGGTCCCTT----
                                                                                                                                                                                                                                    TyrArgArgSerGlyAlaHis-----MetGlyProHisThrPheGlnThrLeuValLeu
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SM00369; LRR_TYP; 1
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38.51%
23.73%
8.98%
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Ras_trnsfrmng
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STRAIM-BRISTOL N2;
Zhu H.J., Graves T., Hawkins M.;
"The sequence of C. elegans cosmid T27C10.";
submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
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Prodom; PD000001; Euk_Pkinase; 1.

SMART; SM00220; S_TKC; 1.

SMART; SM00219; TYFKC; 1.

SMART; SM00219; TYFKC; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

ATP-binding; Hypothetical protein; Transferase.

SEQUENCE 1175 AA; 130667 MW; F4BFBF44DDC1390C CRC64;
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InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; I.
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1602	552 CCAAAGGTGCCTGAG	o V
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1503	444 TACCAGCTGTGTGCCCCGGTACTTCTGCGGGGTCCCCAGCCCCCTCAGGGACATGTTTCC	y Q
1002	:::        983 GlnLysValTrpIleAlaLeuGluLysSerSerLysValGlnMetValGluValGluLys	B.
1443	AGGTCGTCTGGTGCCTGGATGACAAGGCCAAC	Qy
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1383	1333 GCCCCCTCCATGGTTACGTCAGTCGTGTGCAGCTCTGAGGGCAGAGGGGAG	Qy
965	:::     :::        ::: 946 ArgIleSerIleHisHisIleAlaSerAsnAsp	рь .
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1275	TCTGAGGTCTGGTACAGCAATGGGCCGG	Qy
925	916GlyThrIleAspSerProTyrGluIleArg	В
1221	CCCTACCCAGTG	Qγ
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1161	GGTGCGGGGCACCCCAAAGGACAGCTG	γQ
903	886 GluLeuIleSerAspAspValLeuIleLeuIleSerAspLysGlnIleValLeu	B
1101	TAAAAAAGAATTCCTACCTGGTCTTAGCGGGCCTCGCCGATGGGCTTGTGGCTGTG	Qy
885	868 GluThrGlyHisLeuGlnLeuProSerLeuAsnGlyThrLeuIleCysAlaPro	Db
1041	CCCCAACAGGCCTTGGATACTCCAGCTGTCGTCACCTGCTTCTTGGCCGTGCCT	Qy
867	851 TrpSerCysAspGluCysGlyGlnValThrValTyrGlyIleSerLeuHis	DЪ
981	AGCCACCGAGGACCAGAAAATCTACATCTACACCCTCAAGGGCATGTGCCCCTTA	Qy
850	LysValArgAspSerVal	망
921	gggatgaaggtgagctgccagctccagaggtccagagatccctg	Qy
833	CysThrGlnTyrGlyPheValAspGlnLysSer	В
867	TGCA	Qy
813	AspPheGluAlaGlnLeuTrpLeu	D
810	GGAGTACACCGTGGTGTTTTGGGATGGAAAAGAG	Qу
796	spValCysGluLeuGlyGluAlaLeuProProThrGlnLeuMetAlaValGly	B
765	TGTGGGAAGCAGACAGCCTTCTTCTCA	Qy
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Similar to hypothetical protein
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Eukaryota, Metazoa; Chordata; C
Mammalla; Eutheria; Primates; C
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SEQUENCE 221 AA; 241/1 '"
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(TrEMBLrel. 20, Last annotation)
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01-MAR-2001
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Homo sapiens (Human),
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
NCBI_TaxID=9606;
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Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota
Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura
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                             LeuArgAspMetPheProValArgProLeuAspThrGluProProAlaAlaSerHisThr
                   GluLeuGlyThrGlnIleLeuIleHisGlnGluSerLeuThrAspTyrCysSerMetSer
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(TrembLrel. 16, Last sequence up
(TrembLrel. 19, Last annotation
119 fis, clone LNG07978.
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99.60%
32.65%
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Matches:
Conservative:
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Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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01-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submilted (APR-2002) to the EN
EMBL; BC027199; AAH27199.1; -
Hypothetical protein.
SEQUENCE 252 AA; 28042 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. TISSUE-COLON;
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LeuArgAspThrPheSerValGlnProSerValLeuGluThrPro--
                                                                                                 ATGTACCACTCCACCACCTACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCAGCCCC
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84.58%
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25.79%
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Rodentia;
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. 21, Last sequence upo
. 21, Last annotation upo
l protein FLJ23119.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001005; Myb_DNA_binding.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
PROSITE; PS00037; MYB_1; UNKNOWN 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM;
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                                                               CCTGGCTACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAAGGTAGATATG
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                                                                                                             GAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGACACTAAGCCA
                                                                                                                                                                                    TTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCTGCACTGGGCCAC
TACACCGTGGTGTTTTGGGATGGAAAAGAGGGAGTCCAGGAACTACACGGTGGTGAACACACA
                           TTCATGTATGAACTGTGCTGTGGGAAGCAGACAGCCTTCTTCTCATCCCAGGGCCAGGAG
                                                                                                   GluGluValGlnPheArgArgLeuGlnAlaLeuMetMetGluCysTrpAspThrLysPro
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3822.00
100.00%
100.00%
94.18%
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1920	CAGGCCGTGAAGATCCTCGCCGTCAGAGAACCTCATTTGGGTCCCCAGGCGCGGTGGAGAT	1861	. p . Q
1281		1262	
1860	GACGGGGAGACCTTCAGCCAGCACCTG	1801	Qy
1261		1242	Db
12 60	AGGACTCAGACATGCTACATACGCCCGGTGCTGCC	1741	Qy
		1222	Db
1740	TCCCCCTCAAGCCTCCCCAGCTCCCCAGCAAGTTCTTCC	1681	Db Qy
1221		1202	
1680 1201	TCACTCACTGACTACTGCTCCATGTCCTCCTACTCCTCATCC	1621 1182	ДУ
<b>1</b> 6	TCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCAG 		Оу
1560	TTGGACACGGAACCCCCGGCAGCCAGCCAGC	1501	Qy
1161		1142	db
1500 1141	ACCTACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCAGCCCCCTCAGGGACATGTTT	1441 1122	Db Qy
1440 1121	GAGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACTCCACC	1381 1102	ОУ
1380 1101	GAGCCCTACATGGCCCCCTCCATGGTTACGTCAGTCGTGTGCAGCTCTGAGGGCAGAGGG	1321 1082	Db Oy
1320	TGGAGATCTGCAGGCGGCTG	1261	Qy
1081		1062	db
0 0	CCCCTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTAC 	1201 1042	Db Qy
1200	ACAGGTCCAAGTTCAGCATCGCGGATGAAGACGCACGG 	0 1	• Db
1140 1021	TGGCTGTGTTTCCCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTCC 		Db Qy
1001	AAGAATTCCTACCTGGTCTTAGCGGGCCTC	1021	
		982	Оу
1020	CACACCCCAACAGGCCTTGGATACTCCAGCTGTCGTC	961	Ф
981		962	
960	CTGTGGACAGCCACCGAGGACCAGAAAATCTACATCTACACC	901	Фр
961		942	
900	GTGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAAGCTGCCAG	841	Qy
		922	Db
921	${\tt TyrThrValValPheTrpAspGlyLysGluGluSerArgAsnTyrThrValValAsnThr}$	902	D

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Result
No.
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-DB-SBTREMBL_21 -QFMT-fastan -SUFFIX-nJp.rspt -MINNATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DCCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-MODE-LOCAL -OUTEMT-pto -NORN-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09836392_GCGN_1_1_81_Grunat_08042003_090328_22781 -NCPU-6 -TCPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS-1 -XGAPOP=10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                        Score
   3822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seg length: 0 seg length: 2000000000
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Match Length DB
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1 atgctgaggcacctgcggggc.....cttgcactcgcaagagaagg 2184
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14516.352 Million cell updates/sec
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   94.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                      sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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1369 4 Q96JN5
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                                                                                                                                                                                      SUMMARIES
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Q96jn5 homo sapien
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## ALIGNMENTS

190	SULT 1	
٠.	Q96JN5;	
•	-2001	, Created)
	01-DEC-2001 (TrEMBLrel. 19	(TrEMBLrel. 19, Last sequence update)
•	01-JUN-2002 (TrEMBLrel. 21,	, Last annotation update)
	: KIAA1790 protein (Fragment)	-
_	KIAA1790.	
	Homo sapiens (Human).	
`-	Eukaryota; Metazoa; Chordata;	ta; Craniata; Vertebrata; Euteleostomi;
` .	Mammalia; Eutheria; Primates;	es; Catarrhini; Hominidae; Homo.
^	( NCBI_TaxID=9606;	
-	[1]	
Ü	SEQUENCE FROM N.A.	
	TISSUE-BRAIN;	
_	<pre>MEDLINE=21245130; PubMed=11347906;</pre>	1347906;
_	Nagase T., Nakayama M., Nakajima D., Kikuno R.,	kajima D., Kikuno R., Ohara O.;
_	"Prediction of the coding	"Prediction of the coding sequences of unidentified human genes. XX.
•	The complete sequences of	The complete sequences of 100 new cDNA clones from brain which code
-	for large Proteins in vitro.";	0. "."
	DNA Res. 8:85-95(2001).	
٠.	: -!- SIMILARITY: CONTAINS 1	-!- SIMILARITY: CONTAINS 1 WD REPEAT (TRP-ASP DOMAIN).
~	EMBL; AB058693; BAB47419.1; -	•
~	<pre>InterPro; IPR000719; Euk_pkinase</pre>	kinase.

Job time : 57 secs

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Toshima J., Ohashi K., Okano I., Nunoue K., Kishioka M., Kuma K.-I., Miyata T., Hirai M., Baba T., Mizuro K.;

"Identification and characterization of a novel protein kinase,
TESK1, specifically expressed in testicular germ cells.";
J. Biol. Chem. 270:3131-31337(1995).

-I- FUNCTION: DISSPLAYS SERINE/THREONINE-SPECIFIC PHOSPHORYLATION OF
MYELIN BASIC PROTEIN (MBP) AND HISTONE IN VITRO. PROBABLY PLAYS A
CENTRAL ROLE AT, AND AFTER THE MEIOTIC PHASE OF SPERMATOGENESIS.

-I- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN TESTICULAR GERM
CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institute. There are no rest modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.inhors.equires.alicense.agreement (See http://www.inhors.equires.alicense.agreement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- DOMAIN: THE EXTRACATALYTIC C-TERMINAL PART IS HIGHLY RICH IN PROLINE RESIDUES.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-Wistar; TISSUE-Testis;
MEDLINE-96125123; PubMed-8537404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_TYR; PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD000001; Euk_F
SMART; SM00221; STYKC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001245; Ty Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D50864; BAA09460.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                            Transferase; Serine/threonine-protein kinase; ATP-binding.
DOMAIN 52 310 PROTEIN KINASE
NP_BIND 58 66 ATP (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                             BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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 89 ArgSerAsnThrLeuArgGluValGlnLeuMetAsnArgLeuArgHisProAsnIleLeu 108
                                                                      6
                                                                                                        69 ValArgHisArgGlnSerGlyGlnValMetValLeuLysMetAsnLysLeuProSerAsn
                                                                                                                                         4 CTGAGGCACCTGCGGGCCACCGATGCCATG------
                                                     TTCTCCGAGTTCCGGCAGGAGGCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTG
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IPR004040; STY_pkinase.
IPR001245; Tyr_pkinase.
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67987 MW;
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ATP (BY SIMILARITY).
BY SIMILARITY.
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Matches:
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1113	CTGTGTTTCCCGTGGTG	1054	Q .
431	ProLeuThrSerThr-GlnLeuProLeuValAlaSerProGluSerLeuValGlnProGl	412	문
1053	TCCAGCTGTCGTCACCTGCTTCTTGGCCGTGCCTGTTATTAAAAAG	994	Qy
411	sProAlaThrProLeuProLeuValProProSer	392	Db
993	AACACACCCCAA	970	Qy
391	1yAspAsnLeuThrArgValAsnProPheSerLeuArg-GluAspLeuArgGlyGlyLys	372	pb dq
· ~	uSerArgSerArgSerAspLeuPheLeuProProSerProGluSerProProSerTrpG	352	ф
926	GATCCCTGTGGAC	895	Qy
352	SerValProArgGlyGlyProSerAlaThrLeuProArgSerAspProArgL	335	Db.
894	CTGGGATGAAGGTGAGC	835	Qy
334	LeuAlaLysAlaProLeuThrTyrAsnGlnGly	324	<b>D</b> b .
834	GTCCAGGAACTACACGGTGGTG	775	ОУ
323	0	309	ф
774	TCCCAGGGC	715	Qy
308		292	뫄
714	CCGACTTTT	655	Qy .
291	AsnAspCysProLeuProPheLeuLeuLeuAlaIleHisCysCysSerMet	275	ф
654 .	GCAGTTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGACACT	595	Qy
274	GluAspPheGlyLeuAspValProAlaPheArgThrLeuValGly	260	Db
594	CIGGG	535	Qy
259	<pre>:::     </pre>	240	Db
534	TGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCTGCACTG	493	Оу
239	AlaProGluValLeuArgGlyGluLeuTyrAspGluLysAlaAspValPheAlaPheGly	220	Db
492	CCCCAGAGATCAGGCCTCGCATTGTATATGATGAGGAAGGTAGATATGTTCTCCTATGGA	433	Qy
219	ValTyrArgGluGlyAlaArgLysGluProLeuAlaValValGlySerProTyrTrpMet	200	ДĎ
432	CTAGGCGTGGAGGGCACTCCTGGCTACCAG	385	Qy
199	spGlyGlyPheThrAlaValValGlyAspPheGlyLeuAlaGluLysIlePro	182	DЬ
384	CGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCAG	331	Qy
181	isAlaLysGlyValPheHisArgAspLeuThrSerLysAsnCysLeuValArgArgGlu	162	Db
330	CAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTT	271	οу
161 .	LeuSerTrpProValArgLeuHisLeuAlaLeuAspIleAlaGlnGlyLeuArgTyrLeu 1	142	₽
270	CCTGGCCTACCTG	211	Ωy
141	:::    AlaLeuThrGluTyrMetAsnGlyGlyThrLeuGluGlnLeuLeuSerSerProGluPro 1	122	dq
210	GCCTCAACACCGTGCTGTCCGAGAGACGCCAGAGATTCTTCCTTTATACCC	160	Qγ
121	argPheMetGlyValCysValHisGln	109	₽

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                                     SMART; SM00326; SH3; 1.

SMART; SM00219; TYZKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROFIN_KINASE_TYR; PROSITE; PS50011; PROTEIN_KINASE_DOM; PROSITE; PS50001; SH2; 1.

PROSITE; PS50002; SH3; 1.
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P42690;
01-NOV-1995 (Rel.
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Eukaryota; Metazoa; Porifera; Demospongiae;
Haplosclerida; Spongillidae; Spongilla.
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ProDom; PD000093; SH2; 1.
SMART; SM00252; SH2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                         ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00069; pkinase; 1.
PRINTS; PR00401; SH2DOMAIN.
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InterPro; IPR001245; Tyr_pkinase.
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"Multiple src-related kinase genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6055
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11-NOV-1995 (Rel. 32, Created)
11-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
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CACATION: Cytoplasmic (Probable).

ALTERNATIVE PRODUCTS: 2 1soforms; 1 (AC P42686) a
hare); are produced by alternative splicing.

SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN
SIMILARITY: CONTAINS 1 SH2 DOMAIN.

SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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||||||||||||||
-ProProThrPro------SerLeuGlnLeuProGly 623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00017; SH2; 1.
PF00018: SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     PD000001;
                                                                                                                                                                                                                                                                                                                                                                                                                                       PR00109; TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000980; SH2
   Tyrosine-protein kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                  Euk_pkinase; 1.
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ATP-binding; SH2 domain;
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DB:
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Best Local Similarity:
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                                                            CTG
                                                                                                                                                                                                                                    TyrGluValIleThrTyrGlyArgPheProTyrProGlyMetThrAsnAlaGlnValLeu
                                                                                                                                                                                                                                                                                                   ATCAGGCCTCGCATTGTATATGATGAGAAAGGTAGATATGTTCTCCTATGGAATGGTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACTTCTCCGAGTTCCGGCAGGAGGGCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATC
                                     Leu
                                                                                                                                                                                     GluGlnIleGlnGlnSerTyrArgMetProArgProMetGlyCysProGlu--
                                                                                                                                                                                                                                                             TACGAGTTGCTGTCA - - - GGACAGCGCCCTGCACTGGGCCCACCAGCTCCAGATTGCC
                                                                                                                                                                                                                                                                                   AlaAlaMetTyrSerArgPheThrIleLysSerAspValTrpSerPheGlyIleValLeu
                                                                                                                                                                                                                                                                                                                                     GluGluIleTyrGluAlaLysLeuGlyAlaLysPheProIleLysTrpThrAlaProGlu
                                                                                                                                                                                                                                                                                                                                                             CAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACTCCTGGCTACCAGGCCCCAGAG
                                                                                                                                                                                                                                                                                                                                                                                      ---ValGlyGluHisLysIleCysLysValAlaAspPheGlyLeuAlaArgValIleAsp
                                                                                                                                                                                                                                                                                                                                                                                                             GACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                      GluGlnGlnAsnTyrIleHisArgAspLeuAlaAlaArgAsnIleLeu------
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuValAspMetCysSer---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCGCTCAGCAGCCTCAACACCGTGCTGTCCGAGAACGCCAGAGATTCTTCCTTTATACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IleGlnLeuTyrAlaValCysThrLysGluGluProIleTyrIleValThrGluLeuMet
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                                                                                                           CTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACCTTCATGTATGAA
                                                                                                                                                            TTCCGGCGACTGCAGGCGCTCATGATGGAGTGCTGGGACACTAAGCCAGAGAAGCGACCG
                                                                                                                                                                                                              AAGAAGCTGTCCAAGGGCATCCGC-----CCGGTTCTGGGGCAGCCGGAGGAAGTGCAG
                                     489
                                                              735
                                                                                                                                    -LysLeuTyrAlaIleMetMetAspCysTrpArgGluAspProAlaSerArg---
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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Matches:
Conservative:
Mismatches:
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Gaps:
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                                                                                    ProThrPheGluThrLeuSerTrpGln
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TGGGACACT 654	5 CAGCCGGAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAGTGC	Оу 59	
GTTCTGGGG 594 ::::::    LeuValGly 279	5 GGCCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCG         ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	Оу 53 Db 26	
CCTGCACTG 534	3 ATGGTGCTCTACGAGTTGCTGTCAGGACAGCGG :::	Qy 49 Db 24	
TCCTATGGA 492::::::     :::::     AlaPheGly 244	3 GCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTAGATATGTTC          :::	Oy 43 Db 22	
GCTACCAG 432 ::: TyrTrpMet 224	35 TCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACTCCTGG	ОУ 38 Db 20	
AG 384 ::: ysilePro 204	31 GACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCA 	Oy 33 Db 18	_
TGGTCCCTT 330 ArgArgGlu 186	1 CACAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTG 	Qy 27 Db 16	
GCCTACCTG 270         ArgTyrLeu 166	1 CTGGGACACATGCTCACCCAAAAAATAGCCTACCAGATCGCCTCGGGCCTG	Qy 21 Db 14	
TTATACCC 210	O AGCCTCAACACCGTGCTGTCCGAGAACGCCAGAGATTCTTCCT :::    :::    ::::	Qy 16 Db 12	
CGCTCAGC 159	O GCGCTCATCGGCATCAGCATCCACCCGCTCTGCTTCGCCCTGGAGCTCGCGCCC:::   :::    4 ArgPheMetGlyValCysValHisGln	Qy 100 Db 114	
TGCATCGTG 99    ::: AsnIleLeu 113	0 TTCTCCGAGTTCCGGCAGGAGGCCAGCATGCTGCACGCGCTGCAGCACCCC :::	Оу 4 рь 9	
AAGAAC 39     roSerAsn 93	etAsnLysLeuP	Oy 7	
	t'Scores: 2.06e-06 Length: 62 255.50 Matches: 15 Similarity: 33.69% Conservative: 71 al Similarity: 22.87% Mismatches: 24 tch: 6.30% Gaps: 28 1 Gaps: 72 205 (1-2104) There's William (1-62)	ignmen ed. No ore: rcent st Loc ery Ma	
	AIM; 601782; InterPro; IPR000719; Euk_pkinase. InterPro; IPR004040; STY_pkinase. InterPro; IPR004040; STY_pkinase. InterPro; IPR001245; Tyr_pkinase. InterPro; IPR001245; Tyr_pkinase. InterPro; IPR001245; Tyr_pkinase; I. InterPro; IPR001245; Tyr_pkinase; I. InterPro; IPR001245; Tyr_pkinase; I. INTERPO00001; Euk_pkinase; I. INTERPO00001; Euk_pkinase; I. INTERPO00017; PROTEIN_KINASE_TYR; I. INTERPO00019; PROTEIN_KINASE_DOM; I. INTERPO00019; PROTEIN_KINASE_DOM; I. INTERPO000019; PROTEIN_KINASE; ATP-binding INTERPO000019; PROTEIN KINASE; ATP-binding INTERPO000000000000000000000000000000000000	DR MIM; 6 DR InterP DR InterP DR InterP DR Pfam; DR Pfam; DR PROSIT DR TALLE PROSIT DR	

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Qy Db	B . 2	) B	Qy	Дb	Qy	<b>D</b>	Qγ	Db ·	<b>δ</b>	₽ ,	ν	망	ργ	망	Qy	망	Qy	ф	Qy	В	Qy	탕	Qy	Ъ	Qy	Вb	Qy	Дb	Qy	фb	Qy	Вb	Qy	Db
1483 568	553	540	1363	523	1304	503	1294	483	1234	463	1174	443	1144	429	1099	413	1039	394	979	374	966	354	4	342	874	340	814	328	754	317	94	97	655	280
CCCCTCAGGGACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCACC		LeuProArgAla	AGGGGAGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTG		CTGCAGGCGGCTGGAGCCCTACATGGCCCCCCTCCATGGTTACGTCAGTCGTGTGC	  GlnProTrpSerProArgSerGlyProValLeuAsnAsnAsnProProAlaValVa			TCAACAGCGGCTCTGAGGTCTGGTACAGCAATGGGCCGGGCCTCCTTGTCATCGAC	::	agcatcgcggatgaagacgcacggcagaacccctacccagtgaag	uLeuProArgArgMetGluThrAlaLeuProGlyProGlyProProAlaValGlyProSe 4		GlyThrProAlaArgArgCysArgSerLe	GGACAGCTGCTCC	LeuValGlnPr	CGGGCCTC		GCCTTGGATACTCCAGCTGTC	euThrArgValAsnProPheSerLeuArgGluAspL		SerProGluS	AGGACCAGAAAATCTACATCTACACCCTCAA	AspProArgLeu	CCCTGGGATGAAGGTGAGCTGCCAGGCTCCAGGTCCAGAGATCCCTGTGGACAGCCACC	Glypro	CACAGAGAAGGGCCTCATGGAGGTGCAGAGGATGTGC	AlaLeuThrHisAsnGlnGlySerValAlaArgGly3	CAGGAGTACACCGTGGTGTTTTGGGATGGAAAAGAGGAG E	rgThr	AGGACCCGACTTTTGCCACCTTCATGTATGAACTGTGCTGTGGGAAGCAGACA 7		AGAAGCGACCGCTGGCCCTGTCGGTGGTGAGC 6	AspAspCysProLeuProPheLeuLeuLeuAlaIleHisCysCysAsnLeu 2
1542 585	68	552 1482	4 1	540	1362	523	1303	503	.293	83	.233	63	173	43	143	28	.098	13	038	94	78	74	65	.54	933	341	873	139	13	327	53	316	93	296

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HSSP; P08631; lADJ.,
DictyDb; DD03011; pykB.
InterPro; IPR000719; Euk_pkinase.
IPR004040; STY_pkinase.
IPR004040; STY_pkinase.
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SEQUENCE
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PIR; B35670; B35670.
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                      301 AAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTA
                                                                   214 ThrAspMetAlaLeuGlyLeuLeuHisLeuHisSerIleThrIleValHisArgAspLeu
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PD000001; Euk_pkinase; 1.
SM00221; STYKC; 1.
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 MEDLINE-96125123; PubMed-8537404;

Toshima J., Ohashi K., Okano I., Nunoue K., Kishioka M., Kuma K.-I., Miyata T., Hirai M., Baba T., Mizuno K.,

"Identification and characterization of a novel protein kinase,"
TESKI, specifically expressed in testicular germ cells.";

J. Biol. Chem. 270:31331-31337 (1995)

-I- FUNCTION: DISPLAYS SERINE/THREONINE-SPECIFIC PHOSPHORYLATION OF MYELIN BASIC PROTEIN (AMP) AND HISTONE IN VITRO. PROBABLY PLAYS CENTRAL ROLE AT, AND AFTER THE MEIOTIC PHASE OF SPERMATOGENESIS.

-I- DOMAIN: THE EXTRACATALYTIC C-TERMINAL PART IS HIGHLY RICH IN PROLINE RESIDUES.
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Homo sapiens (Human).
Homo sapiens (Human).
'Acria; Metazoa; Chordata;
'Acria; Primates;
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Q15569;
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(Rel. 35, Last sequence update)
(Rel. 40, Last annotation update)
ific protein kinase 1 (EC 2.7.1.-)
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EMBL; D50863; BAA09459.1;

	GGCCAA 1415    :	CGTGTGCAGCTCTGAGGGGAGGAGGGAGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAA	1356	δ
	488	roAlaHisAlaGluHisGlyGly	481	뮹.
	GTCAGT 1355	CTCCCTGGAGATCTGCAGGCGGCTGGAGCCCCTACATGGCCCCCCCC	1296	Ş
1 2 H X	CTGTGC 1295:::   ::   erProP 481	CGGCTCTGAGGTCTGGTACAGCAATGGGCCGGCCTCCTTGTCATCGACTGTGC	1242 461	유
, 	CAACAG 1241   :::   erSerA 461	CGCGGATGAAGACGCACGGCAGAACCCCTACCCAGTGAAGGCCATGGAGGTGGTCAACAG    ::::: :::::         :::  narglleGluargAsnLeuGlnSerProThrGlnPheGlnThrProArgSerSerA	1182 442	8 8
		:::     ServalProlleProvalProThrGlnValGlnAsnTyrG		당 :
n:	CAGCAT 1181	TACDARTTTDARGORGEGGTACTTDGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	_	ξ (
		TTGTGGCTGT	1062	3 5
	414	SerSerProSerProSerSerPro		문 5
<u> </u>	409		398	2 8
	GGCCTT 1001	TACATCTACACCCTCAAGGGCATGTGCCCCTTAAACACACCCCAACAGGCCTT		5
	AAAAATC 948   :::  userH 398	CTGTGGACAGCCACCGAGGACCAGAAAATC	919 378	8 8
	AGATCC 918 ::   ysprop 378	GTGCTGCCCTGGGATGAAGGTGAGCTGCCAGCTCCAGGTCCAGAGATCC ::::::	870 358	8 8
	spPheV 358	ARCACAGAGAAGGGCCTCATGGAGGTGCAGAGGAT	338 5	B 5
Ω Π :	GTG 834    	TGGGATGGAAAAGAGGAGTCCAGGAACTACACGGTGGTG		요 장
	GTGTTT 795 OSerLe 318	TGCTGTGGGAAGCAGACACCCTTCTTCTCATCCCAGGGCCAGGAGTACACCGTGGTGTTT	736 298	B 5
	GAACTG 735 ::: OSerSe 298	CTGTCGGTGGTGÄGCCAGATGAAGGACCCGACTTTTGCCACCTTCATGTATGAACTG	679 286	8 8
	CTGGCC 678	TGCTGGGACACTAAGCCAAAAAGCGACCGCTGGCC	643 269	8 8
0 11 1	MetAsp 268	GTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAG		음 5
	GAGGAA 606 (Thrser 248	CTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGCAGCCGGAGGAA	547 229	용 원
	CACCAG 546 GlnAsp 228	ATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCTGCACTGGGCCACCACCAGCACCAGCAGCTGCTTGCTGTCAGGACAGCGCCCTGCACTGGGCCACCACCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG	493 209	유 원
	      208	:::::::                   ::::::	189	문

Dictyostelium discoideum (Slime mold). Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.		
kinase 2 (EC 2.7.1.112) (Fr		
<pre>16, Created) 16, Last sequence update) 41. Last annotation undat</pre>		
ANDARD;	i.	
12	SULI	
65 roProGlnGlyProArgThrArgMetPheSerAlaGlyProThrGlySer 781	Db 7	
ATTTTCTACCAGTCCTACGAGGA	Qy 21	
45 lyThrSerSerProSerProValValPheThrValGlySerProProSerGlySerThrP 765	Db 7	
ccercre	Оу 20	
25 etGluIleAlaProSerAlaGlyPheGlyGlySerLeuHisProGlyAlaArgAlaGlyG 745	Db 7	
TGCCGTGGTGGCA	0у 19	
05 laAlaPheGlyThrGlnAlaProAspProGlySerThrGluSerLeuGlnGluLysProM 725	Db 7	
GG	Оу 19	
85 roLysGlyProPheGlyArgSerPheSerThrSerArgLeuThrAspLeuLeuLeuLysA 705	Db 6	
74TCCTCGCCGTCAGAGACCTCATTTGGGTCCCCAGGCGCGGTGGAGATGTTATCGTCAT 1931	, Фу 18	
65 erGluValGlyProPheHisGlyGlnProLeuGlyProGlyLeuArgProGlyGluAspP 685	Db 6	
GGACGGGGAGACCTTCAGCCAGCACCTGCAGGC	Оу 18	
:     uLeuAlaArgGlnGlyV	Db 6	
CTGCCTCCGACAGGTCTGAGCATGACCTG	Qy 17	
27 laValProSerPheAspPheProLysThrProSerSerGlnAsnLeuLeuAlaL 645	Db 6	
rgtgcctttctccaccgactgcgaggactcagacatgctacat	Qy 17	
07 ysLeuProAspPheLeuGlnArgAsnProLeuProProIleLeuGlySerProThrLysA 627	9 dd	
	Qy 17	
	Db 5	
- a	. Qy 17	
oProThr <i>t</i>	Db 5	
ATGTCCTCCTACTCCTCATCCCCACCCCGCCAGGCTGCCAGGTCCCCCTCA	Qy 16	
52 ysArgLeuHisSerAlaProAsnLeuSer	Db 5	
TGGGCACGCAGATC	Фу 15	
37 lySerSerAlaProGluHisSerProArgThrSerGlyLeuGlyC 552	Db 5	
CGCCAACCCAAAGGTGCCTGAGGGGGACTCCATCGCGGAC	Фу 15	
      InGlyAlaGluMetArgGlyGly	Db 5	
CCAGCCCCTCAGGGACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCG	0у : 14	
rProGlnValGlyThrIleProGluArgProGlyTrpSe	Db 5	
CCTTGGTGATGTACCACTCCACCACCTACCAGCTGTGTGCCCGGTACTTCTGCGGGG	Qy 14	
89ValLeuAlaArgLysMetSerLeuGlyGlyGlyArgProTyrThrProS 505	Db 4	

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SEQUENCE FROM N.A.
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MEDLINE-98360094; PubMed-9693035;
MEDLINE-98360094; PubMed-9693035;
Murayanagi H., Yan J., Seki N., Yamanouchi Y., Suzuki
Takano T., Murayanatsu M., A., Shirasawa T.;
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Genomics 51:76-85(1998).
-!- TISSUE SPECIFICITY: UBIQUITOUSLY E
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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075385;
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15-JUL-1999 (Rel. 38, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Serine/threonine-protein kinase ULK1 (EC 2.7.1.-)
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

PROSITE; PS500111; PROTEIN_KINASE_DOM; 1.

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DOMAIN 16 278 PROTEIN KINASE.

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SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
APG1/UNC-51/ULK1 SUBFAMILY.
GCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTAGATATGTTCTCCTATGGA
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	Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J., Glbson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C., Tufffeell B. C., Satchwell S.C., Seguin C.,	
	ence and expression of the B95-8 Epstein-Barr v D:207-211(1984)	
วัชช	S SWISS-PROT entry is copyright. It is produced through a coween the Swiss Institute of Bioinformatics and the EMBL o	
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β δ	2092CGGCCAGGCACCACTCTGTGTTTTCATTTTCAAAGGTGCACAACAGTGTCCTTTG 2036                  79 GlyArgProGlyThr	
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roGly 443		В
GCAGC 893	CGTGGCTGTCCACAGGGATCTCTGGACCTGG	Qy
  Arg 42	:::      TrpArgArgArgSerGlyAlaGlnArgGlyH1sProProProGlyAlaG	pb !
AGA 94	06 TATCCAAGGCCTGTTGGGGTGTGTTTAAGGG	Q V
4.		당 :
AGCTGGAG 1007	CTTTTTAATAACAGGCACGGCCAAGAAGCAGGTGACGAC	γQ
roArg 398	379 ProThrargSerGlyAlaAlaAlaGlnArgThrHisArgArgProProGlyCysPr	В
CTAAGA 1067	.GGCCCG	Ωy
roPro 378	359 GlnGluProArgLeuProGlnAspLeuAlaAlaAlaGlnArgCysProAlaGlyProPro	Дb
GCCCC 1115	1138 AGCAGCTGTCCTTTGGGGT	Qγ
Arg 358	352 AlaargLeuProFlu352 AlaargLeuProFlu	명
GTAGG 1139	TCTT	Qy
		뫄
СТССС 1199	ATGGCCTTCACTGGGTAGGGGTI	Qγ
erGly 334		В
AGAGC 1244	NGTCGATGACAAGGAGGCCCGGCCCATT	γ
lyAla 316	297 ProGlyAlaGlyGlnArgProSerGlyProThrGlyGlyArgProAlaAlaProG	B
	GCTCCAGCCGCCTGC	Qy
roPro 296		밁
1337	GCACACGACTGACGTAACCATGGAG	Qy
roGly 279	264ThrHisArgArgProProGlyCysProArgSerAlaArgAsnP	В
1364	TCTGCCCTCA	δδ
263	256 ArgSerGlyAlaAlaAlaGlnArg	밁
TTGGCCT 1409	GAAGTACCGGGCACACAGCTGGTAGGTGGTGGAGTGGTACATCACCAAGGAG	Qγ
hr 25	37 ArgLeuProGlnAspLeuAlaAlaAlaGlnArgCysPro	밁
CCCGC 1469	CGCACGGGAAACATGTCCCTGAGGGGGCTG	٥ ٧
  uPro 236		밁
- വ	CACGTCCGCGATGC	Qy
rgGly 217	::: 	당.
GATGC 1589	36 CCTGGTGGATCAGGATCTGCGTGCCCAGCT	Q
laAla 197	  178 ProSerGlyProThrGlyGlyArgProAlaAlaProGlyAlaProGlyThrProAl	밁
GATT 1	84GTGGGGATGAGGAGTAGGAGGACATGGAGCAGTAG	Qy
lnArg 177	- ARCLISCISSISSISSISSISSISSISSISSISSISSISSISSI	B 4
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CTGTGCCTCCCTGGAGATCTGCAGGCGGCTGGAGCCCTACATGGCCCCCCCC	GlyCysProArgSerAlaArgAsnProG 404	GGTGGYCAACAGCGGCTCFGAGGTCTGGTACAGCAATGGGCCGGGCC	T-MUILCHOWARICHCHARACHCHARACHCCCTACCCAGTGAAGGCCCATGGA 1229		CCCAAAGGACAGCTGCTCCTACCTGTGCTCACACAGAGCAGCGCAACAGGTCCA	roGluArgGlnGlubroArgLeup 364	CCTGGTCTTAGCGGGCCTCGCCGATGGGCTTGTGGCTGTTTTCCCGTGGTGCGGGGCAC 1121		GGATACTCCAGCTGTCGTCACCTGCTTCTTGGCCGTGCCTGTTATTAAAAAGAATTCCTA 1061	roGlyProGlyGlyGlyAlaAlaValProSerGlyAlaThrProHisProGluArgGly- 342	TAAACACCCCAACAGGCCTT 1001	-	CCAGAGATCCCTGTGGACAGCCACCGAGGACCAGAAAATCTACATCTACACCCTCAAGG- 967	rgSerGlyAlaGlnArgGlyHisProProProGlyAlaGlyGlnArgP 303	CCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAGCTGCCAGCTCCAGGT 908			:	GTACACCGT	N1	GAAGGACCCGACTTTTGCCACCTTCATGTATGAACTGTGCTGTGGGAAGCAGACAGCCTT 758	GluargGly-SerGlyProAlaAspProProAlaAlaAlaArgLeuProProGluar		CCGCCCGGTTCTGGGCCAGCCGGGAGAGTGCAGTCCGGCGATGATGATGATGATGATGATGATGATGATGAGAGTGCAGAGAGAG	sersiyerominsiysiyangeroanaanaproGlyanaproGnyTnr 194	TGCCAAGAAGCTGTCCAAGGGCAT	178	ATATGATGAGAAGGTAGATATGTTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCAGG 518	HisProProGlyAlaGlyGlnArgPro 178	CGCCCTAGGCGTGGAGGGCACTCCTGGCTACCAGGCCCCCAGAGATCAGGCCTCGCATTGT 458	GGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCAGTCATTCCATGAGGG 398        ::: GlyAlaGlnArgGly 168	ArgArgArgSer 163
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	FROM N.A. 14270667: PubMed=6087149:		R R R V V
	esvirinae; Lymphocryptovirus.	_ ^	S S S
	dsDNA viruses, no RNA stage		8 8 5
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	rHlsArgArgProProGlyCysProArgSerAlaArgAsnProGlyC	639	DЬ
	GATGCTGCCGTGGTGGC	2001	Qy
638	ProAlaGlyProProProThrArgSerGlyAlaAlaAlaGlnArg	624	Db
2000	GGGCCGAGTCATTGCCGTCTTAAA	1941	Qy
623	uProGlnAspLeuAla	611	DЬ
1940	CCTCATTTGGGTC	1890	Qy
610	oProAlaAlaAlaArgLeuProPı	591	Дb
1889	CATGGACGGGGAGACCTTCAGCCAGCACCTGCAGGCCGTGAAGATCCTCGCCGTCA	1830	Qy
590	ProSerGlyAlaThrPro-HisProGlu	582	Db
1829	CTCAGACATGCTACATACGCCCGGTGCTGCC	1770	Qγ
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1769	TCCCCAGCAAGTTCT	1710	Qy
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1709	ATGTCCTCCTACT:CCTCATCCCCACCCCGCCAGGCTGCCAGGTCCCC	1658	Оу
51	:::	53	dg d
σ	TGGGCACGCAGATCCTGATCCACCAGGAATCACTCACTGACTACTGCT	1602	δ
531	laGlnArgThrHisArgArgProProGlyCysProArgSerAlaArgAsnProGlyCysP	511	Db
1601	GTACAG	1596	Qy
511	spLeuAlaAlaGlnArgCysProAlaGlyProProProThrArgSerGlyAlaAlaA	491	Db
1595	AGGTGCCTGAGGGGGACTCCATCGCGGACGTGAGCATC	1541	Qy
491	ē	471	Db
1540	TGCGGCCCTTGGACACGGAACCCCCGGCAGCCAGCC	1505	Qy
471	lyGlyGlyAlaAlaValProSerGlyAlaThrProHisProGluArgGlySerGlyProA	451	Db
1504	GTCCCCAGCCCCCTCAGGG	1467	Qy
451	oAla····AlaproGlyAlaproGlyThrproAlaAlaproGl	434	뫄
1466	GGCCAACTCCTTGGTGATGTACCACTCCACCACCTACCAGCTGTGTGCCCGGTAC	1407	Qγ
434		423	Дb
4	cgtcagtcgtgtgcagctctgagggcagaggaggaggaggaggtcgtcgtgctgcct	1347	Qy
422	lyCysProArgThrTrpArgArgArgSerGlyAlaGlnArgGlyH1sProProPro	404	Db

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1977 CGTCTTAAAAGCCCCGAGAGC 1996	1917 AGATGTTATCGTCATTGGCCTGGAGAAGGATTCTGAAGCCCAGCGGGGCCGAGTCATTGC 1976    :::       :::    982 roSerThrLeu	1857 CCTGCAGGCCGTGAAGATCCTCGCGGTCAGAGAGACCTCATTTGGGTCCCCAGGCGGGTGG 1916 ::	1797 TGCCTCCGACAGGTCTGAGCATGACCCCCATGGACGGGGAGACCTTCAGCCAGC	1755 CACCGACTGCGAGGACT	1695 TGCCAGGTCCCCCTCAAGCCTCCCCAGCTCCCAGCAAGTTCTTCCAGTGTGCCTTTCTC 1754	1646CTGACTACTGCTCCATGTCCTCCTACTCCTCATCCCCACCCCGCCAGGC 1694                        891 ysLeuSerArgLeuLysProAlaProProProProProAlaAlaSerAlaGlyLysA 910	1614 CACGCAGATCCTGATCCACCAGGAATCACTCA	1554 AAAGGTGCCTGAGGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGG 1613	1528CCGGCAGCCAGCCACACGGCCAGCC 1553	1479 CAGCCCCTCAGGGACATGTTTCCCGTGCGCCCTTGGACACGGAACCC 1527	1445ACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCCC 1478	1417 TCCTTGGTGATGTACCACTCCACCACCT	1357 GTGTGCAGCTCTGAGGGCAAAGGGGAAGGAGGTCGTCTGGTGCCTGGATGACAAGGCCAAC 1416	1313	1298 CCTGGAGATCTGCA	1271 1297	1228 GAGGTGGTCAACAGCGGCTCTGAGGGTCTGGTACAGCAATGGGC 1270	1177 AGCATCGCGGATGAAGACGCACGGC
Qy 279 AAACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTTGACGTCAA 338	Qy 222 GCTCACCCAAAAAATAGCCTACCAGATCGCCTCGGGCCTGGCCT	Qy 186 CGCCAGAGATTCTTC	Qy 126 GCTCTGCTTCGCCCTGGAGCTCGGGCCGCTCAGCAGCACCCTGACCACCGTGCTGTCCGAGAA 185	Qy 72GCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCC 125 :::	Qy 51 CCGGCAGGAGGCAGCATGCT71	1 Gaps: -836-392-8_COPY_22_2205 (1-2184) x YHL1_EBV (1-66	Fred. NO.: 4.03e-07 Letig(II: 2000 Score: 268.00. Matches: 184 Percent Similarity: 29.78% Conservative: 42  Best Local Similarity: 24.24% Mismatches: 272  Query Match: 6.60% Indels: 261	SEQUENCE 660 AA; 66244 MW; 86DAID67A37152A2 C	149 273 1. 274 398 2. 399 523 3. 524 648 4.	EMBL; V01555; -; NC PIR; A03742; QQBE3; Hypothetical proteil DOMAIN 149	modified and this statement is not removed. Usage by and for commerc entitles requires a license agreement (See http://www.isb-sib.ch/announ or send an email to license@isb-sib.ch).	This SWISS-PROT entry is copyright. It is produced thro between the Swiss Institute of Bioinformatics and the the European Bioinformatics Institute. There are no use by non-profit institutions as long as its conte	RA GIBSON 1.0., DECEMBER 3.0., DECEMBER 3.0., DESCRIPTION, RA TUffnell P.S., Barrell B.G., RT "DNA sequence and expression of the B95-8 Epstein Barr virus genome."; RI Nature 310:207-211(1984).	SEQUENCE MEDLINE-8 Baer R.,	Viruses; dsDNA viruses, no Gammaherpesvirinae; Lymphoc NCBI_TaxID=10377;	21-JUL-1986 (Rel. 01, Last sequence up 15-JUL-1998 (Rel. 36, Last annotation Hypothetical BHLF1 protein. Epstein.barr virus (strain B95-8) (Hur	STA	Db 993 laGlyAspGlnProSerSer 999  RESULT 9

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SMART; SM00216; SH3; 1.
SMART; SM00219; TYTKC; 1.
SMART; SM00219; TYTKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00111; PROTEIN_KINASE_DOM;
PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3D-structure;
DOMAIN
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    335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hosphorylation;
                   196 TCTTCCTTTATACCCCTGGGACACATGCTCACCCAAAAAATAGCCTACCAGATCGCCTCG 255
                                                                                            315
                                                                                                                                                                                  295
                                                                                                                                                                                                                                                                   276 AspThrMetGlu---ValGluGluPheLeuLysGluAlaAlaValMetLysGluIleLys 294
                                                                                                                                                                                                                                                                                                                25 GATGCCATGAAGAACTTCTCCGAGTTCCGGCAGGAGGCCAGCATGCTGCACGCGCTGCAG
                                                                                                                                                                                                                             85 CACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCAC-----CCGCTCTGCTTCGCC
                                                                                                                                  CTGGAGCTCGCCGCTCAGCAGCCTCAACACCGTGCTGTCCGAG---AACGCCAGAGAT 195
                                                                                                                                                                             |||||| :::||| |||:::|||:::
| HisProAsnLeuValGlnLeuLeuGlyValCysThrArgGluProProPheTyrIleIle
ValAsnAlaValValLeuLeuTyrMetAlaThr-------GlnIleSerSer
                                                                                     ThrGluPheMetThrTyrGlyAsnLeuLeuAspTyrLeuArgGluCysAsnArgGlnGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on; SH2 domain; SH3 dor
Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                               4.27e-07
269.00
36.05%
24.44%
6.63%
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L -> K (IN REF. 2).
E -> K (IN REF. 2).
S -> T (IN REF. 2).
A -> V (IN REF. 2).
E -> G (IN REF. 3).
E -> G (IN REF. 2).
C -> W (IN REF. 2).
G -> K (IN REF. 2).
R -> K (IN REF. 2).
R -> K (IN REF. 2).
SPS -> APG (IN REF. 2).
G -> A (IN REF. 2).
G -> LS (IN REF. 2).
N -> G (IN REF. 2).
G -> HP (IN REF. 2).
G -> LS (IN REF. 2).
N -> G (IN REF. 2).
R -> G (IN REF. 2).
R -> G (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
MLEICLKLYGCKSKKGLSSSSSCYLE -> MGQQPGKVLGD
QRRPSLPALHFIKGAGKKESSRHGGPHCNVFVEH (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE.
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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domain; Chromosomal
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Matches:
Conservative:
Mismatches:
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TTC 1176 : :nGl 671	1129 GACAGCTGCTCCTACCTGTGCTCACACACACACGCCAACAGGT	Db Qy
65	638 GlyArgAspIleSerAsnGlyAlaLeuAlaPheThrPro	Дb
AG 1128	G	Qy
lu 637	ProGluArgArgGlyAlaGlyGluGluG	Дb
1077	AGAATTCCTACCTGGTCTTAGCGGGC	Qy
rg 617	598 AsnLeuPheSerAlaLeuIleLysLysLysLysLysThrAlaProThrProProLysAry	Дb
AA 1050	CTTGGCCGTGCC	Qy
hr 597	GluArg	ДЪ
TC 1020	GCCCCTTAAACACACCCCAACAGGCCTTGGATACTCCAGCTGTCG	γQ
-P 580	567 laValSerProLeuLeuProArgLysGluArgGlyPro	₽.
CC 960	AGCCACCGAGGACCAGAAAATCTAC	Qy
OA 567	isSerLysGlyG	皮
AG 900	TCATGGAGGTGCAG	Qy
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C3	AACACAGAG	Qy
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824	GAGTACACCGTGGTGTTTTGGGATGGAAAAGAGGAGTCCAGGAACTA	Qy
1уь 512	493 PheGluThrMetPheGlnGlu-SerSerIleSerAspGluValGluLysGlu-LeuGl)	망
AG 771	TTGCCACCTTCATGTATGAACTGTGCTGTGGGAAGCAGACAGCCTTCTTCTCAT	Qy
Ala 492	478 TrpAsnProSerAspArgProSerPheAlaGluIleHisGlnAl	Db
CT 711	GAAGCGACCGCTGGCCCTG	ν
ln 477 .	sProGluLysValTyrGluLeuMetArgAlaCysTrpG	Db.
AC 651	CCGGAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGG	Qγ
et 458	441 ProGlyIleAspLeuSerGlnValTyrGluLeuLeuGluLysAspTyrArgMe	ФФ
TG 591	GATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCGGTT	Qy
Yr 440	421 AspValTrpAlapheGlyValLeuLeuTrpGluILeAlaThrTyrGlyMetSerProTyr	ф
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TA 474	CCAGAGATCAGGCCTCGCATTGTATATGATG	Qy
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ω	316 CTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGAI	Qy
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TT 315	256 GGCCTGGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGACAACAT	Qy

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MEDLINE-90082420;
         "The solution structure
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[5]
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Nature 304:167-169(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Bequence and analysis of the human ABL gene, the BCR gene, and "Sequence and analysis of the human ABL gene, the BCR gene, and regions involved in the Philadelphia chromosomal translocation."; Genomics 27:67-82(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chissoe S.L., Bodenteich A., Wang Y.-F., Wang Y. Cliffon S.W., Crabtree J., Freeman A., Iyer K., McLaury H.-J., Pan H.-Q., Sarhan O.H., Toth S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Lung carcinoma; MEDLINE-95394474; PubMed-7665185;
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Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                            Fainstein E., Marcelle C., Rosner A., Canaani E., G
Dreazen O., Smith S.D., Croce C.M.;
"A new fused transcript in Philadelphia chromosome
lymphocytic leukaemia.";
Nature 330:386-388(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Alternative splicing of from the bcr-abl fused Cell 47:277-284(1986).
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                                 STRUCTURE BY NMR OF SH3
                                                                               heteronuclear
                                                                                                                MEDLINE-93101588;
                                                                                                                                                                      "Three-dimensional solution
                                                                                                                                                                                             STRUCTURE BY NMR OF MEDLINE-92370689; Pu
                                                                                                                                                                                                                              "Inokuchi K., Futaki M., Dan K., Nomura T.;
"Sequence analysis of the mutation at codon
variation of codon 837 of c-abl gene.";
Leukemia 8:343-344(1994).
                                                                yerduin M., Mayer B.J., Rios C.B., Baltimore D., Cowburn "secondary structure of Src homology 2 domain of c-abl by neteronuclear NMR spectroscopy in solution."; 270c. Natl. Acad. Sci. U.S.A. 89:11673-11677(1992).
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92370689; PubMed-1505033;
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219; PubMed=3021337;
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Marcelle C., Rosner
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Gokkel E.
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PITR; A25582; TVHUA
PITR; A25582; TVHUA
PDB; 1AB2; 31-JAN-94
PDB; 1ABL; 01 NOV-94
PDB; 1ABL; 04-SEP-97
DB; 1AMO; 28-JAN-98
B; 1AWO; 28-JAN-98
Yew; HGNC: 76; AFF**
                                             Pfam; PF00017; SH2; 1.
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PRINTS; PR00401; SH2DOMAT
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Pisabarro M.T., Serrano L., Wilmanns
Pisabarro M.T., Serrano L., Wilmanns
Pisabarro M.T., Serrano L., Wilmanns
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MEDLINE-95199229; PubMed-7892170;
Pisabarra M.T., Ortiz A.R., Serrano L., W
"Homology modeling of the Abl-SH3 domain.
Proteins 20:203-215(1994).
PRINTS;
ProDom;
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J. Mol. Biol.
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Nam H.-J., Haser W.G., Roberts T.
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SIMILARITY: CONTAINS 1 SH2 |
SIMILARITY: CONTAINS 1 SH3 |
DATABASE: NAME—Atlas Genet.
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DISEASE: PARTICIPATES IN A T(9;22)(Q34;011) CHR
TRANSLOCATION THAT PRODUCES A BCR-ABL ONCOGENE
CHRONIC MYELOID LEUKEMIA (CML), ACUTE MYELOID I.
ACUTE LYMPHOBLASTIC LEUKEMIA (ALL).
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CATALYTIC ACTIVITY: ATP + a
tyrosine phosphate.
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SIMILARITY: CONTAINS 1 SH3 DOMAIN.
DATABASE: NAME=Atlas Genet. Cytogenet. Oncol: Haematol.;
WWW="http://www.infobiogen.fr/services/chromcancer/Genes/ABL.html".
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              PR00401; SH2DOMAIN.
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PD000001; Euk_pkinase;
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	HIT 8  _HUMAN STANDARD; PRT; 1130 AA.  P00519; Q16133; Q18869; Q13870; 21-JUL-1986 (Rel. 01, Created) 01-APR-1990 (Rel. 14, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Proto-oncogene tyrosine-protein kinase ABL1 (EC 2.7.1.112) (p150) (d-ABL).	RESULT ABL1_HI	
	1870 AAGATCCTCGCCGT 1883 ::	Ωb	
1869 133	1852 CAGCACCTGCAGGCCGTG 1	Qy	
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1551 539	492 GACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCACGCCACACGGCCAAC	Дb	
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Viruses; Retroid viruses; Ret:
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EMBL; K00010; AAA46470.1; -.
PIR; A00627; TYMVGM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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Nature 304:167-169(1983).
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21-JUL-1986 (Rel.
15-JUN-2002 (Rel.
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PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00109; TYRKINASE.
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the European Bioinformatics Institute
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P., Smith M.J.,
tl. Acad. Sci. U
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01-FEB-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M3K9_HUMAN
P80192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mitogen-activated protein kinase kinase kinase
lineage kinase 1) (Fragment).
MAP3K9 OR MLK1 OR PRKE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _HUMAN
                                                                                                NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                InterPro; iPR000719; Euk_pkinase.
InterPro; iPR002299; Ser_thr_pkinase.
InterPro; iPR001245; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
SMART; SM00219; TyrKC; 1.
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                                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dorow D.S., Devereux L., Dietzsch E., de Kretser T.;
"Identification of a new family of human epithelial protein kinas
containing two leucine/isoleucine-zipper domains.";
Eur. J. Blochem. 213:701-710(1993).

-i- TISSUE SPECIFICITY: EXPRESSED IN EDITHELIAL TUMOR CELL LINES
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                        DOMAIN
DOMAIN
                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew;
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PIR; $32467; $32467.
PIR; JU0229; U00229.
HSSP: P12931; 1FMK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Colon epithelium;
MEDLINE-93238756; PubMed-8477742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1735 TCTTCCAGTGTGCCTTTCTCCACCGACTGCGAGGAC-----TCAGACATGCTACATACG
                                                                                                                                                                                                                 ATP-binding.
                                                                                                                                                                                                                                       Transferase;
                                                                                                                                                                                                                                                             PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00108; PROTEIN_KINASE_ST; PROSITE; PS50011; PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MIM; 600136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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       44975
    MW;
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
LEUCINE-ZIPPER 1 (BY SIMILARITY).
LEUCINE-ZIPPER 2 (BY SIMILARITY).
ARG/LYS-RICH (BASIC).
AN; DBEINR7D31047FD8 CRC64;
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kinase;
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Alignment Scores:
Pred. No.:
                      Query Match:
DB:
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Best Local Similarity:
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PROSITE; PS00109;
PROSITE; PS50011;
PROSITE; PS50001;
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SEQUENCE
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BINDING
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1123
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; AAA37136.1;
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CAA30411.
CAA30412.
CAA30413.
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PROTEIN_KINASE_DOM;
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22.96%
6.90%
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SH2.
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                                                                                                                                                                                                                                                        HLKLLVLDV (IN ISOFORM II).
MLEICLKLVGCKSKKGLSSSSSCYLE ->
                                                                                                                                                                                                                                                                                           PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
MLEICLKLYGCKSKKGLSSSSSCYLE -> MSQRWTYTKCR
VQRDPALPFM (IN ISOFORM III).
MLEICLKLYGCKSKKGLSSSSSCYLE -> MISFDLLSDEL
                                                                                                                                                                                                                                                                                                                                                                                               ATP
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NUCLEAR LOCALIZATION
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                                                                                                                                                                           -> VGDW (IN REF. 2).
284F0830644AFD8F CRC64;
                                                                           Length:
Matches:
Conservative:
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indels:
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in; Alternative s
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rAsnLeuPheSerAlaLeuIleLysLysLysLysLysMetAlaProThrProProLysAr
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                                      ACCGTGGTGTTTTGGGATGGAAAAGAGGAGTCCAGGAACTACACGGTGGTGAACACAGAG
                                                                           gGlyProProAspGlySerLeuAsnGluAspGluArgLeuLeuProArgAspArgLysTh
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	4 AAAGCCCGAG 1993        4 yThrProGlu 807	1984 804	Db Qy
1983 804	ATCGTCATTGGCCTGGAGAAGGATTCTGAAGCCCAGCGGGGCCGAGTCATTGCCGTCTTA ::: ::	1924 794	D Q
1923 793	GCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCCAGGCGCGGTGGAGATGTT 	1864 778	d Qy
1863 777	GACAGGTCTGAGCATGACCTGACCCCCATGGACGGGGAGACCTTCAGCCAGC	1804 771	g S
1803 770	GTGCCTTTCTCCACCGACTGCGAGGACTCAGACATGCTACATACGCCCGGTGCTGCCTCC 	1744 763	g 9
1743 762	<pre>t cccccccagccagccacgccccccacaccccccccccc</pre>	1684 743	gg dy
1683 742	CTGATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCTACTCCTCATCCCCA	1624 727	д 9
1623 726	GAGGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCAGATC 	1564 709	B 8
1563 708	o — o	1504 701	g Q
1503 701	TGCG	1468 686	å S
1467 686	- AGGCCAACTCCTTGGTGATGTACCACTCCACCACCTACCAGCTGTGTGCCCGGTACTTC	1409	В <sub>б</sub>
1408 666	GTCGTGTGCAGCTCTGAGGGCAGAGGGGAGGAGGTCGTCTGGTGCCTGGATGACA	1354	å Vo
1353 646	GTTACGTGTTACGTGTTACGTGTTACGTGTTACGT	1345 626	B 8
1344 626	CGGCTGGAGCCCT                 yLeuGlySerProGlyGlyLeuGlyValGlyP	1315	р 8
1314 606	TGGTACAGCAATGGGCCGG    ::: sGlySerCysGlyAspLeu	· 1255 586	B 5
125 <b>4</b> 586	GCACGGCAGAACCCCTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTC	1195 575	g Q
1194 574	TGCTCCTACCTGTGCTCACACACACACCCAAGAGTCCAAGTTCAGCATCGCGGATGAAGAC	1135 561	g å
1134 560	GCCTCGCCGATGGGCTTGTGGCTGTGTTTCCCGTGGTGCGGGGCACCCCAAAGGACAGC	1075 554	д Q

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RESULT
ABL1_MC
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P00520; Q61252; Q61253; Q61255; Q61255; Q61257; Q61258; Q61259; Q61250; Q61261; P97896;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1980 (Rel. 13, Last sequence update)
15-JUN-2002 (Rel. 41, Last sanotation update)
Proto-oncogene tyrosine-protein kinase ABL1 (EC 2.7.1.112) (p15)
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Mus.musculus (Mouse),

Mus.musculus (Mouse),

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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               use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (see http://www.isb-or send an email to license@isb-sib.ch).
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"High-resolution crystal structures of tyrosine kinase SH3 domains complexed with proline-rich peptides.";
Nat. Struct. Biol. 1:546-551(1994).
-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bernards A., Paskind M., Baltimore D.;
"Four murine c-abl mRNAs arise by usage of two transcriptional promoters and alternative splicing.";
Oncogene 2:297-304(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 85-182 FROM N.A. MEDLLNE-84106840; PubMed-6319018; Wang J.Y. Ledley F. Goff S., L "The mouse c-abl locus: molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chissoe S.L., Bodenteich A., Wang Y.-F., Wang Y.-P., Burian D., Clifton S.W., Crabtree J., Freeman A., Iyer K., Jian L., Ma Y., McLaury H.-J., Pan H.-Q., Sarhan O.H., Toth S., Wang Z., Zhang (Helsterkamp N., Groffen J., Roe B.A.; "Sequence and analysis of the human ABL gene, the BCR gene, and "segions involved in the Philadelphia chromosomal translocation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-187 FROM N.A. (ISOF MEDLINE=95394474; PubMed=7665185;
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MEDLINE=88068561; PubMed=3317402;
                                                                                        the European Bioinformatics Institute.
                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF MEDLINE*95393198; PubMed=7664083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE SPLICING.
MEDLINE-88202920; Pub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 36:349-356(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 27:67-82(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oppi C., Shore S.K., Reddy E.P.;
"Nucleotide sequence of testis-derived c-abl cDNAs: implications for testis-specific transcription and abl oncogene activation.";
Proc. Natl. Acad. Sci. U.S.A. 84:8200-8204(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: 4 ISOFORMS; I (SHOWN HERE), II, III AND IV; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: WIDELY EXPRESSED.
SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. ABL
                                                                                                                                                                  SIMILARITY: CONTAINS 1 SH2 DOMAIN. SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                       tyrosine phosphate.
SUBCELLULAR LOCATION: CYTOPLASMIC; THE MYRISTOYLATED C-ABL PROTEIN
                                                                                                                                                                                                                                                                                                    WAS REPORTED TO BE NUCLEAR
                                                                                                                                                                                                       SUBFAMILY
                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed-3283651;
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                                   (See http://www.isb-sib
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g and characterization.
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MetGluPheCysAlaGlnGlyGlnLeuTyrGluValLeuArgAlaGlyArg-----

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InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        within the nervous system, predominantly expressed in neurons enriched in synaptic terminals.

-i- PTM: Autophosphorylated on ser/Thr. Phosphorylated in cytosol under basal conditions and dephosphorylated when membrane.
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-!- SUBCELLULAR LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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InterPro; IPR000719;
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CTGGAGCTCGCGCCCCCAGCAGCCCTCAACACCCGTGCTGTCCGAGAACGCCAGAGATTCT 198
                                           HisProAsnIleIleThrPheLysGlyValCysThrGlnAlaProCysTyrCysIleLeu
                                                                                      CACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCCGCTCTGCTTCGCC-----
                                                                                                                                 AlaValLysLysValArgAspLeuLysGluThrAspIleLysHisLeuArgLysLeuLys
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K->A: NO CATALYTIC ACTIVITY.

E->A: NO CHANGE.

V -> A (IN REF. 2).

KI. -> NV (IN REF. 2).
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٠	TGCCAGCTCC	895	Qy	
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GTGAGC 894		844	Qy	
uLysGlu 487	ArgAlaAsnAsnLeuTyrMetGluLeuAsnAlaLeuMetLeuGlnLeuGluLe	468	Db	
GAG 843	1	823	Qy	
LeuGlu 467	ArgArgGluGluLeuArgHisAlaLeuAspIleArgGluHisTyrGluArgLys	448	DЬ	
822	1	805	Qγ	
MetArg 447	GluLysIleLysSerGluGlyThrCysLeuHisArgLeuGluGluGluLeuVal	428	В	
804	ACCGTGGTGTTTTGGGATGGA	784	Qy	
uHisPhe 427	ProGlnGluThrTyrPheLysSerGlnAlaGluTrpArgGluGluValLysLe	408	밁	
GAGTAC 783	AAGCAGACAGCCTTCTTCTCATCCCAGGGCCAG	745	Qy	
SerThr 407	IleAlaSerAlaAsp	399	Ъ	
TGTGGG 744	GTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACCTTCATGTATGAAC	685	Qy	
LeuAsp. 398	CysTrpAsnSerLysProArgAsnArgProSerPheArgGlnIleLeuLeuHis	379	Dр	
CTGTCG 684	TGCTGGGACACTAAGCCAGAGAAGCGACCG	643	Qy	
g.,	ProValProSerSerCysProAsp	363	Db	
ရ	CCGGTTCTGGGGCAGCCGGAGGAAGTGCAGTTCCG	583	0	
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ATCCGC 582	GCACTGGGCCACCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGG	529	Qy	
rAlaile 351	<pre>                                     </pre>	332	Дb	
528	GTGCTCTACGAGTTGCTGTCAGGACAGCGCCCT	496	Qy	
GlyVal 331	:::   ProGluValIleArgAsnGluProValSerGluLysValAspIleTrpSerPheGl	312	Дb	
GGAATG 495	CCAGAGATCAGGCCTCGCATTGTATATG	436	Qy	
pmetala 311	LysGluLeuSerAspLysSerThrLysMetSerPheAlaGlyThrValAlaTr	292	В	
CAGGCC 435	AGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACTCCTGG	379	Qy	
Thrser 291	<pre>::: IleThrTyrAspAspVal</pre>	277	망	
ATTTCG 378	GTGTGGTCCCTTGACGTCAAGGAGCAC	319	Qy	
MetLeu 276	MetAsnTyrLeuHisLeuHisLysIleIleHisArgAspLeuLysSerProAsnMetLeu	257	문	
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                                                                    Mata M., Merritt S.E., Fan G., Yu G.G., Holzman L.B.;
"Characterization of dual leucine zipper-bearing kinase, a mixed lineage kinase present in synaptic terminals whose phosphorylation state is regulated by membrane depolarization via calcineurin.";
J. Biol. Chem. 271:16888-16896(1996)
                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ICR X Swiss Webster; TISSUE-Brain;
MEDLINE-96365388; PubMed-8769565;
Blouin R., Beaudoin J., Bergeron P., Nadeau A., Grondin G.;
"Cell-specific expression of the ZPK gene in adult mouse tissues.";
DNA Cell Biol. 15:631-642(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           060700; p70286;
16-007-2001 (Rel. 40, Created)
16-007-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Mitogen-activated protein kinase kinase kinase 12 (EC 2.7.1.37)
(Leucine-zipper protein kinase) (ZPK) (Dual leucine zipper bearing
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                                                                                                                                                                                                                                                                                                                                          STRAIN-CD-1: TISSUE-Brain;
MEDLINE-95074107; PubMed-7983011;
HOLEMAN L. B., Werritt S.E., Fan G.;
"Identification, molecular cloning, and characterization of dual leucine zipper bearing kinase. A novel serine/threonine protein kinase that defines a second subfamily of mixed lineage kinases.";
J. Biol. Chem. 269:30808-30817(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE-96279269; PubMed-8663324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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                             Biol. Chem. 271:16888-16896(1996).
FUNCTION: May be an activator of the JNK/SAPK pathway.
Phosphorylates beta-casein, histone 1 and myelin basic
CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
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                                                                                                                                                                                                                                                                                        muse by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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Oncogene 12:641-650(1996).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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(MAPK-upstream kinase) (MUK).
MAP3K12 OR MUK.
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PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.
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Transferase; Serine/threonine-protein kinase; ATP-binding;
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SMART; SM00221; STYKC; 1.
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HSSP; P12931;
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6-OCT-2001 (Rel.
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SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES MAP KINASE KINASE SUBFAMILY.
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, V		TAC 783	745 AAGCAGACAGCCTTCTTCTCATCCCAGGGCCAG	Qy
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Qy		TCG 684	643 TGCTGGGACACTAAGCCAGAGAAGCGACCGCTGGCCCTGTCG	γQ
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gg ,			259 CTGGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTG ::::	를 <sup>5</sup>
0		Gly 223	7	Ъ
J 5		iGGC 258	199 TCCTTTATACCCCTGGGACACATGCTCACCCAAAAAATAGCCTACCAGATCGCCTCGGG	· Q
? {		206	190 MetGluPheCysAlaGlnGlyGlnLeuTyrGluValLeuArgAlaGlyArg	DЪ
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? <b>5</b>		Leu 189	170 HisProAsnIleIleThrPheLysGlyValCysThrGlnAlaProCysTyrCysIleLeu	DЪ
i S		138	85 CACCCCTGCATCGCGCGCTCATCGGCATCAGCATCCACCCGCTCTGCTTCGCC	QY.
P B	,		ב	В
Qy		CAG 84	28 GCCATGAAGAACTTCTCCGAGTTCCGGCAGGAGGCCCAGCATGCTGCACGCGCTGCAG	Qy
Db			9-836-392-8_COPY_22_2205 (1-2184)	0S-09
Qy			Best Local Similarity: 22.40% Mismatches: 257 Query Match: 7.28% Indels: 236 DB: Gaps: 31	Best Query DB:
D Qy			ment Scores:  1.78e-08  No.:  295.50  Matches:  1.78e-08  Conservative:	Alignm Pred. Score: Percen
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Mitogen-activated protein kinase kinase kinase
DOMAIN
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                                                                                                                                                                                                                                                                                                    InterPro; IPR000719; Euk_pkinase.
InterPro; IPR004040; STY_pkinase.
InterPro; IPR002290; Ser_thr_pkina
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U07358; AAA67343.1; HSSP; P12931; 1FMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was a second of the state of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of the second of th
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Biochem. Biophys. Res. Commun. 202:613-620(1994).
-i- FUNCTION: May be an activator of the JNK/SAPK pathway.
Phosphorylates beta-casein, histone 1 and myelin basic pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Leucine-zipper protein kinase) (ZPK).
MAP3K12 OR ZPK.
                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:6851; MAP3K12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Teratocarcinoma;
MEDLINE-94311945; PubMed-8037767;
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SMART; SM00221; STYKC; 1.
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                                                                                                                Phosphorylation;
DOMAIN 125
                                                                                                                                                             Transferase;
                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          associated (By similarity).
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES MAP KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: Highly expressed in brain and kidney. PTM: Autophosphorylated on Ser/Thr. Phosphorylated in cytosol under basal conditions and dephosphorylated when membrane-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: ATP + a protein =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFACTOR:
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                                                                                                                                                                                                           PS00107; PROTEIN_KINASE_ATP; I
PS00108; PROTEIN_KINASE_ST; 1
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                                                                                                                                                                  Serine/threonine-protein kinase; ATP-binding,
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ATP (BY SIMILARITY).
POLY-GLU
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Best Local Similarity:
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SMART; SM00221; STYKC; 1.
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InterPro; IPR001452; SH3.
InterPro; IPR00140; STY_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00018; SH3; 1.
Pfam; PF00069; pkinase; 1.
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EMBL; Z48615; CAA88531.1;
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PROSITE; PS50011;
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAP KINASE KINASE SUBFAMILY. SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                        {\tt GlnGluAlaArgLeuPheGlyAlaLeuGlnHisProAsnIleIleAlaLeuArgGlyAla}
                                                     CysLeuAsnProProHisLeuCysLeuValMetGluTyrAlaArgGlyGlyAlaLeuSer
                                                                                         AGCATCCACCCG-----CTCTGCTTCGCCCTGGAGCTCGCGCCCCAGCAGCCTCAAC 168
                                                                                                                                             CAGGAGGCCAGCATGCTGCAGCGCTGCAGCACCCCTGCATCGTGGGCGCTCATCGGCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation een the Swiss Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way.
                     ACCGTGCTGTCCGAGAACGCCAGAGATTCTTCCTTTATACCCCTGGGACACATGCTCACC
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                                                                       LysGlySerAspGlyAlaSerProProAlaSerProSerIle---
                                                                                                                                                                                                                                                                                {\tt ArgGluLeuHisLeuLeuMetCysGlnLeuSerGlnGluLysProArgValArgLysArg}
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·IleProArgLeuArgAlaIleArg
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Run on:
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-MODEL-frame+_n2p.model -DEV=xlh
-Q-cgn2_1/GSPTQ_spool_VG90886392/runat_08042003_090327_22769/app_query.fasta_1.2375
-Q-cgn2_1/GSPTQ_spool_VG90886392/runat_08042003_090327_22769/app_query.fasta_1.2375
-DB-SwissProt_40 -QFMT-fastan -SUFFIX-n2p.rsp -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MTRIX-bicsum62 -TRANS-human40 cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pot -THR_MAX=100 -THR_KIN-0 -ALIGN-15
-MODE-LOCAL -OUTFMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-2000000000
-USER-US09836392_@CGN_1.1_16 @runat_08042003_090327_22769 -NCPU-6 -ICPU-3
-USER-US09836392_@CGN_1.1_16 @runat_08042003_090327_22769 -NCPU-6 -ICPU-3
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-USER-US09836392_@CGN_1.1_16 @runat_08042003_090327_22769 -NCPU-6 -ICPU-3
-NCALTXEDUT-30 -THREADS-1 -NCAPOP-10 -NCAPOENT-7
-YGAPOP-10 -YGAPEXT-0.5 -DELOP-6 -DELEXT-7
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match Length DB
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YHL1_EBV
ULK1_HUMAN
KYK2_DICDI
TESK_HUMAN
SRK4_SPOLA
TESK_RAT
ROR1_MOUSE
ULK1_MOUSE
ROR1_HUMAN
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M3KC_RAT
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arabidopsis	drosophila	drosophila	gallus gall	cani	homo sapien	dictyosteli		homo s		mus mu	arab	ratti	homo	homo	mus I		spon		arabido	dugesia tig	drosoph	cerat	homo	arak	homo sapien	homo sapien	/

## LIGNMENTS

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MEDLINE-93238756; PubMed-8477742; Dorow D.S., Devereux L., Dietzsch E., de Kretser T.; Dorow D.S., Devereux L., Dietzsch E., de Kretser T.;  Identification of a new family of human epithelial protein kinases containing two leucine/isoleucine-zipper domains.";  Eur. J. Biochem. 213:701-710(193).  -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoproteinI- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND SKELETAL MUSCLEI- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.	SEQUENCE FROM N.A.  TISSUE-Brain; MEDLINE-95249256; PubMed-7731697; MEDLINE-95249256; PubMed-7731697; Katoh M., Hirai M., Sugimura T., Terada M.; "Cloning and characterization of MST, a novel (putative) serine/threonine kinase with SH3 domain."; Oncogene 10:1447-1451(1995).  [3] SEQUENCE OF 244-480 FROM N.A. TISSUE-Color cattablum.	FROM FRAIN; 96128 S., D. D. D. D. D. D. D. D. D. D. D. D. D.	

SUMMARIES

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15
MODE=LOCAL -OUTFMT=pto -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
USER-US09836392_eCGN_1_1_52_erunat_08042003_090327_22761 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
WARN_TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPPEXT=0.5 -FGAPPOP=6 -FGAPEXT=7
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12516.961 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA19
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antifungal; antiparasitic; sarcollosis; inflammation; asthma; arthritis; cardiovascular disorder; severe combined immunodeficiency; SCID; vaccine; hyperproliferative disorder; atherosclerosis; brain disorder; leukaemia; multiple sclerosis; Alzheimer's disease; vascular dementia; thrombosis; gene therapy; neurodegenerative disorder; gastrointestinal disorder; cancer; lymphoma; blood coagulation disorder; trauma; cerebrovascular disorder; tendonitis; Human; protein tyrosine kinase receptor; PTK; antibacterial; antiviral; disorder; autoimmune disorder; allergy; neoplasm

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The invention relates to human protein tyrosine kinase (PTK) receptors and their corresponding cDNA molecules. PTK receptors are useful in providing immunological probes for differential identification of the tissues or cell types present in a biological sample. PTK is used in methods for the diagnosis, prevention and treatment of various disorders related to PTK such as immune system disorders (severe combined immunodeficiency (SCID) inflammation); hyperproliferative disorders (neoplasm, sarcoidosis); cardiovascular disorders (arrhythmia, atherosclerosis); central nervous system disorders (multiple sclerosis), neurodegenerative disorders (Alrhahmer's disease, Parkinson's disease); blood coagulation disorders (Alrhahmer's disease, Parkinson's disease); blood coagulation disorders (Alrhahmer's disease); respiratory disorders (asthma, thing); crohn's disease); respiratory disorders (asthma, thing); crohn's disease); respiratory disorders (asthma, thing); crohn's disease); respiratory disorders (asthma, thing); crohn's disease); respiratory disorders (asthma, thing); crohn's disease); respiratory disorders (asthma, thing); crohn's disease); respiratory disorders (asthma, thing); crohn's disease); respiratory disorders (asthma, thing); crohn's disease); respiratory disorders (asthma, thing); crohn's disease); respiratory disorders (asthma, thing); crohn's disease); respiratory disorders (asthma); thing); crohn's disease); respiratory disorders (asthma); thing); crohn's disease); respiratory disorders (asthma); thing); crohn's disease); respiratory disorders (asthma); thing); crohn's disease); respiratory disorders (asthma); thing); crohn's disease (asthma); thing); crohn's disease (asthma); thing); crohn's disease (asthma); thing); crohn's disease (asthma); thing); crohn's disease (asthma); thing); crohn's disease (asthma); thing); crohn's disease (asthma); thing); crohn's disease (asthma); thing); crohn's disease (asthma); thing); crohn's disease (asthma); thing); crohn's disease (asthma); thing); crohn's disease 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infections caused by bacteria, viruses, fungi and parasit useful for screening therapeutic compounds. PTK is used a vaccine to raise an immune response against infectious
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The present invention relates to albumin fusion proteins comprising therapoutic protein X and human albumin (HA, also known as numan for albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapoutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological

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                                                                                                              12-APR-2000;
25-APR-2000;
21-DEC-2000;
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Synthetic.
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1926	7 GTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCCAGGCGCGGTGGAGATGTTATC	1867	40
620			40
1866	7 AGGTCTGAGCATGACCTGACCCCCATGGACGGGGAGACCTTCAGCCAGC	1807	da Vo
1806 580	AGGACTCAGACATGCTACATACGCCCGGTGCTGCCTCCGAC	174 56	B 6
1746	7 CGCCAGGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCAGCTCCCCAGCAAGTTCTTCCAGTGTG	168	da
560		54	Vo
1686	7 ATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCTACTCCTCATCCCCACCC  -  -  -  -  -  -  -  -  -  -  -  -  -	162	g.
540		52	VQ
1626 520	7 GGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCAGATCCTG	<u> </u>	ρ. δ
1566	7 CGGCCCTTGGACACGGAACCCCCGGCAGCCAGCCÄACACGGCCAAAGCTGCCTGAG	150	
500			VQ 40
1506 480	7 CAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCAGCCCCCTCAGGGACATGTTTCCCGTG		B 6
1446 460	7 GTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACCACCTAC	138	ad Vo
1386	GCAGCTCTGAGGGCAGAGGGGAGGAG		dd
440			Vo
1326	7 GGGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCTGGAGATCTGCAGGCGGCTGGAGCCC 		אַס עַס
1266 400	GTCAACAGCGGCTCTGAGGTCTGGTACAGCAAT 	y 120 5 38	29 9
1206 380	7 TGCTCACACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATGAAGACGCACGGCAGAAC	y 114 5 36	Db.
1146.	7 GGGCTTGTGGCTGTGTTTCCCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTGCTCCTACCTG	108	dg
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1086 340	7 TTCTTGGCCGTGCCTGTTATTAAAAAGAATTCCTACCTGGTCTTAGCGGGCCTCGCCGAT	102 32	Db Qy
1026	CCCAACAGGCCTTGGATACTCCAGCTGTCGTCACCTGC	30	Db
320			Qy
966	7 GTCCAGAGATCCCTGTGGACAGCCACCGAGGACCAGAAAATCTACATCTACACCCTCAAG	90	D Qy
300		28	
906	7 GGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAGCTGCCAGCTCCAG	26	dd
280			Qy

Claim 11;

Page 491-493; 534pp; English.

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N-PSDB; AAD33718.
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Wei P, Ebner R,
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Shi Y, Choi GH, Fis
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CC AAD33692-AAD33736 represent cDNAs corresponding to 21 human secreted protein genes, and AAE21191-AAE21235 represent the proteins they encode. AAE21236-AAE21280 represent human secreted proteins they encode. CC AAE21236-AAE21280 represent human secreted proteins are useful for preventing, ctreating or ameliorating medical conditions, e.g., by protein or gene ctherapy. Pathological conditions can be diagnosed by determining the most therapy. Pathological conditions can be diagnosed by determining the presence of mutations in the new genes. Specific uses are described for each of the CC and include developing products for the diagnosis or treatment of the can be a conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the diagnosis or treatment of conditions of the conditions of the diagnosis or treatment of conditions of the conditions of the diagnosis or treatment of conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the conditions of the
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US-09-836-392-8\_COPY\_22\_2205 (1-2184) x AAE21217 (1-706)

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No :

Alignment Scores:

Score:

Query Match:

Percent Similarity: Best Local Similarity:

2.07e-273 3707.00 100.00% 100.00% 91.35%

Length:
Matches:
Conservative:
Mismatches:
Indels:

706 706 0

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	160	141 TyrGlyMetValLeuTyrGluLeuLeuSerGlyGlnArgProAlaLeuGlyHisHisGln	Дb
	546	63	Qy
	140	121 TyrGlnAlaProGluIleArgProArgIleValTyrAspGluLysValAspMetPheSer	Db
	486		Qy.
	120	-	Db
	426	367 TACGGGATTTCCAAGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACTCCTGGC	Qy
	100	81 AspAsnIleLeuValTrpSerLeuAspValLysG1uHisIleAsnIleLysLeuSerAsp	DЬ
	366		Qy
	08	61 IleAlaSerGlyLeuAlaTyrLeuHisLysLysĀsnIleIlePheCysAspLeuLysSer	Дb
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	60	41 AlaargaspSerSerPheIleProLeuGlyHisMetLeuThrGlnLysIleAlaTyrGln	DЬ
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	126	67 ATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCCG :	Qy

An isolated nucleic acid molecule (I) comprising a polynucleotide which encodes a polypeptide useful in the diagnosis and treatment of disorders e.g. immune disorders -

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                                                            TTCTTGGCCGTGCCTGTTATTAAAAAGAATTCCTACCTGGTCTTAGCGGGGCCTCGCCGAT
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                                                                                                                                                                   Albumin fusion protein; therapeutic protein X; human albumin; human serum albumin; HSA; cancer; reproductive disorder; digestive disorder; immune disorder; rendocrine disorder; haematopoietic disorder; neural disorder; connective disorder; cytostatic; antiinfertility; antiinflammatory; antiulcer; immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropineuroprotective; antiparkinsonian; antimicrobial; neuroleptic; osteopathic; antiarthritic.
                                           12-APR-2000; 2000US-229358P
25-APR-2000; 2000US-199384P
21-DEC-2000; 2000US-256931P
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                                                                                                                                        Homo sapiens.
Synthetic.
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WPI; 2002-010886/01.
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New fusion protein for treating disease e.g. diabetes comprises an albumin fused to a therapeutic protein  $\boldsymbol{\cdot}$ 

Claim 1; Page 1566-1569; 2102pp; English.

The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and diagnosing disorders such as cancer, reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoletic disorders, neural disorders (e.g. alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningliis, schizophrenia), and connective disorders (e.g. osteoporosis, arthitis). ABG63326-ABG65518 represent albumin fusion proteins of the invention.

#X##X#X55555555555555555555555555

## Sequence 706 AA;

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607 181	547 161	487 141	427 121	367 101	307 81	247 61	187	127 21	67	-836-	Ma nen
GTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAGGCTGGGACACTAAGCCAGAGAAG 666	CTCCAGATTGCCAAGAAGCTGTCCAAGGCATCCGGCCCGGTTCTGGGGCAGCCGGAGGAA 606 	TATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAGCGCCCTGCACTGGGCCCACCACCACCACCACCACCACCACCACCACCACCA	TACCAGGCCCCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTAGATATGTTCTCC 486	TACGGGATTTCGAGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACTCCTGGC 426	GACAACATTCTGGTGTGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTATCTGAC 366 	ATCGCCTCGGGCCTGGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTGAAGTCG 306 	GCCAGAGATTCTTCCTTTATACCCCTGGGACACATGCTCACCCAAAAAATAGCCTACCAG 246 	CTCTGCTTCGCCCTGGAGCTCGCGCCGCTCAGCAGCCTCAACACCGTGCTGTCCGAGAAC 186	ATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCCG 126	392-8_COPY_22_2205 (1-2184) x ABG64872 (1-706)	t Scores: 7.05e-273 Length: 706 .: 3700.00 Matches: 705 Similarity: 99.86% Conservative: 0 al Similarity: 99.86% Mismatches: 1 tch: 91.18% Indels: 0 Caps: 0

GTG 17         18   18	GCCTCCCCAGCTCCCCAGCAAGTTCTTCCAGT 	pb dd
Pro	27 ATCCACCAGGAATCACTCACTGACTGCTGCATGCTCCTACTCCTCATCCCCA	DP Ad
CTG 1	GTACAGTGAGGAGGTGGGCACGCAGATC 	dg V
GAG 1	TTGGACACGGAACCCCGGCAGCCAGCCACACGGCCAACCCAAAGGTGCCT 	Дb
GTG 1      Val 4	47 CAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCAGCCCCCTCAGGGACATGTTTCCC	Db Qy
TAC 1	ACTCCTTGGTGATGTACCACTCCACC 	Оу Въ
ര — ഒ	27 TACATGGCCCCCTCCATGGTTACGTCAGTCGTGTGCAGCTCTGAGGGCAGAGGGGAG 	ду Оу
CCC 1	ATCGACTGTGCCTCCCTGGAGATCTGCAGGCGGCTGGAG 	dd VQ
AST 1	07 CCCTACCCAGTGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTACAGC 	Дy
AAC 1      Asn 3	47 TGCTCACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATGAAGACGCACGGCAG 	ду Оу
CTG 1	87 GGGCTTGTGGCTGTGTTTCCCGTGGTGCTGCGGGGCACCCCAAAGGACAGCTGCTCCTAC 	ОУ
GAT 1     Asp 3	27 TTCTTGGCCGTGCCTGTTATTAAAAAGAATTCCTACCTGGTCTTÅGCGC 	g V
TGC 1	GCATGTGCCCCTTAAACACACCCCAACAGGCCTTGGATACTCCAGCTGTCGTCACC 	g 6
AAG 9 III Lys 3	07 GTCCAGAGATCCCTGTGGACAGCCACCGAGGACCAGA 	gy Vy
CAG 90	47 GGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAGCT 	DP DP
AAG 84	87 GTGGTGTTTTGGGATGGAAAAGAGGAGTCCAGGAACTACACGGTGGTGAACACAGAG 	β δ
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                                                                                                                                                                               Key
Peptide
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; immune disorder; antiallergic; antirheumatic; rheumatoid arthritis; breast neoplasia; breast cancer; antiarthritic; neurological disease; Alzheimer's disease; Parkinson's disease; trauma; Tourette syndrome; encephalitis; cytostatic; haemostatic; anaemia; mania; antiinfalmmatory; ophthalmalogical; dermatological; immunostimulatory;
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(HUMA-) HUMAN GENOME SCI INC
                           18-AUG-2000; 2000US-226282P
                                                     17-JAN-2001;
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                                                     2001WO-US01435
                                                                                                                                                 /label= Signal_peptide
25..706
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1..24
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                                                                                                                                     "Human mature secreted protein"
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and their corresponding secreted proteins are useful for preventing.

C treating or ameliorating medical conditions, e.g., by protein or gene
therapy. Pathological conditions can be diagnosed by determining the
amount of the new protein in a sample or by determining the presence of
mutations in the new genes. Specific uses are described for each of the
21 genes, based on the tissues in which they are most highly expressed,
and include developing products for the diagnosis or treatment of
themune or autoimmune diseases e.g. AIDS (acquired immune deficiency
syndrome), asthma, anaemia and rheumatoid arthritis, breast neoplasia
and breast cancer, neurological diseases e.g. Alzheimer's disease,
cand breast cancer, neurological diseases, Fourette syndrome,
meningitis, demyelinating disease, peripheral neuropathies, meoplasia,
trauma, congenital malformations, spinal cord injuries, toxic
neuropathies induced by neurotoxins, peripheral neuropathies, multiple
sclerosis, ischaemia and infarction, haemorrhages, schizophrenia, mania,
dementia, depression, panic disorder, learning disabilities, ALS,
altered behaviours e.g. disorders in feeding, sleep patterns, balance
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Moore
Ni J;
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                                                           sensory, reproductive and digestive systems, behavioural disorders and hyperproliferative disorder. The present sequence represents a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Page 472-474; 534pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An isolated
                                                                                                      perception, encephalitis, disorders in cardiovascular,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ed nucleic acid molecule (I) comprising polypeptide useful in the diagnosis and e.g. immune disorders -
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                                           of the invention.
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Sequence 706

Alignment Scores
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306		Qy 247	_
60	AlaArgAspSerSerPheIleProLeuGlyHisMetLeuThrGlnLysIleAlaTyrGln	рь 41	_
246	- 63	Qy 187	_
40	LeuCysPheAlaLeuGluLeuAlaProLeuSerSerLeuAsnThrValLeuSerGluAsn .	Db 21	-
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20	MetLeuHisAlaLeuGlnHisProCysIleValAlaLeuIleGlyIleSerIleHisPro	Db 1	_
126	٠.	Оу 67	_
	US-09-836-392-8_COPY_22_2205 (1-2184) x AAE21194 (1-706)	JS-09-836-	_
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29-MAR-2000;
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Key Domain

Location/Qualifiers 1280..1549

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Best Local
Query Match
US-09-836-392-8_COPY_22_2205 (1-2184)
                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                            The invention relates human kinases (PKIN) and their corresponding CC nucleic acid sequences. PKIN and its DNA are useful for diagnosing, CC treating and preventing cancer, an immune system disorder (e.g., CC acquired immune deficiency syndrome (AIDS), Addison's disease, allergy, CC affecting growth and development (e.g., arteriosclerosis, cirrhosis, CC affecting growth and development (e.g., hypertension, myocardial) CC infarction, Goodpasture's syndrome), and a lipid disorder (e.g., fatty CC liver, Gaucher's disease, Niemann-Pick's disease, hypertcholesterolaemia, CC hyperlipidaemia, obesity), and for assessing the effects of exogenous CC condition or a disease associated with the expression of PKIN in a CC condition or a disease associated with the expression of PKIN in a CC condition or a disease or composition comprising PKIN or an agonist of PKIN is useful in a number of drug screening techniques and to analyse CC PKIN is useful in a number of drug screening techniques and to analyse CC the proteome of a tissue or cell type. PKIN DNA is useful for creating and in somatic or germline gene therapy. The present sequence is human or part of pkin writerin.
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Yao MG, R
Gandhi AR,
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27-OCT-2000;
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0 4	AAGTOGAACAACATTCTGGTCTGGTCCCTTGACGTCAAGAACAACATCAACATCAAGCT	ـــــــــــــــــــــــــــــــــــــ	8 8
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		aggcttgcactcgcaagagaa	21	δõ
	2006	87 GlyTrpGlyAlaArgGluPheAspIlePheTyrGlnSerTyrGluGluLeuGlyArgLeu	19	Д
	2160	GCTGGGGCGCCAGGGAGTTCGACATTTTCTACCAGTCCTACGAGGAGCTGGGCCGGC	21	Q,
	1986	rValValCysThrPheGluAsnGluAsnThrGluTrpCysLeuAlaValTrpAr	19	멅
	2100	ACACTGTTGTGTGCACCTTTGAAAATGAAAACACAGAGTGGTGCCCTGGCCGTCTGGA	20	ξQ
	96		19	문 :
	Š	1 ТТААААЯССССВАGAGCTGACTCCGCATGGGGTGCTTGGTGGATGCTGCCGTGGTGGTGGCAAA	. 19	o O
	1946	27 ValIleValIleGlyLeuGluLysAspSerGlyAlaGlnArgGlyArgValIleAlaVal	19	뫄
	1980	TTATCGTCATTGGCCTGGAGAAGGATTCTGAAGCCCAGCGGGGCCGAGTCATTGCCGT	19	δō
	1926	07 GlnalaValLysIleLeuAlaValArgAspLeuIleTrpValProArgArgGlyGlyAsp	. <u>1</u> 9	뫄
	1920	AGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCCAGGCGCGGTGGAGA	1.8	γΩ
	1906	87 SerAspArgSerGluHisAspLeuThrProMetAspGlyGluThrPheSerGlnHisLeu	18	뫄
	1860	CCGACAGGTCTGAGCATGACCTGACCCCCATGGACGGGGAGACCTTCAGCCAGC	18	Q.
	1886	67 SerValProPheSerThrAspCysGluAspSerAspMetLeuHisThrProGlyAlaAla	18	D)
	1800	GTGTGCCTTTCTCCACCGACTGCGAGGACTCAGACATGCTACATACGCCCGGTGCTGC	17	. ο
	1866	47 ProProArgGlnAlaAlaArgSerProSerSerLeuProSerSerProAlaSerSerSer	18	D)
	1740	CACCCCGCCAGGCTGCCAGGTCCCCCTCAAGCCTCCCCAGCTCCCCAGCAAGTTCTTC	16	Qy
	1846	27 IleLeuIleH1sGlnGluSerLeuThrAspTyrCysSerMetSerSerTyrSerSerSer	18	DЬ
	1680	TCCTGATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCTACTCCTCATC	. 16	γQ
	1826	07 ProGluGlyAspSerIleAlaAspValSerIleMetTyrSerGluGluLeuGlyThrGln	18	Дb
	1620	CTGAGGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTGGGCACGCA	15	δõ
	1806	87 ProValArgProLeuAspThrGluProProAlaAlaSerHiSThrAlaAsnProLysVal.	17	밁
	1560	CCGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCAGCCA	15	δõ
	1786	67 ThrTyrGlnLeuCysAlaArgTyrPheCysGlyValProSerProLeuArgAspMetPhe	17	DЪ
	1500	CCTACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCAGCCCCCTCAGGGACATGTT	14	γQ
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	4	1 GAGGAGGTCGTCTGGTGCCTGGATGATGAGAGAGAGAGAG	μ ω	Q Q
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•	1380	21 GAGCCCTACATGGCCCCCCCCCATGGTTACGTCAGTCGTGTGCAGCTCTGAGGGCAGAGG	13	γQ
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                                                                                                                             Alignment
                                 US-09-836-392-8_COPY_22_2205 (1-2184)
                                                                                         Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnostics, responsible f biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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23-AUG-2000;
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maging; diagnostic; genetic disorder
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    TCGGACAACATTCTGGTGTGGTCCCTT--
                      GlnAlaAlaArgAlaIleGluTyrLeuHisArgArgArgIleIleTyrArgAspLeuLys
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	1215	GCACGGCAGAAC	1195	~
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	1194	AGGTCCAAGTTCAGCATCGCGGATGA	1165	~<
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	951	AGCTGCCAGGTCCAGGAGATCCCTGTGGACAGCCACCGAGGACCAGAAAATCTA	892	~
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                                                                                                                                                                                                                                                                                                                                                                      Human; cytostatic; antisense gene therapy; screening; protein kinase; cancer; liver; colon; tumour; inflammation; arthritic synovium; MAP3K11; enzyme; mitogen activated protein kinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1324 CCCTACATGGCCCCCTCCATGGTTACGTCAGTCGTGCAGCTCTGAGGGCAGAGGGGAG 1383
                                Yoganathan T,
                                                                                                                                                                                                                               20-SEP-2001; 2001WO-IB02237
                                                                                                                                                                                                                                                                                                    WO200224947-A2
                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human mitogen activated protein kinase, MAP3K11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE22763;
                                                                                                                                                                                                                                                                  28-MAR-2002
                                                                   (KINE-) KINETEK PHARM INC.
(UYBR-) UNIV BRITISH COLUMBIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SerThrProThrHisGlyAlaAlaLysSer 2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCATCCCCACCCCGCCAGGCTGCCAGGTCC 1704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACGCAGATCCTGATCCACCAGGAATCACTCACTGACTACTGCTCCATGTCCTCCTACTCC 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IleSerValPheArgProTyrGluAsnGluIleLysSerIleIleThrLeuSerLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tyr---IleGlyThrThrTrpGlyCysLeuIleValAlaGluLeuH1sThrLeuArgPro
                                Delaney AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GlnTleSerAlaLeuAlaAlaHisAsnSerGluLeu 2206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ATCGACTGTGCCTCCCTGGAGATCTGC---AGGCGGCTGGAG
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N-PSDB; AAD36139.

Diagnosing cancer, comprises determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase or upregulation of expression of the protein kinase, in the cancer

Claim 1; Page 60-62; 87pp; English.

The invention relates to a method for screening biologically active agent that modulates cancer associated protein kinase function. The invention also relates to a method for diagnosing cancer comprising determining the upregulation of expression of a nucleic acid sequence encoding a protein kinase. The method is useful for diagnosing cancer. A protein kinase is useful for screening biological agents that modulate cancer associated protein kinase function. Downregulating the activity of protein kinase is useful for inhibiting the growth of a cancer cell, e.g. liver or colon cancer. A nucleic acid encoding protein kinase is useful to screen biopsy derived tumours and inflammatory samples such as arthritic synovium, for amplified DNA in the cell or increased expression of corresponding mRNA or protein and is also useful to detect differences in expression levels such as molecular weight, amino acid and nucleotide sequences between the kinase, MAP3K11.

Sequence 847 AA;

Qy	Db Oy	β Q	D 49	B 8	B 64	В <b>2</b>	g 84	Å Å	4g VQ	us-09	Alignr Pred. Score Percer Best 1 Query DB:
y 559AAGAAGCTGTCCAAGGGCATCCGCCCGGTTCTGGGGCCAGCCGGAGGAAGTGCAG	y 508 TTGCTGTCAGGACAGCGCCCTGCACTGGGCCACCACCAGCTCCAGATTGCC	y 448 CCTCGCATTGTATATGATGAGAAAGGTAGATATGTTCTCCTATGGAATGGTGCTCTACGAG	y 388 TTCCATGAGGGCGCCCTAGGCGTGGAGGGCACTCCTGGCTACCAGGCCCCAGAGATCAGG :::           5 275 HisLysThrThrGinMetSerAlaAlaGlyThrTyrAlaTrpMetAlaProGluValIle	y 328 CTTGACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCAGTCA	y 280AACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTGGTGTGGGTCC :::                :::          ::: b 235 ValProValIleHisArgAspLeuLysSerAsnAsnIleLeuLeuLeuGlnProIleGlu	y 226 ACCCAAAAATATAGCCTACCAGATCGCCTGGGCCTGGGCCTACCTGCACAAGAAA	166 AACACCGTGCTGCCGAGAACGCCAGAGATTCTT :::    ::: 202 SerArgAlaLeuAlaGlyArgArg	y 112 ATCAGCATCCACCCGCTCTGCTTCGCCCTGGAGCTCGCGCCGCTCAGCAGCCTC	y 52 CGGCAGGAGGCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGC	-09-836-392-8_COPY_22_2205 (1-2184)	NO.: 4.69e-17 NO.: 337.50 : 34.098 Local Similarity: 24.628 Match: 8.328
TTCTGGGGCAGCCGGAGGAAGTGCAG 612	ACCAGCTCCAGATTGCC 558           :::       spCysLeuAlaValAlaTyrGlyVal 334	TCTCCTATGGAATGGTGCTCTACGAG 507	CTGGCTACCAGGCCCCAGAGATCAGG 447 :::          :::  YrAlaTrpMetAlaProGluValIle 294	CTGACTACGGGATTTCGAGGCAGTCA 387 ::   :::   ::: hraspPheGlyLeuAlaArgGluTrp 274	ACATTCTGGTGTGGTCC 327         :::  snIleLeuLeuLeuGlnProIleGlu 254	TGGCCTACCTGCACAAGAAA 279 ::          ::: lethisTyrLeuHisCysGluAlaLeu 234	CCTTTATACCCCTGGGACACATGCTC 225	TGGAGCTCGCGCCGCTCAGCAGCCTC 165	ACCCCTGCATCGTGGCGCTCATCGGC 111 	x AAE22763 (1-847)	Length: 847 Matches: 195 Conservative: 75 Mismatches: 241 Indels: 283 Gaps: 38

Qy 1283TCATCG 1288	
Db 639LysLeuIleGlnArgAlaLeuLeuArgGlyThrAlaLeuLeuAlaSerLeu 655	
-1223 CCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTACAGCAATGGGCCGGGCCTCCTTG 1	-
QY 1163 ACAGGTCCAAGTTCAGCATCGCGGATGAAGACGCAGGGAAACCCCTACCCAGTGAAGG 1222	
1106 CCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTCCTACCTGTGCTCACACACA	
OY 1055 ATTCCTACCTGGTCTTAGCGGGCCCTGGCCGATGGGCCTGTGGGCTGTGTTC 1105	
567	
QY 1010 CAGCTGTCGTCACCTGCTTCTTGGCCGTGCCTGTTATTAAAAAGA 1054	
Oy 950 ACATCTACACCCTCAAGGGCATGTGCCCCTTAAACACACCCCAACAGGCCTTGGATACTC 1009 ::::::               Db 556 SerAsnGlyGluArgArgAlaCys	
536 GluProAlaGluProGlyGlnAlaTrpGlyArgGlnSerProArgArgLeuGluAspSer 555	
Qy 923GGACAG	
Db 516 ValPheGluValGlyProGlyAspSerProThrPheProArgPheArgAlaIleGlnLeu 535	
Qy 897 CCAGCTCCAGGTCCAGGATCCCTGT 922	
Qy 879 TGGGATGAAGGTGAGCTG 896	
476 GlyThrPheLysArgSerLysLeuArgAlaArgAspGlyGlyGluArgIleSerMetPro	
855	
456 GluLeuThrLeuLeuGlnGlnValAspArgGluArgProHisValArgArgArgArg 47	
85	
Db 436 GluGlnLeuArgArgArgGluHisLeuLeuAlaGlnTrpGluLeuGluValPheGluArg 455	-1
416 GIULEULEUSERAIGGIUGIUGLULEUTNIRAIGALAALAARGGIUGINAIGSEIGINALA 43	
818 81	(A)
Db 396 GlnGluGlyTrpLysArgGluIleGlnGlyLeuPheAspGluLeuArgAlaLysGluLys 415	
Qy 792 GTTTTGGGATGGAAAAGAGGAGTCCAG818	
Db 376 LeuGluAlaLeuGluAlaGlnValLeuArgGluMetProArgAspSerPheHisSerMet 395	
QY 733 CTGTG-CTGTGGGAAGCAGACAGCCTTCTTCTCATCCCAGGGCCAGGAGTACACCGTGGT 791	
Db 367ProAspPheAlaSerIleLeuGlnGln 375	
Qy 673 CTGGCCCTGTCGGTGGTGAGCCAGATGAAGGACCCGACTTTTGCCACCTTCATGTATGAA 732	
.351	
GGAGTGCTGGGACACTAAGCCAGAGAAGCGACCG 67	
Db 335 AlaValAsnLysLeuThrLeuProIleProSerThrCysProGluPro 350	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1826 CCCCCATGGACGGGAGACCT---TCAGCCAGCACCTGCAGGCCGTGAAGATCCTCGCCG 1882
20-APR-1994;
20-APR-1993;
                                                                                                                              US5849895-A.
                                                                                                                                                                                                    NMDA-activated
                                                                                                                                                                                                                                                                                             23-FEB-1999
                                                                                                                                                                                                                                                                                                                               AAW87504;
                                                                                                                                                                                                                                                                                                                                                                   AAW87504 standard; Protein; 1061 AA
                                                      20-APR-1994;
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                     Human; N-methyl-D-aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                         830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGAGACCTCATTTGGGTCCCCAGGCGCGCGGTGG 1916
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                                                                                                                                                                                                                                                                                                                                                                                                                                         aGlnThrLysAspMetGlyAlaGlnAlaProTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProPheTrpAspSerProProAlaAsn-ProPheGlnGlyGlyProGlnAspCysArgAl 830
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                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                    cation-selective
 94US-0231193.
93US-0052449.
                                                      94US-0231193.
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                                                                                                                                                                                                                       receptor; NMDAR2C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----GlyProArgProSerProLeuProSerPro
                                                                                                                                                                                                    ion channel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ·---ArgProSerProLeuArgSer
                                                                                                                                                                                                                                                                                                                                                                                                                                         841
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                                                                                                                                                                                                    glutamate receptor
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Alignment Scores: Pred. No.:
                                                                                                                        (AAV8289) Inserted between nucleotides 23050 and 2351, as set forth in AAV82889. The cDNA sequence is derived from clone NMDA24. The NMDAR subunits contribute to the formation of NMDA-activated cation-selective ion channels. In addition to being useful for the production of NMDA receptor subunit proteins, the nucleic acids are also useful as probes to identify and isolate nucleic acids encoding related receptor subunits. Functional glutamate receptors can be assembled from several NMDA receptor subunit proteins of one type (homomeric) or from combinations of subunit proteins of different types (heteromeric). The present invention also comprises methods for using such receptor subunits to identify and characterise compounds which affect the function of such receptors, e.g. agonists, antagonists and modulators of glutamate receptor function. The invention also comprises methods for determining whether unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 19
                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a human N-methyl-D-aspartate (NMDA) receptor subunit (NMDAR). The nucleic acid sequence does not contain the 860 5'-most nucleotides, has an additional 11 nucleotides (AAV82891) between nucleotides 1300 and 1301, an additional 24 nucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding N-methyl-D-aspartate receptor subunit assembly of functional glutamate receptor subunits
                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Columns 261–268; 203pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Daggett LP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SIBI-) SIBIA NEUROSCIENCES
                                                                                                          protein(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-069812/06
DB; AAV82910.
                                                                                                          are
                                                                 1061 AA;
                                                                                                            functional
                                                                                                              as
                                                                                                              NMDA
                                                                                                              receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for the
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Pred. No.: 1.59e-16 Length: 245
Score: 331.00 Matches: 245
Percent Similarity: 30.47% Conservative: 64
Best Local Similarity: 24.16% Mismatches: 313
Query Match: 8.16% Indels: 392
DB: 20 Gaps: 57
US-09-836-392-8\_COPY\_22\_2205 (1-2184) x AAW87504 (1-1061)

Q B	9 b 9	p dy	40 A	ру	Qy Db	ор Ор	gg dy	р <sub>у</sub>	р У У	94 60	р <sub>ь</sub> оу	D oy	g v	Дb	dg Qy	Db Qy	Db .
544ProThrGlySerGly550 1217 TGAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCT 1255	1097 CTGTGTTTCCCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTCCTACCTGTGCTCACACA 1156	1052 AGAATTCCTACCTGGTCTTAGCGGGCCCTCGCCGATGGGCTTGTGG 1096	1001 TGGATACTCCAGCTGTCGTCACCTGCTTCTTGGCGTGCCTGTTATTAAAA 1051	941 AGAAAATCTACATCTACACCCTCAAGGGCATGTGCCCCTTAAACACACCCCAACAGGCCT 1000	881 GGATGAAGGTGAGCTGCCAGGTCCAGAGATCCCTGTGGACAGCCACCGAGGACC 940	821 ACTACACGGTGGTGAACACAGAGAAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTG 880 :::                              439 GlyLeuLysIleSerThrHisLeuSerAlaSerAlaArgCysProThrAlaAlaArgSer 458	767 CCCAGGGCCAGGAGTACACCGTGGTGTTTTGGGATGGAAAAGAGGAGTCCAGGA 820     ::::::    	719CTTCATGTATGAACTGTGCTGTGGGAAGCAGACAGCCTTCTTCTAT 766         ::::: ::: 399 PheTrpSerGlyProSerLeuLeuSerSerSerProAspThrArgProThrTrpPro 418	TGGCCCTGTCGG     CysProSer	617GCGAATGCAGCCGCTCATGATGGAGGTCTGGGACACTAAGCCAGAGAAGCGACCGC 673	ት። ይ	503 ACGAGTTGCTGTCAGGACAGCGCCCTGCACTGGGGCCACCAGCTCCAGATTGCCAAGA 562	443 TCAGGCCTCGCATTGTATATGATGAGAAAGGTAGATATGTTCTCCTATGGAATGGTGCTCT 502	392 ATGAGGGCCCCTAGGCGTGGAGGGCACTCCTGGCTACCAGGCCCCAGAGA 442	335 TCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCAGTCATTCC 391	296ACCTGAAGTCGGACAACATTCTGGTGTGGTCCCTTGACG 334	
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סא מם	D V D	0 P Q	) bb 04	p da	2 B 2	S. B. 8	P	o do	o p :	ð þ	Q D 5	? B 5	? B 5	2 B 5	Q D 5	당 말 :	Qv Qv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
CC mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
CC rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
CC conternial, parasitic, fungal, viral, protozoal and helminthic infections)
CC growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
CC cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
CC vascular disease (arteriovenous fistula, hypertension, vasculitis,
CC aneurysms, congestive heart failure, angina pectoris, myocarditis,
CC ischaemic heart disease, chronic bronchitis, lung tumours); lipid
CC disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
CC disorder (fatty compound and in gene therapy. The present sequence
CC is human PKIN-5 protein.
                                                                                                                                                                                                                                                       US-09-836-392-8_COPY_22_2205 (1-2184)
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07-JUL-2000;
13-JUL-2000;
25-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                corresponding cDNAs. A composition containing PKIN agonist is useful for treating a disease or condition associated with decreased expression of PKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with overexpression of PKIN. The disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, atherosclerosis, anaemia, allergies, adult respiratory distress syndrome, atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
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Lo TP, Kh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, a diseases such as cancer, comprise human kinase polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases such as cancer,
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dhn MR, He A, Thornco...
"han F, Recipon SA,
"han F, Act VS, Than"
AGAGATTCTTCCTTTATACCCCCTGGGACACATGCTCACCCAAAAAATAGCCTACCAGATC
                                    MetLeuValMetGluLeuAlaSerLysGlySerLeuAspArgLeuLeuGlnGlnAspLys
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                                                                        TGCTTCGCCCTGGAGCTCGCGCCGCTCAGCAGCCTCAACACCGTGCTGTCCGAGAACGCC
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Flanagan P,
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                                                                                                                                                                                                                                          No.:
  459
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                       TGCTTCGCCCTGGAGCTCGCGCCGCTCAGCAGCCTCAACACCGTGCTGTCCGAGAACGCC
                                                                                                                                                                                                                                                      Scores:
MetLeuValMetGluLeuAlaSerLysGlySerLeuAspArgLeuLeuGlnGlnAspLys 478
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protein kinase #54. protein kinase; disorder; immune related PTK; STK; cancer; cardiovascular neurological disorder; disease;

infectious disease;

Homo sapiens.

22-NOV-2000; 2000WO-US32085

99US-0167482

(SUGE-) SUGEN INC.

Whyte Clary ם מ Manning . و, Sudarsanam Ś Martinez

2001-343950/36

Nucleic acids encoding human kinase polypeptides, useful for preventing diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections

433pp; English.

AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel protein kinases have been identified as members of the tyrosine or serine/threonine kinase (PTK and STK) families. The polynucleotides encoding protein kinases and the polypeptides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoletic origin), cardiovascular disease (e.g. HIV) and reproductive disorders (e.g. infertility). Additionally, polynucleotides encoding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays. The protein kinase polypeptides may be used as antigens in the professional protein kinase polypeptides may be used as antigens in the professional protein kinase polypeptides may be used as antigens in the professional protein kinase polypeptides may be used as antigens in the professional prof of antibodies against the protein kinases and acmodulators of protein kinase expression and ac disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. Parkinson's disease), inflammatory disorders (e.g. asthma), infectious disease, (e.g. utv.) s antigens in the production in assays to identify

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US-09-836-392-8_COPY_22_2205 (1-2184) x AAU03554 (1-909)
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                                                                                                          GCCATGAAGAACTTCTCCGAG-----
                                   CTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCCGCTC 129
                                                                        AlaValLysIlePheAsnLysHisThrSerLeuArgLeuLeuArgGlnGluLeuValVal 438
LeuCysHisLeuHisHisProSerLeuIleSerLeuLeuAlaAlaGlyIleArgProArg
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327.50
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26.10%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 argAlaProGluValAlaArgGlyAsnValIleTyrAsnGlnGlnAlaAspValTyrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCTCGGGCCTGCCCTGCACAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGAC
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GlyIleAlaGlnTyrCysCysArgMetGlyIleLysThrSerGluGlyThrProGlyPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGATTTCGAGGCAGTCATTCCATGAGGGCCCCTAGGCGTGGAGGGCACTCCTGGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTATCTGACTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuLysGluAsnProGlnGluArgProThrSerAlaGlnValPheAspIleLeuAsnSer
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                                                                                                                                                                                                                                                                                                                                                                                    GluSerTrpIleValSerGlyThrGlnSerGlyThrLeuLeuValIleAsnThrGluAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AlaAspSerArgIleLeuCysLeuAlaLeu------ValHisLeuProValGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt AspArgGlyGlnLeuSerPheLeuAspLeuAsnThrGluGlyTyrThrSerGluGluValue}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MetValAlaThrHisHisAsnSerArgAsnAlaSerIleTrpLeuGlyCysGlyHisThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCTTCTCATCCCAGGGCCAGGAGTACACCGTGGTGTTTTGGGATGGA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AlaGluLeuValCysLeuThrArgArgIleLeuLeuProLysAsnValIleValGluCys 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGACTTTTGCCACCTTCATGTATGAACTGTGCTGTGGGAAGCAGACA-----GCC
                                                                                                             AspGlyLysLouAlaILePhe
                                                                                                                                                                                                      TyrCysAsnSerPheSerLysGlnSerLysGlnLysAsnPheLeuLeuValGlyThrAla
                                                                                                                                                                                                                                                  TTGGCCGTGCCTGTTATTAAA----
                                                                                                                                                                                                                                                                                            GlyLysLysArgHisThrLeuGluLysMetThrAspSer-----ValThrCysLeu
                                                                                                                                                                                                                                                                                                                                          ATGTGCCCCTTAAACACACCCCCAACAGGCCTTGGATACTCCAGCTGTCGTCACCTGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCCTGTGG-----ACAGCCACCGAGGACCAGAAAATCTACATCTACACCCTCAAGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----CACCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGCCCG
                       Protein; 1212
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                                                                                                                                                                             US-09-836-392-8_COPY_22_2205 (1-2184) x AAW87503 (1-1212)
                                                                                                                                                                                                                                                   Best Local Similarity:
                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                    Score:
                                                                                                                                                                                                                                                                                                                                                                                                          receptor subunit (NMDAR): The nucleic acid sequence does not contain the 366 5'-most nucleotides, by the insertion of il nucleotides between nucleotides 1300 and 1301, nor the 15 nucleotides at positions 1960-1974, nor the 1061 3' nucleotides, as set forth in AAV82889. The CDNA sequence is derived from clone NMDAR1. The NMDAR subunits contribute to the formation of NMDA-activated cation-selective ion channels. In addition to being useful for the production of NMDA receptor subunit proteins, the nucleic acids are also useful as probes to identify and isolate nucleic acids encoding related receptor subunits. Functional classifies of one type (homomeric) or from combinations of subunit proteins of one type (homomeric) or from combinations of subunit proteins of different types (heteromeric). The present invention also comprises compounds which affect the function of such receptors, e.g. agonists, antagonists and modulators of glutamate receptor function. The invention also comprises methods for determining whether unknown protein(s) are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a human N-methyl-D-aspartate (NMDA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding N-methyl-D-aspartate receptor subunit assembly of functional glutamate receptor subunits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Daggett LP,
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NMDA-activated cation-selective ion channel; g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human N-methyl-D-aspartate receptor subunit encoded by clone NMDA22
                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Columns 253-262; 203pp; English.
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20-APR-1993;
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 122
                                    497
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ACCCGC--
                                                                       AGC--
                                  {\tt AlaSerLeuTrpTrpProSerProSerSerCysSerSerThrSerAlaLeuSerAlaThr}
                                                                                                          ProSerProProArgProSerTrpSerHisIlcAlaLeuGlnCysGlyCysLeuSerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              NMDA receptor
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93US-0052449.
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                                                                                                                                                                                                                 1.36e-15
319.00
33.25%
25.73%
7.86%
20
                                                                       -ACCCCTGCATCGTGGCGCTCATCGGCA-----TCAGCATCC 121
                                                                                                                                                                                                              Conservative: Mismatches: Indels: Gaps:
                                                                                                                                                                                                                                                                                      Length:
Matches:
     TCTGCTTCGCCC
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     139
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ਲੇ ਵੱ	140 537	TGCTGTCCGAGAACGCCAGAGATT 1      /   	51
Ÿ	197	CCTTTATACCCCTGGGACACATGCTCACCCAAAAAATAGCCTACCAGATCGCCT 2	53
ō	552		71
Ÿ	254	CCTGAAGTCGG 3	07
σ	572	rArgProThrTrpProProSerSerLysSerAsnThrSerThrLeu	87
4	308	AACATTCTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGC 3	58
ō	588	rGlyLeuLysIleSerThr 6	03
Ÿ	359	GCCCTAGGCGTGGAGGGCA 4	18
ō	604	IsLeu	14
¥	419	ATTGTATATGATGAGAAGGTAGATA 4	7.8
ō	615	cAlavalThrThrValThr 6	26
¥	479	ACGAGTTGCTGTCAGGACAGCGCCCTGCACTGGGCC 5	. 80 ·
ŏ	627	ysThrProThrTrpSerSerSerThrSerAlaArgTrpArg 6	0
¥	539	GCCAAGAAGCTGTCCAAGGGCATCC 5	80
ŭ	641	ArgSerProAlaSerArgTrpGlySerTrpMetProSerSerMetMetLeuLeuSer 6	60
¥	581	GGCGACTGCAGGCGCTCATGATGG 6	40
ŏ	661	erThrThrTrpGlnAlaArgThrArgAlaAlaSerTrp 6	73
¥		AAGCGACCGCTGGCCCTGTCGGTGG 6	88
ō	674	erProLeuGlyLeuAlaArgSerLeuLeuProLeuAlaThrAlaSerProCysArg 6	92
¥	689	ATGTATGAACTGTGCTGTGGGAAGC 7	48
õ	692	6	92
Ÿ	749	GACAGCCTTCTTCTCATCCCAGGGCCAGGAGTACACCGTGGTGTTTTGGGATGGAA 8	05
õ	693	7	04
4	806	GAGAAGGGCCTCATGGAGG 8	59
ŏ	705	SerTrpGlyThrGluArgHisArgAsnTrpArgGlnCys 7	19
¥	860	TGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAGCTGCCAGGTTCCAGGTCCAGAGAT 9	.16
ŏ	720	ySerGlnGlySerAlaArgMetArgArgThrArgAlaAlaSerTrpThrSerThrThr 7	39
Ϋ́	917		34
ŏ	7,40	laSerSerThrCysCysTrpTrpProTrpGlyTrpProCysTrpSerSerPro 7	59
¥	935	CCAGAAAATCTACATCTACACCCTCAAGGGCATGTGCCCCTTAAACACACCCCCAAC 9	94
ŏ	760	CysAlaThrArgCysProThrHisProSer 7	77
¥	995	GGCCGTGCCTGTTA 1	045
ŏ	778	SerAlaGlyAlaSerThrAlaAlaSerAlaGlyCys 7	95
7 4	خة د	GCTTGTGGCTGTGTTTC 1	
ō	/96	ArgAlaSerProAlaHisArg 8	02

1134		Db
1954	1937TGGAGAAGGATTCTGAAG 1	Qy
1114	1095 ProValThrAlaThrAlaProGlySerProAlaProGlyGlyLeuTrpGlyThrAlaAla	Db
1936 .	CAGAGACCTCATTTGGGTCCCCAGGCGCGGTGGAGATGTTATCGTCATTGGCC	Qy
1094	roThrProThrCysHisCysAlaGlyGlyLeuSerValLeuThrPheHis	Db
1882	GTGAAGATCCTCGCCG	QΨ
1077	1058 ArgArgAlaSerArgGlnGlyProProProGlySerThrAspSerThrSerAlaCysThr 1	Db
1864	CCATGGACGGGGAGACCTTCAGCCAGCACCT	Qy
1057	1038 ProAlaGlyAlaTrpArgArgArgSerArgCysAlaCysArgSerThrGlyArgProAla :	Db.
1804	CACCGACTGCGAGGACTCAGACATGCTACATACGCCCGGTGCTGCCTCCG	Qy
1037	:::	타
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5 6	CVICTOR TO THE TAXABLE TO THE TAXABL	? 5
0 0	8 ACAGTGAGGAGCTGGGCACGCAGATCCTGATCCACCAGGAATCAC :::	γ. γ
980	962 AlaAlaProSerSerArgSerSerArgSerProArgSerTrpArgThrCysArgCys	Дb
1597	ACACGGCCAACCCAAAGGTGCCTGAGGGGGACTCCAT	Qy
961		밁
1537	CAGGGACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCA	Qy
941	 	밁
1486	CTACCAGCTGTGTGCCCGGTACTTCTGCGGGGTCCCCCAGCCCCC	γO
921	 	밁
1441	GGAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACTCCACCA	οy
904	aArgArgLeuCysAlaGlyLeuArgSerProArgAlaAlaPro	밁
1381	CAGCTCTGAGGGCAGAGGGG	δō
884	 rArgAlaProArgAlaGlyAsp	В
1357	TGGTTACGTCAGTCG	Qγ
864	HisArgProProAlaArgProArgGlyLeuAla.	В
1318	CAATGGGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCTGGAGATCTGCAGGCGGC	Qy
847	834ThrProTrpThrAlaProLeuAlaProSerArgIleGlyVal 8	Дb
1261	TGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTACA	Qy
833	820 ArgPheCysArgGlnProAlaThrTrpProArgArgAlaAla 8	Дb
1201	GGATGAAGACGCACGGC	Qy
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1150	1106 CCGTGGTGCGGGGCACCCCAAAGGACAGCTGCTCCTACCTGTGCT 1	VQ

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AIDS; seizures; cell proliferative disorder; cancer; adenocarci
leukaemia; lymphoma; melanoma; myeloma; sarcoma; developmental
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                  31-AUG-2000;
08-SEP-2000;
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14-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           enzyme; PKIN-12 protein; immune system disorde deficiency syndrome; thymic hypoplasia; Crohr ogical disorder; epilepsy; Charcot-Marie-Tooth
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression of PKIN, particularly immune system disorders (e.g. acquired immune deficiency syndrome (AIDS), thymic hypoplasia, Crohi's disease, anaemia, asthma), neurological disorders (e.g. epilepsy, Charcot Marie-Tooth disease or setzures), cell proliferative disorders (e.g. cancers such as adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma, sarcoma) and developmental disorders (e.g. Down's syndrome). They are also used in gene therapy and protein therapy. The present sequence is human PKIN-12 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-SEP-2000;
06-OCT-2000;
13-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding such proteins. PKIN sequences of the invention are useful for diagnosing, treating or preventing disorders associated with aberrant expression of PKIN, particularly immune system disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human kinases, useful for diagnosing, treating or preventing system disorders (e.g. Crohn's disease), neurological disorders epilepsy), or cell proliferative disorders (e.g. cancers such as
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                                                                                                                                                                                                                                     ProAsnLeuCysLeuValMetGluPheAlaArgGlyGlyProLeuAsnArgValLeuSer
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                      ATGCTGCACGCGCTGCACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCCG
ProllelleHisArgAspLeuLysSerSerAsnIleLeuIleLeuGlnLysValGluAsn
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R, Ding L, Patterson C, Y
M, Elliott VS, Lu Y, Ison
Burrill JD, Marcus GA,
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                                                                                                                                                                                                                                                                           -CTCTGCTTCGCCCTGGAGCTCGCGCCCCCAGCAGCCTCAACACCGTGCTGTCC
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Policky JL,
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Au-Young J,
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Thangavelu K;
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)AM, Lal PG;
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GACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCGAGGCAGTCA

1133	1080	
N	602 GlyThrLeuGlyGlnLysGluLeuAlaSerGlyAspGluGlyLeuLysSerLeuValAsp	
1079	CT	بيا
601	 yGluGluGluLysArgAlaProLysLysLysGlyArgThrTrpGly-Pro	
1073	TAAAAAGAATTCCTACCTGGTCTTAGC	1
582	ysThrTrpGlyArgSerSerValValProLysG	
1045	1045	Ë
562	:     :::::: aSerProThrIleIleProArgLeuArgAlaI	
1045	CCAGCTGTCGTCACCTGCTTCTTGGCCGTGCCTGTTA	
542	522 eraspPheGlnHisLysPheThrValGlnAlaSerProThrMetAspLysArgLysSerL	
1001		
N 6	02 ysGlyLysPheArgLysSerArgLeuLysLeuLysAspGlyAsnArgIleSerLeuProS	
2	47	
502	82 rgGluLeuAsnIleIleIleHisGlnLeuCysGlnGluLysProArgValLysLysArgL	
946	CCCTGTGGACAGCCACCGAGGACCAGAAAA	
482	oo/ white rectrements the more recorded to the control of the cont	
462	43 GIULEUAFGINTITPGIUGIUGULEUThrArgAlaAlaLeuGlnGlnLysAsnGlnGlu	
0	43 GAAGGCCTCATGGAGGTGCAGAG	
442	23 GlnAspAsnTrpLysHisGluIleGlnGluMetPheAspGlnLeuArgAlaLysGluLys	
842	ACAGA	
422	403 LeuThrThrIleGluGluSerGlyPhePheGluMetProLysAspSerPheHisCysLeu	
791	GGAAGCAGACAGCCTTCTTCTC-ATCCCAGGGCCAGGAGTACACCGTGGT	
402	394ProSerPheThrAsnIleLeuAspGln	
732	ATGTATGAA	
393	aspCysTrpAsnProAspProHisSerArg	
672	TGGAGTGCTGGGACACTAAGCCAGAGAAGCGACCG	
377	luPro	•
612	CTGTCCAAGGGCATCCGCCCGGTTCTGGGGCAGCCGGAGGAAGTGCAG	
361	yrGlyVal	
558	TCAGGACAGCGCCCTGCACTGGGCCACCACCAGCTCCAGATTGCC	
	;; ysGlySerAspValTrpSerTyrGlyValLeuLeuTrpGlu	
	atatgatgagaaggtagatatgttctcctatggaatggtgctctacgag	
321	02 HisargThrThrLysMetSeralaaAlaGlyThrTyrAlaTrpMetAlaProGluVallle	
	204 7.me7.e04.0.0.0.2038.0.4.m.0.204.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0.0	
301	283 GlyAspLeuSerAsnLysIleLeuLysIleThrAspPheGlyLeuAlaArqGluTrp	

1976 942	1917 AGATGTTATCGTCATTGGCCTGGAGAAGGATTCTGAAGCCCAGCGGGCCCGAGTCATTGC	Оу
22	902 rLeuLeuAlaSer-ArgSerProSerSerAsnGlyLeuSerProSerProGlyAlaG	DЬ
9	57 CCTGCAGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCCAGGCGCGG	Qy
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882	62 lGluArgPheLysArgAspPr	Db
1796		Qy
862	845 uAlaProProLeuSerProCysThrHisAsnProLeuValAsnValArgVa	В
1785	CCAGTGTGCCTTTCTCCACCGACTGCGAGGA	Qy
845		ф
1733	TCCCCCTCAAGCCTCCCAGC	Qy
825	   :::   IleSerGluCysAsnSe	DB DB
1691	CTACTCCTCAT	Qy
812	805 oSerAlaSerLeuThrLeuLeu	Д
1634	GEACGTGAG	Qγ
0	gLysLeuPheLysLysGluGluProMetLeuLeuLeuGlyAsp	<b>В</b> .
1574	GAACCCCGGCAGCCAGCCACACGGCCAACCCAAAGGTGCCTGAGGGGGGA	0γ
785	 erArgProArg	DЬ
1520	AGGGACATGTTTCCCGTGCGGCCCTTGGAC	Qy
765	H	Db
1487	AGCCCCC	Qγ
745	lAlaLe	В
1475	GCCCGGTACTTCTGCGGG	Qγ
725	722ArgArg	р
1454	-6	Qy
721	704 AlaThrSerThrProGlnLeuThrProThrAsnSerLeuLysArgGlyGlyAla	Дb
1394	AGCTCTGAGGGCAGAGGG	οy
703	pGlyAspGlyProSerSerAspGlyIleF	탕
1346	TCTGCAGGCGGCTGGAGCCCTACATGGCCCCCCTCCA	οy
683	.668GlnHisSerProSerGlnSerTyrLeuCysIleProPheProArgGly	₽
1301	1254 CTGGTACAGCAATGGGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCT	Qy
667	653GluAspGluAspSerGlyGlySerGlyGluSerArgLeu	Db
1253	ARGCCATGGAGGTGGTCAACAGC	Qy
652	641 ProAlaLeuProGlyPheThrSerLeuMetGluMet	р
1193	ACCTGTGCTCACACACAC	Qγ

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-DB-PIR_73 -OFMT-fastan -SUFFIX-mip.rufr -MINATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START-1 -RND--1 -MATRIX-blosum62 -TRANS-human40:cdi -LIST-45
-DCCALIGN-200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-OUTPMT-pto -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09836392_eCGN_11_38_erunat_0804200_090328_22799 -NCPU-6 -ICPU-3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-NARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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## ALIGNMENTS

A; Dolecule type: DNA A; Molecule type: DNA A; Residues: 1-1090 <2HU> A; Cross-references: EMBL: AF098504; PIDN: AAC67413.1; GSPDB: GN00019; CESP: T27C10.5 RESULT 1 T33475 δÃ 밁 δÃ R; Zhu, H.J.; Graves, T.; Hawkins, M. submitted to the EMBL Data Library, October 1998 A; Description: The sequence of C. elegans cosmid T27C10. A; Reference number: Z21354 A; Accession: T33475 US-09-836-392-8\_COPY\_22\_2205 (1-2184) x T33475 (1-1090) Best Local Similarity: Query Match: Pred. No.: A;Map position: 1 A;Introns: 182/3; 260/2; 319/2; 796/3; 826/3; 979/3; 1038/2 Score: Percent Similarity: A;Status: hypothetical protein T27ClO.5 - Caenorhabditis elegans ۱; Gene : Species: Caenorhabditis elegans;
Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999 Accession: T33475 CESP: T27C10.5 preliminary; translated from GB/EMBL/DDBJ CCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCCGCTCTGCTTCGCCCTTGGAGCTC 147 9.15e-13 403.50 41.26% 24.36% 9.94% Conservative: Mismatches: Indels: Length: Matches: Gaps:

477 ProAsnValIleGlyLeuValGlyValCysThrPheProLeuSerLeuValValGluLeu 496

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TA 20 :: eu 51	48 GCGCCGCTCAGCAGCCTCAACACCGTGCTGTCCGAGAACGCCAGAGAT:          :::     :::   97 AlaProLeuGlyAlaLeuAsnGlnLeuLeuGlySerH18ArgLy8Alac	р <i>9</i>

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	Cys 951	<pre>? GlySerGluThrIleHisThrIleAspMetGluMetAlaSerGlnAsnTyrValThrCys</pre>	932	рь
•	AAC 1551	GTGCGGCCCTTGGACACGGAACCCCCGGCAGCCAGCC	1504	Ωy
	Pro 931	ArgGlnValThrGlySerLeuAspIleArgLysValMetPro	918	Дb
	CCC 1503	TACCAGCIGIGIGCCCGGTACTICIGCGGGGTCCCCAGC	1444	Qy
•	Lys 917	GlnLysValTrpIleAlaLeuGluLysSerSerLysValGlnMetValGluValGluLys	898	밁
	CACC 1443	GAGGTCGTCTGGTGCCTGGATGACAAGGCCAACTCCTTGGTGATGTACCACTCCAC	1384	8
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	GGGAG 1383	GCCCCTCCATGGTTACGTCAGTCGTGCAGCTCTGAGGGCAGAGGG	. 1333	δ
	Tyr 880	ArgIleSerIleHisHisIleAlaSerAsnAspSerPheSerPheSerSerSerLeuTyr	. 861	망
	ATG 1332	CTCCTTGTCATC GACTGTGCCTCCCTGGA	1276	δõ
-	 	ThrAlaThrPheLeuGlyAsnGlySerThrArgGlnIleTrpAlaGlyHisSerG	841	타
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	AAG 1221	AACAGGTCCAAGTTCAGCATCGCGGATGAAGACGCACGGCAGAA	1162	Qy

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                                                                                                                                                                                                                                     EMBL:AL049914; GSPDB:GN00062; ATSP:F6E21.
se: cultivar Columbia; BAC clone F6E21
   2.14e-08
315.00
54.55%
35.50%
7.76%
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              Length:
Matches:
Conservative:
Mismatches:
Indels:
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1999
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                                                                                                                                                                                                                                                                                                                                                         B.G.;
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            A;Map position: 2
C;Superfamily: kinase-related
                                                                                                                                                    Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant rearence number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                 probable protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: (02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
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                                                                                 A; Cross-references:
                                                                                                 A; Molecule type: DNA
A; Residues: 1-407 <STO>
                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                   M.; Koo, H.; Moffat,
                                                                                                                                                                                                                     euss, D.; Nierman,
                                                                                                                                                                                                                                                   R; Lin, X.; Kaul,
                                                   Gene:
                                                                 Genetics
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                                                   At2g24360
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                                                                                                                                                                                                                  S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuj
fat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; '
n, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.;
                                                                                 GB:AE002093;
              transforming
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                                                                                 NID: g4337195;
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                                                                             PIDN:AAD18109
              protein
                 kinase
                                                                                                                                                                                    Arabidopsis thaliana
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E.; Umayam, L.; Tal
                                                                                 GSPDB: GN00139
                 homology
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jii, C.Y Tallon, Venter

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C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_charge
C;Accession: S68178; 138044; S32468
R;Dorow, D.S.: Devereux, L.: Tu, G.F.; Price, G.; Nicholl, J.K.;
Bul. J. Bicchem. 234, 492-500, 1995
A;Title: Complete nucleotide sequence, expression, and chromosom
A;Reference number: S68178; MUID: 96128179; PMID: 8536694
A;Accession: S68178
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A;Cross-references: EMBL:X90846; NID:g971419; R;Katoh, M.; Hirai, M.; Sugimura, T.; Terada,
                                      A; Molecule type: mRNA
A; Residues: 1-954 <DOR>
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                          PID:g971420
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A; Residues: 1-461, 'A'
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F;104-112/Region: protein kinase ATP-binding motif F;384-405/Region: leucine zipper motif F;419-440/Region: leucine zipper motif F;449-463/Region: basic F;125,145,222,224/Active site: Lys, Glu, Asp, Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncogene 10, 1447-1451, 1995
A;Title: Cloning and characterization of MST,
A;Reference number: I38044; MUID:95249256; PMJ
A;Accession: I38044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: mixed-lineage protein kinase 2; protein kinase homology; SH3 hom C;Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific F;23-76/Domain: SH3 homology <SH3> F;96-364/Domain: protein kinase homology <KIN>
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A;Map position: 19q13.1-19q13.2
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A;Cross-references: EMBL:248615; NID:g758593; PIDN:CAA88331.1; PID:g758593
R;Dorow, D.S.; Devereux, L.; Dietzsch, E.; de Kretser, T.
Eur J. Biochem 213, 701-710, 1993
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A; Residues: 244-464, 'AQAAGRRQPHQPALWL' <DO2>
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GAGTTGCTGTCAGGACAGCGCCCTGCACTGGGCCACCAGCTCCAGATTGCC-----
                                             IleArgLeuSerLeuPheSerLysSerSerAspValTrpSerPheGlyValLeuLeuTrp
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_	AGGTCCAAGTTCAGCATCGCGATGAAG	1160	O <sub>V</sub>
557	SerArgGlyGlyProProLysLysGluGluLeuValGlyGlyLysLysLysGlyArg	539	D
1159	TGGTGCGGGGCACCCCAAAGGACAGCTGCTCCTACCTGTGCTCACACACAG	1104	Qy
538	SerGlySerSerSerGlyGlySerGlyThrTrp	528	Дb
1103	TCGCCGATGGGCTT	1044	νQ
527	LeuThrProValAspCysGlyGlySerSer	518	망
1043	IGT	984	Qy
517.	:::	510	Дb
983	CTTAA	936	Qy
509	LysGlySerAspGlyAlaSerProProAlaSerProSerIle	496	рь
935	CCCTGGGATGAAGGTGAGCTGCCAGCTCCAGGTCCAGAGATCCCTGTGGACAGCCACCGA	876	Qy
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415	LeuArgAlaAlaGlnGluGln	396	дд
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818		789	γo
375	ArgLeuGluVallleGluGlnSerAlaLeuPheGlnMetProLeuGluSerPheHisSer	356	망
788	C-ATCCCAGGGCCAGGAGTACACCGT	730	δô
355	ProAspPheGlySerIleLeuLys	348	Дb
729	TGCCACCTTCATGTAT	670	QΥ
347	<b>4</b> –	332	Дb
669	TAAGCCAGAGAAGCGA	610	γo
331	ValalaMetAsnLysLeuThrLeuProIleProSerThrCysProGluPro	315	밁
609	CGCCCGGTTCTGGGGCAGCCGGAGGAAGTG	559	Qy
314	GluLeuLeuThrGlyGluValProTyrArgGluIleAspAlaLeuAlaValAlaTyrGly	295	망

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7305 tein kinase hom	A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1091 <man> A;Residues: 1-1091 <man> A;Cross-references: EMBL:L13738; NID:g307304; PIDN:AAA53570.1; PID:g307C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; prot</man></man>	02222
ty of p21(cdc4	ex, E.; Leung, T.; Sallhuddin, H.; Tan, L.; Lim, L. 363, 364-367, 1993 shon-receptor tyrosine kinase that inhibits the GTPase activisence number: S33596; MUID:93268389; PMID:8497321 sion: S33596	D D D Z R
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1510	1452 -GTGTGCCCGGTACTTCTGCGGGGTCCCCAGCCCCTCAGGGACATGTTTCCCGTGCGGC	р 29
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GCCCGGTTCTGGGGCAGCCGGAGGAAGTGCAGTTCCGGCGACTGCAGGAGGCGCTCATGATG 639 	Qy 580 CGCCCGGTTCTGGGGCAGCCG           ::    Db 405 ArgLeuproArgPro
ACCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATC 579 :::           :::         euasnGlySerGlnIleLeuHisLysIleAspLysGluGlyGlu 404	Qy 523 CGCCTGCACTGGGCCACCACCACCACCCCCCCCCCCCCC
AGAAGGTAGATATGTTCTCCTATGGAATGGTGCTCTACGAGTTGCTGTCAGGACAG 522 	Qy 466 GAGAAGGTAGATATGTTCTCC     :: Db 365 HisalaserAspThrTrpMet
GAGGGCACTCCTGGCTACCAGĠCCCCAGAGATCAGGCCTCGCATTGTATATGAT 46 	Qy 409 GTGGAGGGCACTCCTGGC
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AAGTCGGACAACATTCTGGTGTGGTCGCTTGACGTCAAGGAGCACATCAACATCAAGCTA 36 ::    :::   ::: AlaAlaArgAsnLeuLeuAlaThrArgAspLeuValLysIle 32	Qy 301 AAGTCGGACAACATTCTGGTG:::    :::   ::: Db 310 AlaAlaArgAsnLeuLeuLeu
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	ignment Scores:  6.89e-0  ad. No.: 304.00  ore: 35.60%  st Local Similarity: 24.13%  st Local Similarity: 7.49% :
ase; tyrosine-specific protein kinase; homology <kin> ATP-binding motif</kin>	C;Keywords: ATP; phosphotransfer F;180-448/Domain: protein kinase F;188-196/Region: protein kinase

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ATCGCGG       oProArg	GACACGG	-CCCGGT       aProGly	AAGGCCAACTCCTTG     ::: SerAlaGlnThrAla	LeuGluAs	CCCCTCCA []]	spAspPh	GTAÇAGCAATGGGC     ValvalAspTrpAs	pProAl	ProTyrGlyProAl	AGGTCCA	lyAlaGluValThr	GCTTGTGGC            	nAspProl		gProProG	  uTyrLeuc	/AspSerAs <sub> </sub> CCAGCTGTC	PACATCTACAC	lyLeuSerAl	CAGGTCCAGAG	FIGCAGAG	,
, G	AACCCCCGG	ACTTCTG	റ റ	pAsnLeu	CTCCATGGTTACGTCAGTCGTGCAGCTCTGAGGGCAG 	CGACTGTGC :::    pPheGluIleCys	)CGGG	  aserGlup	AlaAlaLeuP	TIC	valThrLe	CTGTGTTTC      LeuAlaLys	euSe		lnHis	:::    rLeuGlyAsnPro	SPPTO	ACCCTC	aGlnAs	ATC	gThrLeuCysValGly	3
	GGCAGCCA          	GGGGTC	TGATGTACCACTCCACCA :::::: lullePheGlnAlaLeuG	uPheLeuPr	GTCAGTCO ::: ThrasnTy	TGCCTCC     :::  CysSerIleA	roLeuF	0 (	ProG	AGCATCGCGGATGAAGACGC	uIleAs	ProSe	AspPh	;	LeuGlyGly	) OMetAsp	-ArgHis	AAGGGCA	pIleSer	CCTGTGGA	CysvalG	,
AGTG	AGCCACAI	CCCAGCC	CACTCCACC ::: GlnAlaLeu	Q₽ ;	TGTGCA	CTCCCTGGI ::: :lleAsnSei	oProp	:::  aGlyThrAlaArg	roGlyAlaAlaGlyHis CATGGAGGTGGTCAACA	atgaag <i>i</i>	Phe	ngcgg AlaAr	pPheLysArgLe		lyvaltysty	  spProProAs	CysTrp- TGGCCGT	TGTGCCC	SerGlnProL		     yProPhe	) 
GAGC	CGGCCAA	CCTCAGO         	- Q	GGAGGAG         nGlyGlyG	CTCTGAC	CTGGAGATCTGCA     snSerThrLeuVa	CTCCTTGTCAT       ::: roProAlaTyr	ir e	a AG	CGCACGG	luGlu	gGCACCCCA         gValProGl	euGlyLe		CCTACCTG       :: ysProThrTy	spLeuLeuS	G1	CTTAAAC	bLeuGlnAsı	CGAGG	ProArg	 
3GGCACGC	AGCCAGCCACACGCCAACCCAAAGGTG     	GGACATGT 	ACCTACCAGCTGTGT :::   :: lnGlnGlu-CysMe	AGGGGAGGAGGTCGTCTG :::        ::: roginglyglyglyLys	AGGGCAG III oGluGlnAl	DAGGCGGCT     /alGlyAla	AT ;; yrAspAs	roLeu	G Y≱-	ACGGCAGAACC	CCTACCTGTG     Proval	AAAGGACA lyThrLys	yLeuArgLys		CTGGTCTT.  ::: TTYTASPP	 uSerValG	-ArgHisCysTrpGlyPheProAs TGCTTCTTGGCCGTGCCTGTTATTAAAAAG	ACACCCC	nSerPhe		AsnValVal	
AG 16	9TG 155	150 790	NGT 145	G 139 - 751	137 aA 733	G 132  -   713	128 pv 693	sp 673	-L 653 AG 1251	CC 1209	GC 1149 634	AGC 1134     SA1 616		1081	TA 1071 Pr 576	S	As 536 AG 1053	99	II 519	937	49	<b>1</b> 0
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US-09-836-392-8_COPY_22_2205 (1-2184) x JC5399 (1-888)	7.23% Indels: 2 Gaps:	2.29e-07 293.50 ty: 33.38% arity: 23.25%	F:472-500/Region: leucine zipper motif F:557-888/Region: glycine-serine-proline rich #status predicted Alignment Scores:	156-404/Domain: kinase catalyti 156-404/Domain: protein kinase 164-172/Region: protein kinase 421-449/Region: leucine zipper	Tyr-specific pro	Molecule type: mRNA Residues: 1-888 <amat> Comment: This enzyme is involved i Genetics:</amat>	Title: Identification of a du Reference number: JC5399; MUI Accession: JC5399 Status: nucleic acid sequence	C;Date: 07-Jul-1997 #sequence_revision 18-Jul-1997 #text_change 28-May-1999 C;Accession: JC5399 R;Matsul, N.; Sarkar, G.; Shuto, T.; Marrs, J.; Bronk, J.T.; Mizuno, K.; Bolander, M.E. Biochem. Biophys. Res. Commun. 229, 571-576, 1996	RESULT 7 JC5399 dual leucine zipper kinase (EC 2.7) - rat C:species: Rattus norvegicus (Norway rat)	OY 2071 AACACAGAGTGGTGCCTGGGCCGTCTGGAGGGGCTGGGGCGC 2111 ::: :::::	Qy 2026 GCCGTGGTGGCAAAGGACACTGTTGTGTGCACCTTTGAAAATGAA 2070	QY 1966 CGAGTCATTGCCGTCTTAAAAGCCCGAGAGCTGACTGCGCATGGGGTGCTGGTGGATGCT 2025 ::   ::	QY 1906 AGGCGCGGTGGAGATGTTATCGTCATTGGCCTGGAGAAGGATTCTGAAGCCCCAGCGGGGC 1965  B78 spproLysTyr	QY 1846 TTCAGCCAGCAGCAGCCGTGAAGATECTCGCCGTCAGAGAGCCTCATTTGGGTCCCC 1905	Qy 1786 ACGCCCGGTGCCTCCGACAGGTCTGAGCATGACCTGACC	QY 1726 CCAGCAAGTTCTTCCAGTGTGCCTTTCTCCACCGACTGCGAGGACTCAGACATGCTACAT:1785	QY 1670ACTCCTCATCCCCACCCCGCCAGGCTGCCAGGTCCCCTCAAGCCTCCCCAGCTCC 1725	QY 1621 ATCCTGATCCACCAGGAATCACTGACTGACTGCTCCATGTCCTCCT 1669
95	Qy 844 AAGGGCCTCATG :::    ::: Db 488 ArgGluLeuArgArg	Oy 814 TCCAGGAAC     Db 468 ArgAlaAsnAs	Qy 796Db 448 ArgArgGlyGl	Oy 778Db 428 GluLysIleLy		Qy 685 GTGGTGAGCCAGA :::     Db 399 IleAlaSerAla-	Qy 643 TGCTGGGACAC	Qy 583 CCGGTTCTGGG        Db 363 ProValProSe	Qy 529GCACT	Qy 496 GTGCTCTACGA       :::   Db 332 ValLeuTrpGl	Qy 436 CCAGAGATCAG	Qy 379 AGGCAGTC ::::::       Db 292 LysGluLeuSe	Qy 319 GTGTGGTCCCT ::: Db 277 IleThrTyrAs	Qy 259 CTGGCCTACCT :::    :: Db 257 MetAsnTyrIl	Oy 199 TCCTTTATACC	Qy 139 CTGGAGCTCGC :::    Db 223 MetGluPheCy	Qy 85 CACCCCTGCAT	Qy 28 GCCATGAAGAA    :::    Db 183 AlaValLysLy
w	AAGGGCCTCATGGAGGTGCAGAGGATGTGCTGCCCTGGGATGAAGGTGAGC 894 :::    :::    :: ArgGluLeuLeuArgArgAlaGlnAlaLeuGluArgArgCysProGlyLeuLeuLysSer 507	TCCAGGAACACAGGGTGGTGAACACAGAG 843	TGGGATGGAAAAGAGGAG 813 TrgArgGlyGluPheArgHisAlaLeuAspIleArgGluHisTyrGluArgLysLeuGlu 467			TIGGTGAGCCAGATGAAGGACCCGACTTTTGCCACCTTCATGTATGAACTGTGCTGTGGG 744 ::::	TGCTGGGACACTAAGCCAGAGAAGCGACCG	CCGGTTCTGGGGCAGCAGGAGGAAGTGCAGTTCCGGCGACTGCAGGCGCTCATGATGGAG 642	GCACTGGGCCACCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGC 582 :::   ::    ::    ::    ::       ::	STGCTCTACGAGTTGCTGTCAGGACAGCGCCCT	CCAGAGATCAGGCCTCGCATTGTATATGATGAGAAGGTAGATATGTTCTCCTATGGAATG 495        ::: ProGluValIleArgasnGluProValSerGluLysValAspIleTrpSerPheGlyVal 331	AGGCAGTCATTCCATGAGGGCGCCCTAGGCGTGGAGGGCACTCCTGGCTACCAGGCC 435 	STGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTATCTGACTACGGGATTTCG 378 :::	CTGGCCTACCTGCACAAGAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATTCTG 318 :::    :::	ICCTTTATACCCCTGGGACACATGCTCACCCAAAAATAGCCTACCAGATCGCCTCGGGC 258	CTGGAGCTCGCGCCCCCACCAGCCTCAACACCCTGCTGCTGCCGAGAACGCCAGAGATTCT 198	DACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCACCCGCTCTGCTTCGCC 138                ::           ::               ::               ::                     ::               ::	3CCATGAAGAACTTCTCCGAGTTCCGGCAGGAGGCCAGCATGCTGCACGCGCTGCAG 84    :::

	C 1911	S CAGCACCTGCAGGCCGTGAAGATCCTCGCCGTCAGAGACCTCATTTGGGTCCCCAGGCGC	Qy 1852
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	iC 1851	GGTGCTGCCTCCGACAGGTCTGAGCATGACCTGACCCCCA	Oy 1792
	- 770	9 ValAspSerGluValGluLeu-ProProSerGlnArg	Db 759
	C 1791		Оу 1732
	A 1731 u 758	<pre>12 TCCTCATCCCCACCCCGCCAGGCTGCCAAGGTCCCCCAAGCTCCCCAGCA ::::::      </pre>	Qy 1672 Db 739
		GGCACGCAGATCC	<u>.</u> د
	G 1611 S 724	2 CCAAAGGTGCCTGAGGGGGACTCCATCGCGGACGTGAGCATCATGTACAGTGAGGAGCTG 	Qy 1552 Db 709
	.C 1551 - 708.	)2 GACATGTTTCCCGTGCGGCCCTTGGACACGGAACCCCCGGCAGCCAGC	Qy 1492 Db 701
	- 700		Db 682
	G 1491	a	Qy 1456
	1 682		Db 662
	T 1455	<b>ω</b>	Qy . 1402
	1 662	2	Qy 1352 Db 642
		aCyspropr	
	- 1351	7CCTCCATGGTTACGT	Оу 1337
	1 622		Db 602
	- 1336	GAGATCTGCAGGCGGCTGGAGCCCTACA	Оу 1303
	G 1302 1 602	5 TGGTACAGCAATGGGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCTG :::      :: ::       2 sAlaSerAlaLysGlySerCysGlyAspLeuProValLeuArgAlaAlaLeuProProH1	Qy 1255 Db 582
·			Db 575
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	- 560	:::       4 aLeuSerGlyValGlyLeu	Db 554
	C 1134		Ωy 1075
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	3 1074	GTCGTCACCTGCTTCTTGGCCGTGCCT	Oy 1015
	T 1014 h 544	5 TACACCCTCAAGGGCATGTGCCCCCTTAAACACCCCCAACAGGCCTTGGATACTCCAGCT :     :::	Qу 955 рь 527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serine/threonine protein kinase (EC 2.7.1.-) DLK - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 24-Sep-1999
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A;Accession: A55318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-888 <HOL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Status: preliminary
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                                                                                             LysGluLeuSerAspLysSerThrLysMetSerPheAlaGlyThrValAlaTrpMetAla
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1353	GTTACGTCA	1345	δδ
626	  LeuGlySerProGlyGlyLeuGl	6	В
1344	ACATGGCCC	1315	Qγ
606	:::	586	용
1314	GTACAGCAATGGGCCGGGCCTCCTTGTC	1255	Q.
586	:::    -ArgGlyLysThrArgHisArgLysAlaSerAlaLy	575	뭥
1254	AGGTGGTCAACA	1195	Ş
574	ProGlyCysProLysGlyProProSerProGlyArgSerArg	561	8
1194	TCACACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATGAAG	1135	δ
560	aLeuSerGlyValGlyLeu	554	В
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1074	GTCACCTGCTTCTTGGCCG	1015	Ş
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1014	ACACCCTCAAGGGCATGTGCCCCCTTAAACACACCCCAACAGGCCTTGGATACTCCAG	955	Ϋ́
527	-HisProSerArgGlyLeuLeuHisGlyAsnThrMetGluLysLeuIleLysLysArgAs	508	₽
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804	ACCGTGGTGTTTTGGGATGGA	784	δ
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783	CTTCTCATCCCAGGGCCAG	<b>4</b>	γ
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684	TGCTGGGACACTAAGCCAGAGAAGCGACCG	643	₹ 5
378	GlyPheLysIleLeuLeuArgGln	363	문
642	GTGCAGTTCCGGCGAÇTGCAGGCGCTCATGATGG	583	δ
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582	GCACTGGGCCACCACCAGCTCCAGATTGCCAAGAAGCTGTCCAAGGGCATCCGC	529	Ϋ́
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528	GTGCTCTACGAGTTGCTGTCAGGACAGCGCCCT	496	υy

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                                                                                               A;Molecule type: mRNA
A;Residues: 1-1123 <OPP>
A;Cross-references: GB:JU2995; NID:g191566; PIDN:AAA88241.1; PID:g309084
A;Experimental source: clone A16
R;Ben-Neriah, Y; Bernards, A.; Paskind, M.; Daley, G.Q.; Baltimore, D.
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                                                                                                                                                                                                                                                                                                                                                                   kinase-related transforming protein (abl) (EC 2.7.1.-) type I - mouse N;Alternate names: protein-tyrosine kinase abl C;Species: Mus musculus (house mouse) C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 18-Jun-1999 C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991 #text_change 18-Jun-1999 C;Accession: A39962; A24773, S00771; A00626
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                                                                                                                                                                                                                                                                         A;Title: Nucleotide sequence of testis-derived c-abl cDNAs: implications for testis-s
A;Reference number: A39962; MUID:88068561; PMID:3317402
                                                   A; Title: Alternative
                                                                                                                                                                                                                           A;Status:
                                                                                                                                                                                                                                             A; Accession: A39962
                                                                                                                                                                                                                                                                                                                          R;Oppi, C.; Shore, S.K.; Reddy, Proc. Natl. Acad. Sci. U.S.A. 8
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cernative 5' exons in c-abl mRNA.
number: A90877; MUID:86133550; PMID:3512096
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Qy 1219 AAGGCCATGGAGGTGGTCAACAGCGGCTCTGAGGTCTGGTACAGCAATGGCCGGCC	474 420 531 440 591	415 405 475 421 532
	375 . 384 414 404	316 CTGGTGTGGTCCCTTGACGTCAAGGAGCACATCAACATCAAGCTATC           11    370 LeuValGlyGluAsnHisLeuValLysValAl 376 TCGAGG
GATACTCCAGCTGTCGTCACCTGCTTGTGGCCGTGCCTGTTATAAAAAGAATTCCTAC :::    :::         59proLysAlaSerAsnGlyAlaGlyValProAsnGlyAlaPheArgGluProGlyAs 63 CTGGTCTTAGCGGGGCCTCGCCCGATGGGCTTGTGCTGTGTTTCCCGTGGTGCGGGCACC    :::	334 255 349 315 369	Db 315 ThrigiupheMetThrTyrGlyAsnLeuLeuAspTyrLeuArgGluCysAsnArgGlnGlu Qy 196 TCTTCCTTTATACCCCTGGGACACATGCTCCACCAAAAAATAGCCTACCAGATCGCCTCG
617 gserSerSerPheArgGluMetAspGlyGlnProAspArgArgGly 632  883 ATGAAGGTGAGCTGCAGGTCCAGGTCCAGAGATCCCTGTGGACAGCCACCGAGGACCAG 942     ::      ::		276 85 295
67		Alignment Scores:  Pred. No.:  280.00  Score:  Percent Similarity:  34.69%  Best Local Similarity:  22.96%  Duery Match:  6.90%  DB:  US-09-836-392-8_COPY_22_2205 (1-2184) x A39962 (1-1123)  Ov 25 GATGCCATGAAGAACTTCTCCGGAGTTCCGGGAGGGGGAGGAGGGCAGCAGCAGGCGCTGCAGG
7 6 7 2	SH2 homology; hoprotein; phc	nase abl; protein ki utophosphorylation; yy <kin> iding motif</kin>
478 TrpAsnProSerAspArgProSerPheAlaGluIleHISGInAlaPheGluThrMetPhe 49/ 687	1; PID:949838 Db Baltimore, D. Qy oterization. Db	A;Cross-references: EMBL;X07539; NID:949837; PIDN:CAA30411.1; PID:9498 R;Wang, J.Y.J.; Ledley, F.; Goff, S.; Lee, R.; Groner, Y.; Baltimore, Cell 36, 349-356, 1984 A;Title: The mouse c-abl locus: molecular cloning and characterization A;Reference number: A00626; MUID:84106840; PMID:6319018 A;Accession: A00626 A;Molecule type: DNA A;Residues: 85-127,'C',129-182 <wan> C;Genetics:</wan>
41 ProGlyIleAspLeuSerGlnValTyrGluLeuLeuGluLysAspTyrArgMet 92 GGGCAGCCGGAGGAAGTGCAGTTCCGGCGACTGCAGGGCGCTCATGATGGAGTGCTGGGAC :::      59 GluArgProGluGlyCysProGluLysValTyrGluLeuMetArgAlaCysTrpGln 52 ACTAAGCCAGAGAAGCGACCGGTGGCCCTGTCGGTG	promoters and alt	D. y usage of two tran 0; PMID:3283651

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mixed lineage protein kinase 1 - human C; Species: Homo sapiens (man) C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_cha C; Accession: S22467; JU0229 R; Dorow, D.S.; Devereux, L.; Dietzsch, E.; de Kretser, T. Eur. J. Blochem. 213, 701-710, 1993 A; Title: Identification of a new family of human epithelial A; Reference number: S32467; MUID:93238756; PMID:8477742 A; Accession: S32467 A; Molecule type: mRNA A; Residues: 1-394 <DO2> C; Genetics:
A;Gene: GDB:MLK1
A;Gross-references: GDB:141921; OMIM:600136
A;Gross-references: GDB:141921; OMIM:600136
A;Map position: 14924.3-14931
G;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol C;Keywords: ATP; leucine zipper; phosphotransferase; serine/threonine-specific protein
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F;9-17/Region: protein kinase ATP-binding F;289-310/Region: leucine zipper motif F;324-345/Region: leucine zipper motif
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F;1-268/Domain: catalytic <CAT>
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LeuThrThrIleGluGluSerGlyPhePheGluMetProLysAspSerPheHisCysLeu
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                                      CTGTGCTGTGGGAAGCAGACAGCCTTCTTCTC-ATCCCAGGGCCAGGAGTACACCGTGGT
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probable protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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Best Local Similarity:
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A; Residues: 1-546 <STO>
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Accession: D84555
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Gene: At2g17700
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278.50
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F;361-621/Domain: protein kinase homology <K
F;369:377/Region: protein kinase APP-binding
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                                                                                                                                                                                                                                                                            CACCCCTGCATCGTGGCGCTCATCGGCATCAGCATCCAC-----CCGCTCTGCTTCGCC
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                                                      GGCCTGGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATT
                                                                                                                             TCTTCCTTT ATACCCCTGGGACACATGCTCACCCAAAAAATAGCCTACCAGATCGCCTCG
                                                                                                                                                                 ThrGluPheMetThrTyrGlyAsnLeuLeuAspTyrLeuArgGluCysAsnAigGlnGlu
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gag-abl polyprotein - Abelson murine leukemia virus %;Contains: amino end of core shell protein p30; core protein p15; inner coi C;Species: Abelson murine leukemia virus %;Note: host Mus sp. (mouse) C;Date: 14-Nov-1983 #sequence_revision 09-Sep-1994 #text_change 11-Jun-1999 C;Accession: A03931; A06627; A93955 K;Reddy, E.P.; Smith, M.J.; Srinivasan, A. proc. Natl. Acad. Sci. U.S.A. 80, 3623-3627, 1983 A;Title: Nucleotide sequence of Abelson murine leukemia virus genome: Struct A;Reference number: A93955; MUID:83221648; PMID:6304726 A;Accession: A03931
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PID:g331888
as Glu
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135	715 lGlyLeuSerLysAlaSerSerGluGluMetArgValArgArgHisLysHisSerSerGl 7	В
1371	GGCCCCCTCCATGGTTACGTCAGTCGTGTGCAGCTCTGAG	γo
115	695 ySerAlaSerGlyMetGlyThrProAlaThrAlaGluProAlaProProSerAsnLysVa 7	ğ
1311	GGTACAGCAATGGGCCGGGCCTCCTTGTCATCGACTGTGCCTCCCTGGAGATCTGC	QY
595	690 sGluhlaThrLysGl 6	뫄
1251	GAAGGCCATGGAGGTGGTCAACAGCGGCTCTGAG	Qy
069	679 rAlaSerProSerSerGlyLeuSerH1sLysLy 6	밁
1191	ACACAGCCAACAGGTCCAAGTTCAGCATCGCGGATGAA	Qy
579	677Ginvaith 6	망
1131		δõ
576	662 nLysAlaSerProProSerLeuThrProLysLeuLeuArgArg 6	밁
1071		δ
62	653 rArgThrCysArgAlaAlaGluG1 6	밁
1011		Ωy
553	642SerMetLeuGlnAlaproGluLeuProThrLysTh 6	밁
951	GGACAGCCACGAGGACCAGAAAATCTAC	οy
541	627 ValGluLysGluLeuGlyLysArgGlyThr-ArgGlyGlyAlaGly 6	밁
391	AGAGGATGTGCTGCCCTGGGATGAAGGTG 8	Q
626	611 H1sGlnAlaPheGluThrMetPheGlnGluSerSerIleSerAspGlu 6	밁
831	ATGGAAAAGAGGAGTCCAGGAACTACACGGTG	Qy
610	606SerPheAlaGluIle 6	밁
771	GTGGGAAGCAGACAGCCTTCTTCTCATCCCAG	ý V
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1	15 CCCACALCARCARCARCACCACCACCACCACCACCACCACCACCACC	Ş
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505	91 LeuValGlyGluAsnHisLeuValLysValAlaAspPheGlyLeu 5	망
375	16 CTGGTGTGGTCCCTTGACGTCAAGGACAACAATCAAGCTATCAAGCTACGGGATT 3	γQ

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106 ATCGGCATCAGCATCCACCCG-----CTCTGCTTCGCCCTGGAGCTCGCGCCGCTCAGC 159

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Query Match:
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A; Introns: 69/2; 107/3;
A; Note: F8D20.290
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                                                                    US-09-836-392-8_COPY_22_2205 (1-2184) x T04683 (1-553)
                                                                                                                                                                                                     Pred. No.:
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A;Residues: 1-553 <BEV>
A;Cross-references: EMBL:AL031135
A;Experimental source: cultivar CC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F8D20.290 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C;Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-May-1999 C;Accession: T04683
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Accession: T04683
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                                  46 GAGTTCCGGCAGGAGGCCAGCATGCTGCACGCGCTGCAGCACCCCTGCATCGTGGCGCTC 105
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                                                                                                              3.17e-06
270.50
48.36%
30.33%
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A;Accession. A;Accession type: DNA A;Nolecule type: DNA A;Residues: 1-1171 <CHO>
A;Residues: 1-1171 <CHO>
A;Cross-references: EMBL:AL096859; GSPDB:GN00061; ATSP:T6H20.
A;Cross-references: Cultivar Columbia; BAC clone T6H20
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Best Local Similarity:
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                       Query Match:
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'Species: Arabidopsis thaliana (mouse-ear cress)
'Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change
'Accession: T12956
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C;Date: 03-Aug-1994 #sequence_revision 17-Nov-1995 #text_change 04-Feb-2000
C;Accession: S08519; A25582; A00625; E38268
R;Fainstein, E.; Einat, M.; Gokkel, E.; Marcelle, C.; Croce, C.M.; Gale, R.:
Oncogene 4, 1477-1481, 1989
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                         R;Shtivelman, E.; Lifshitz, Cell 47, 277-284, 1986
                                                                                                                 A;Title: Nucleotide sequence analysis of human abl and bcr-abl cDNAs A;Reference number: S08519; MUID:90082420; PMID:2687768 A;Accession: S08519
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                                           B.;
                                         Gale, R.P.; Roe, B.A.;
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   the human abl
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F;248-256/Region: protein kinase AFP-binding motif
F;248-750/Binding site: carbohydrate (Asn) (covalent) #status
F;271/Active site: Lys #status predicted
F;393/Binding site: phosphate (Tyr) (covalent) (by autophospho
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A;Title: Putative tyrosine kinases expressed in K-562 human A;Reference number: A38268; MUID:91062349; PMID:2247464
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F;127-217/Domain: SH2 homology <SH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 360-423, 'GK', 426 <GRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Homology between phosphotyrosine acceptor site of human c-abl A;Reference number: A00625; MUID:83245023; PMID:6191223 A;Accession: A00625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-139,'P',141-158,'S',160-444,'R',446-458,'K',460-718,'V',720-836,'W',838-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-836-392-8_COPY_22_2205 (1-2184) x TVHUA (1-1130)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A25582; A; Accession: A25582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Status: nucleic acid sequence not shown; not compared with ;Molecule type: mRNA ;Residues: 365-420 <PAR>
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                                                                                                                                     AlaMetGluTyrLeuGluLysLysAsnPheIleHlsArgAspLeuAlaAlaArgAsnCys
                                                                                                                                                                         GGCCTGGCCTACCTGCACAAGAAAAACATCATCTTCTGTGACCTGAAGTCGGACAACATT
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                                                           -GluAsnHisLeu---ValLysValAlaAspPheGlyLeu
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ySerSerSerLysArgPheLeuArgSerCysSerAlaSerCysValProH1sGlyAlaLy
                                                                                                                   GAGGTGGTCAACAGCGGCTCTGAGGTCTGGTACAGCAATGGGC----
                                                                                                                                                       yAlaLeuArg---GluSerGlyGlySerGlyPheArgSerPro---
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